

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:28:13 ; Search time 97.25 Seconds
(without alignments)
67.608 Million cell updates/sec

Title: US-10-612-162A-1

Sequence: 1 VVARSMGKEDLIWELL 17

Scoring table: BLOSUM62

Gapor 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%

Listing first 45 summaries

```
Database :
1: Geneseqp1.6Dec04:*
2: Geneseqp1.980s:*
3: Geneseqp1.990s:*
4: Geneseqp2.000s:*
5: Geneseqp2.001s:*
6: Geneseqp2.002s:*
7: Geneseqp2.003s:*
8: Geneseqp2.004s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query			ID		Description
No.	Score	Match	Length	DB	ID	
1	86	100.0	17	8	ADG66075	Adg66075 Human CD7
2	86	100.0	200	8	ADP030379	Adp030379 Human see
3	86	100.0	220	8	ADH89432	Adh89432 Human tcr
4	86	100.0	371	8	ADL70790	Adl70790 Transferr
5	86	100.0	539	4	AAU02980	AAU02980 Angioten
6	86	100.0	575	6	ABR82321	ABr82321 Human met
7	86	100.0	643	8	ABM83778	ABm83778 Human dle
8	86	100.0	645	8	ABM83783	ABm83783 Human dle
9	86	100.0	646	4	AAU02938	AAu02938 Angioten
10	86	100.0	665	4	AAU02937	AAu02937 Angioten
11	86	100.0	679	6	ABP72820	ABp72820 Human tcr
12	86	100.0	679	8	ADH89360	Adh89360 Human tcr
13	86	100.0	679	8	ADKL5869	Adkl5869 Mature hu
14	86	100.0	679	8	ADL70732	Adl70732 Human tcr
15	86	100.0	679	8	ADL24413	Adl24413 Human tcr
16	86	100.0	696	1	APF03084	APf03084 Sequence
17	86	100.0	698	2	AAK12499	AAk12499 Human tcr
18	86	100.0	698	2	AAK66492	AAk66492 Human tcr
19	86	100.0	698	2	AAW54354	AAw54354 Human tcr
20	86	100.0	698	3	AAYS0717	AAy50717 Human ser
21	86	100.0	698	8	ABP72819	ABp72819 Human tcr
22	86	100.0	698	7	ADDA4282	ADd44282 Human tcr
23	86	100.0	698	7	ADF74796	ADf74796 Human NO
24	86	100.0	698	7	ADF74800	ADf74800 Human NO
25	86	100.0	698	8	ADH34559	Adh34559 Human tcr

ALIGNMENTS

26	86	100.0	698	8	ADH89359	Adh89359	Human	chr8
27	86	100.0	698	8	ADH15868	Adh15868	Human	chr8
28	86	100.0	698	8	ADL70721	Adl70721	Human	chr8
29	86	100.0	698	8	ADL24412	Adl24412	Human	chr8
30	86	100.0	698	8	ADP21259	Adp21259	Human	chr8
31	86	100.0	1074	2	AAW07621	Aaw07621	LDLR/TF	C
32	86	100.0	1410	2	AAW07622	Aaw07622	LDLR/TF	C
33	86	100.0	1410	6	ABU04139	Abu04139	Human	exp
34	86	100.0	1418	4	AAU2831	Aau2831	Novel	hum
35	86	100.0	1418	6	ABU04138	Abu04138	Human	exp
36	76	88.4	685	8	ADL70768	Adl70768	Bovine	chr8
37	76	88.4	685	8	ADL24462	Adl24462	Bovine	chr8
38	76	88.4	704	8	ADP21260	Adp21260	Bovine	chr8
39	75	87.2	676	8	ADL70764	Adl70764	Bovine	chr8
40	75	87.2	676	8	ADL24458	Adl24458	Rabbit	chr8
41	71	82.6	689	3	AAV49270	Aav49270	Lactoferr	
42	71	82.6	708	2	AAAR1037	Aaar1037	Dyactolin	
43	71	82.6	708	2	AAW09343	Aaw09343	Bovine	la
44	71	82.6	708	2	AAW57318	Aaw57318	Bovine	la
45	71	82.6	708	2	AAW86022	Aaw86022	Bovine	la

RESULT 1

ADG46075	standard; peptide; 17 AA.
ADG46075	
ADG46075:	
25-MAR-2004	(first entry)
Human CDR peptide fragment #1.	
antibody: carbohydrate-deficient transferrin: CDT;	
non-glycosylated transferrin; alcoholism; alcoholic; diagnosis; human.	
Homo sapiens.	
EP1378521-A1.	
07-JUN-2004.	
19-MAY-2003; 2003EP-00011334.	
05-JUL-2002; 2002DE-01030550.	
(DADE-) DADE BEHRING MAREBURG GMBH.	
Althaus H;	
WPI: 2004-073743/08.	
New antibody specific for carbohydrate-deficient transferrin, useful for	
diagnosis of alcoholism, can bind its target in solution, eliminating	
need for immobilization.	
Claim 4; SEQ ID NO 1; 21pp; German.	
This invention describes a novel antibody that, in aqueous solution,	
binds selectively to carbohydrate-deficient transferrin (CDT) without	
having to bind CDT to a solid phase. The invention also describes an	
antibody that binds selectively to CDT at regions containing the	
sequences VVARSWGKEDIDWELL, TTEDSIATKMGADAMSLDGF, SKTWSGLNLSPPN and	
YKYLDEEVKAV (ADG46075-ADG46078) and an immunoassay for detecting CDT	
using the antibodies of the invention. The antibodies of the invention	
are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The	
antibodies are obtained by immunisation with non-glycosylated	
transferrin, or a fragment, then generation of hybridomas by standard	
fusion of spleen and myeloma cells. Hybridomas are then selected for	
production of antibodies that specifically bind CDT from the aqueous	
phase. The antibodies are useful for diagnosis of alcoholism, CDT, which	

CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
CC alcohols. The antibodies allow direct detection of CDR in solution,
CC eliminating the need for immobilizing it on a solid phase (as required
CC when using known antibodies). ADG46075-ADG46094 represent CDR peptide
CC fragments used in the method of the invention.

CC Sequence 17 AA:

Query Match 100.0%; Score 86; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSWGKEDLIWELL 17
1 VVARSWGKEDLIWELL 17

ADP30379 standard; protein, 200 AA.

ADP30379;

12-AUG-2004 (first entry)

Human secreted protein SEQ ID #1146.

Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
cancer; inflammatory; immune; human secreted protein.

Homo sapiens.

WO2004035732-A2.

29-APR-2004.

28-AUG-2003; 2003WO-US026780.

29-AUG-2002; 2002US-0406576P.

29-AUG-2002; 2002US-0406579P.

29-AUG-2002; 2002US-0406585P.

29-AUG-2002; 2002US-0406588P.

29-AUG-2002; 2002US-0406608P.

29-AUG-2002; 2002US-0406611P.

29-AUG-2002; 2002US-0406612P.

29-AUG-2002; 2002US-0406640P.

29-AUG-2002; 2002US-0406642P.

29-AUG-2002; 2002US-0406646P.

29-AUG-2002; 2002US-0406653P.

29-AUG-2002; 2002US-0406655P.

29-AUG-2002; 2002US-0406666P.

17-SEP-2002; 2002US-0410946P.

17-SEP-2002; 2002US-0410947P.

17-SEP-2002; 2002US-0410948P.

17-SEP-2002; 2002US-0410949P.

17-SEP-2002; 2002US-0410953P.

17-SEP-2002; 2002US-0410957P.

17-SEP-2002; 2002US-0410958P.

17-SEP-2002; 2002US-0410959P.

17-SEP-2002; 2002US-0410960P.

17-SEP-2002; 2002US-0410961P.

17-SEP-2002; 2002US-0411019P.

17-SEP-2002; 2002US-0411022P.

17-SEP-2002; 2002US-0411023P.

17-SEP-2002; 2002US-0411024P.

17-SEP-2002; 2002US-0411032P.

17-SEP-2002; 2002US-0411035P.

17-SEP-2002; 2002US-0411037P.

17-SEP-2002; 2002US-0411041P.

17-SEP-2002; 2002US-0411045P.

17-SEP-2002; 2002US-0411046P.

17-SEP-2002; 2002US-0411048P.

17-SEP-2002; 2002US-0411052P.

17-SEP-2002; 2002US-0411055P.

17-SEP-2002; 2002US-0411073P.

17-SEP-2002; 2002US-0411082P.

17-SEP-2002; 2002US-0411082P.

17-SEP-2002; 2002US-0411101P.

17-SEP-2002; 2002US-0411111P.

18-APR-2003; 2003US-0463700P.

18-APR-2003; 2003US-0463708P.

18-APR-2003; 2003US-0463715P.

18-APR-2003; 2003US-0463732P.

02-MAY-2003; 2003US-0467199P.

02-MAY-2003; 2003US-0467201P.

02-MAY-2003; 2003US-0467203P.

02-MAY-2003; 2003US-0467230P.

19-MAY-2003; 2003US-0471306P.

19-MAY-2003; 2003US-0471336P.

22-MAY-2003; 2003US-0472420P.

22-MAY-2003; 2003US-0472430P.

09-JUN-2003; 2003US-0476609P.

09-JUN-2003; 2003US-0476641P.

08-JUL-2003; 2003US-0485218P.

08-JUL-2003; 2003US-0485223P.

08-JUL-2003; 2003US-0485224P.

08-JUL-2003; 2003US-0485325P.

14-JUL-2003; 2003US-0486446P.

14-JUL-2003; 2003US-0486480P.

15-JUL-2003; 2003US-0486891P.

15-JUL-2003; 2003US-0486969P.

08-AUG-2003; 2003US-0493341P.

08-AUG-2003; 2003US-0493370P.

08-AUG-2003; 2003US-0493373P.

08-AUG-2003; 2003US-0493577P.

(FIVE-) FIVE PRIME THERAPEUTICS INC.

Williams LT, Chu K, Lee B, Hestir K, Beaurang PA, Behrens D,

Halenebeck RF, Huang MM, Kothakota S, Halshan L, Himmelman T,

Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;

WPI, 2004-348436/32.

New nucleic acid molecule for diagnosing, preventing or treating diseases
such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
genetic, bacterial and viral diseases.

Claim 1; SEQ ID NO 2377; 428bp; English.

The present invention relates to an isolated nucleic acid molecule
encoding a polypeptide which is believed to be cyostatic,
antiinflammatory, immunosuppressive, antibacterial and virucidal. The
composition and methods are useful for diagnosing, preventing and
treating diseases such as proliferative (e.g. cancer), inflammatory,
immune, metabolic, genetic, bacterial and viral diseases. The present
sequence represents a human secreted protein. The present sequence is
available on WIPOMEB and is not in the specification.

Sequence 200 AA:

Query Match 100.0%; Score 86; DB 8; Length 200;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSWGKEDLIWELL 17
1 VVARSWGKEDLIWELL 17

DB 124 VVARSWGKEDLIWELL 140

RESULT 3

ADH89432 standard; protein, 220 AA.

ADH89432

ADH89432;

XX 15-APR-2004 (first entry)
XX Human transferrin fusion protein-related mTF PREX0080 protein SegID76.
XX fusion protein; transferrin protein; glycosylation;
XX antibody variable region; cytosolic; antibacterial; virucide;
XX anti-parasitic; immunosuppressive; anti-arthritic; gene therapy;
XX septic shock; endotoxic shock; cachexia syndrome; bacterial infection;
XX viral infection; parasitic infection; neoplasm; autoimmune disease;
XX arthritis; graft rejection; PREX0080; mTF.
XX Unidentified.
XX US2003226155-A1.
XX 04-DEC-2003.
XX 10-MAR-2003, 2003US-00384060.
XX 30-AUG-2001; 2001US-0315745P.
XX 30-NOV-2001; 2001US-0334059P.
XX 30-AUG-2002; 2002US-00231494.
XX 30-AUG-2002; 2002US-0406977P.
XX (BIORE-) BIOREXIS PHARM CORP.
XX Sadeghi H, Prior CP, Turner A;
XX MPI; 2004-022093/02.
XX N-PSDB; ADL70789.
XX New fusion protein comprising a transferrin protein exhibiting reduced
XX glycosylation fused to at least one antibody variable region, useful for
XX preparing a composition for treating e.g., septic shock, neoplasm or
XX autoimmune disease.
XX Example 2; SEQ ID NO 76; 82pp; English.
XX This invention relates to a novel fusion protein which comprises a
XX transferrin protein exhibiting reduced glycosylation fused to at least
XX one antibody variable region. The invention may be useful for the
XX development of compounds with cytostatic, antibacterial, virucide,
XX anti-parasitic, immunosuppressive or anti-arthritic activity. In addition,
XX the sequences disclosed may be useful for gene therapy. The fusion
XX protein is useful for preparing a composition for treating a disease or
XX disease symptom in a patient for example septic shock, endotoxic shock,
XX cachexia syndrome associated with bacterial, viral or parasitic
XX infections, neoplasm, autoimmune disease, arthritis or adverse effects
XX associated with treatment for preventing graft rejection. The present
XX sequence is that of a protein which was used in the exemplification of
XX the invention.
XX Sequence 220 AA;
XX
XX Query Match 100.0%; Score 86; DB 8; Length 220;
XX Best Local Similarity 100.0%; Pred. No. 4; 7e-06;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 VVARSWGKEDLIWELL 17
XX 183 VVARSWGKEDLIWELL 199
XX
XX RESULT 4
XX ADL70790
XX ID ADL70790 standard; protein; 371 AA.
XX
XX AC ADL70790;
XX
XX 03-JUN-2004 (first entry)
XX DT Transferrin N-domain protein, SEQ ID 63.
XX DE

XX Immunosuppressive; Haemostatic; Anti-allergic; Antiasthmatic;
XX Dermatological; Anti-inflammatory; Antibacterial; Vasotropic;
XX Nephrotoxic; Neuroprotective; Cytostatic; Cerebroprotective; Vulnerary;
XX Antiparkinsonian; Nootropic; Cardiant; Antianaemic; Antithrombotic;
XX Thrombolytic; Anticoagulant; Gastrointestinal; Respiratory; transferrin;
XX Tf; transferrin fusion protein; Tf fusion protein.
XX Synthetic.
XX WO2004020588-A2.
XX 11-MAR-2004.
XX 28-AUG-2003; 2003WO-US026779.
XX 30-AUG-2002; 2002US-0406977P.
XX 10-MAR-2003; 2003US-00384060.
XX 09-JUL-2003; 2003US-0485404P.
XX (BIORE-) BIOREXIS PHARM CORP.
XX Prior CP, Turner AJ, Sadeghi H;
XX MPI; 2004-239175/22.
XX N-PSDB; ADL70789.
XX Novel library containing several fusion proteins each of which comprises
XX first transferrin polypeptide fused to at least one second peptide,
XX PT useful for screening for transferrin fusion protein having the particular
XX activity.
XX Example 13; SEQ ID NO 63; 243pp; English.
XX The present invention relates to a library (1) of modified fusion
XX proteins of transferrin (Tf) and therapeutic proteins with increased
XX serum half-life or serum stability. Preferred fusion proteins include
XX those modified so that the Tf moiety exhibits no or reduced
XX glycosylation, iron binding and/or Tf receptor binding. The transferrin
XX fusion proteins are useful for treating, preventing or ameliorating
XX disorders or diseases of endocrine system, nervous system, immune system,
XX respiratory system, cardiovascular system, diseases and/or disorders
XX relating to cell proliferation, and/or diseases or disorders relating to
XX blood. The modified fusion proteins are useful in diagnosis, prognosis,
XX prevention and/or treatment of autoimmune disorders; diseases and
XX disorders of haematopoietic cells (e.g., leukopenia, neutropenia, anaemia
XX and thrombocytopenia); allergic reactions such as allergic asthma,
XX anaphylaxis, IgE-mediated allergic reactions such as asthma, rhinitis and
XX eczema; inflammatory conditions e.g., inflammation associated with
XX infection (e.g., septic shock, sepsis), ischaemia-reperfusion injury,
XX nephritis, Crohn's disease, multiple sclerosis, respiratory disorders
XX (asthma and allergy), gastrointestinal disorders (inflammatory bowel
XX disease), cancers (e.g., gastric, ovarian, lung, bladder), CNS disorders
XX (multiple sclerosis, stroke, traumatic brain injury, neurodegenerative
XX disorders such as Parkinson's disease, Alzheimer's disease), etc. The
XX fusion protein is also useful as an adjuvant to enhance anti-bacterial or
XX anti-fungal immune responses, anti-parasitic immune responses, etc. The
XX fusion protein is also useful for treating monoclonal gammopathy of
XX undetermined significance (MGUS), Waldenstrom's disease, plasmacytomas,
XX adult respiratory distress syndrome, for stimulating wound repair, for
XX preventing or treating infections of joints, bones, skin, etc. The fusion
XX protein is also useful for treating or preventing thrombosis, myocardial
XX infarction, cancers, thrombocytopenia, sickle cell anaemia,
XX glomerulonephritis, cardiac arrest, edema, pulmonary embolism,
XX atherosclerosis, etc. In an example from the invention, a system of Tf
XX peptide display for generating peptide sequences uses the N-domain of Tf
XX incorporated into the pIII protein and the insertion of random peptides
XX within the Tf scaffold. The present sequence was used to illustrate this
XX example.
XX Sequence 371 AA;
XX
XX Query Match 100.0%; Score 86; DB 8; Length 371;
XX

Best Local Similarity 100.0%; Pred. No. 8.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSNGKEDLIWELL 17
Db 274 VVARSNGKEDLIWELL 290

RESULT 5
AAU02980

ID AAU02980 standard; protein; 539 AA.

XX AAU02980;

DT 12-SEP-2001 (first entry)

DE Angiotensin converting enzyme (ACEV) splice variant protein #80.

XX Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW platelet-derived endothelial cell growth factor; cardiovascular disease;
KW cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW myocardial infarction; coronary arterial thrombosis; renal disease;
KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW nonarctoidic pulmonary granulomatous disease; endothelial abnormality;
KW vascular disorder; atherosclerosis.

XX Homo sapiens.

PN WO200136632-A2.

XX 25-MAY-2001.

PD 17-NOV-2000; 2000WO-IL000766.

XX 17-NOV-1999; 99IL-00132978.

PR 10-DEC-1999; 99IL-00133455.

XX (COMP-) COMPUEN LTD.

XX Levine Z, David A, Azar I, Khosravi R, Bernstein J;

PI MPI; 2001-336004/35.

DR N-PSDB; AAS06080.

PT Novel alternative splicing variants e.g. variant of angiotensin
XX converting enzyme (ACEV), useful in identifying candidate compounds
XX capable of binding to the variant and to detect anti-variant antibodies.

XX Claim 4; Fig 80; 519pp; English.

XX The sequence represents an angiotensin converting enzyme splice variant
XX (ACEV) polypeptide. The polypeptides of the invention include variants of
XX granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
XX platelet-derived endothelial cell growth factor, cyclin-dependent kinase
XX inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal
XX polypeptide receptor 2. The polypeptides and their associated nucleic
XX acids are useful for identification of variant sequences and detection of
XX candidate compounds capable of binding the molecules. The sequences of
XX the invention can be used in the treatment and diagnosis of various
XX disorders including cardiovascular diseases such as arteriosclerosis,
XX myocardial infarction and coronary arterial thrombosis, renal diseases
XX such as diabetic nephropathy, muscular diseases such as hypertrophy,
XX immune disorders such as immune complex nephritis, multiple sclerosis,
XX cancer, sarcoidosis, nonarctoidic pulmonary granulomatous diseases such
XX as atherosclerosis and vascular pathologies involving an endothelial
XX abnormality such as deep vein thrombosis

XX Sequence 539 AA;

Query Match 100.0%; Score 86; DB 4; Length 539;

Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSNGKEDLIWELL 17
Db 143 VVARSNGKEDLIWELL 159

RESULT 6
ABR82321

ID ABR82321 standard; protein; 575 AA.

XX ABR82321;

DT 06-NOV-2003 (first entry)

DE Human metalloprotein (MEPR) polypeptide (Id-7509328CD1).

XX MEPR; metalloprotein; anti-HIV; antiallergic; antiinflammatory; human;
KW antianemic; antiparkinsonian; noctropic; anticonvulsant; cytostatic;
KW antiartherosclerotic; antiasthmatic; immunosuppressive; antithyroid;
KW heptocarcinoma; dermatological; antidiabetic; nephrotoxic; antigen;
KW thymometric; neuroprotective; osteopathic; antiarthritic; uterine;
KW antiparasitic; antihelminthic; antiproliferative; antiproliferative; virucide;
KW antirheumatic; haemostatic; antibacterial; protozoacide; fungicide;
KW gene therapy; transgenic.

XX Homo sapiens.

PN WO2003060089-A2.

XX 24-JUL-2003.

PD 14-JAN-2003; 2003WO-US001485.

XX 14-JAN-2002; 2002US-0348769P.

PR 18-JAN-2002; 2002US-0350701P.

PR 19-MAR-2002; 2002US-0366059P.

PR 10-MAY-2002; 2002US-0379907P.

XX (INCY-) INCYTE GENOMICS INC.

XX Kable AE, Griffin JA, Gorvad AE, Becha SD, Richardson TW;

PI Emerling BM, Chien D, Jin P, Chawla NK, Yue H, Khare R, Margulis JP;

PI Tang YF;

XX MPI; 2003-598523/56.

DR N-PSDB; ACP35812.

PT New human metalloproteins and polynucleotides, useful for diagnosing,
XX treating or preventing autoimmune or inflammatory disorders (e.g. AIDS,
XX allergy or anemia), multiple sclerosis, osteoarthritis, cancer or
XX hepatitis.

XX Claim 1; Page 146-148; 153pp; English.

XX The invention relates to novel human metalloproteins (MEPR) and encoding
XX polynucleotides. The human MEPR polypeptides, polynucleotides and
XX modulators are useful for diagnosing, treating or preventing disorders
XX associated with aberrant expression of MEPR, particularly cell
XX proliferative disorders (e.g. arteriosclerosis, atherosclerosis,
XX cirrhosis, hepatitis, paroxysmal nocturnal hemoglobinuria, polycythemia
XX vera, psoriasis, primary thrombocytopenia or cancer), developmental
XX disorders (e.g. renal tubular acidosis, anemia or mental retardation),
XX neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or
XX epilepsy), autoimmune/inflammatory disorders (e.g. AIDS, allergies,
XX asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease,
XX diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout,
XX Graves' disease, Hashimoto's thyroiditis, irritable bowel syndrome,
XX multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's
XX syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,
XX bacterial, fungal, parasitic, protozoan or helminthic infections. The
XX polynucleotides encoding MEPR are useful for creating transgenic animals

CC to model human disease. Sequences ABR82316-323 represent the human MEPR
CC polypeptides of the invention
XX
SQ Sequence 575 AA;
Query Match 100.0%; Score 86; DB 6; Length 575;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 17, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
QY 1 VVARSWGKEDLIWELL 17
DB 147 VVARSWGKEDLIWELL 163
RESULT 7
ABM83778
ID ABM83778 standard; protein; 643 AA.
AC ABM83778;
XX
XX
DT 18-NOV-2004 (first entry)
XX
XX Human diagnostic and therapeutic pprotein SEQ ID NO:4027.
DE
XX
XX gene therapy; human diagnostic and therapeutic polynucleotide; dittp.
KM
XX
OS Homo sapiens.
XX
XX WO2004023973-A2.
XX
XX 25-MAR-2004.
XX
XX 12-SEP-2003; 2003WO-US028227.
XX
XX 12-SEP-2002; 2002US-0410259P.
XX
XX 12-SEP-2002; 2002US-0410260P.
XX
XX
XX (INCY-) INCYTE CORP.
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
PI Hartschorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kitton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
XX MPI; 2004-329368/30.
XX
XX N-PSDB; ACN42430.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
XX in diagnosing a condition, disease or disorder associated with human
XX molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
XX in gene mapping.
XX
XX Claim 27; Page: 190pp; English.
XX
XX The invention relates to novel diagnostic and therapeutic polynucleotides
XX selected from one of the 2722 sequences defined in the specification. A
XX polynucleotide of the invention may have a use in gene therapy. The human
XX diagnostic and therapeutic polynucleotides (dittp) or polypeptides may be
XX used to diagnose a particular condition, disease or disorder associated
XX with human molecules, e.g. cell proliferative disorders,
XX autoimmune/inflammatory disorder, developmental disorder, endocrine
XX disorder, neurological disorders, gastrointestinal disorders, or
XX infections caused by virus, bacteria, fungi or parasite. The dittp
XX molecules may also be used in genetic mapping, in identifying individuals
XX from minute biological samples, in detecting single nucleotide
XX polymorphisms, as molecular weight markers, and for somatic or germline
XX gene therapy. The present sequence represents a dittp protein of the
XX invention. Note: The sequence data for this patent is not represented in
XX the printed specification, but was obtained in electronic format directly

CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 643 AA;
Query Match 100.0%; Score 86; DB 8; Length 643;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 17, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
QY 1 VVARSWGKEDLIWELL 17
DB 251 VVARSWGKEDLIWELL 267
RESULT 8
ABM83783
ID ABM83783 standard; protein; 645 AA.
AC ABM83783;
XX
XX
DT 18-NOV-2004 (first entry)
XX
XX
XX Human diagnostic and therapeutic pprotein SEQ ID NO:4032.
DE
XX
XX gene therapy; human diagnostic and therapeutic polynucleotide; dittp.
KM
XX
OS Homo sapiens.
XX
XX WO2004023973-A2.
XX
XX 25-MAR-2004.
XX
XX 12-SEP-2003; 2003WO-US028227.
XX
XX 12-SEP-2002; 2002US-0410259P.
XX
XX 12-SEP-2002; 2002US-0410260P.
XX
XX
XX (INCY-) INCYTE CORP.
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
PI Hartschorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kitton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
XX MPI; 2004-329368/30.
XX
XX N-PSDB; ACN42435.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
XX in diagnosing a condition, disease or disorder associated with human
XX molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
XX in gene mapping.
XX
XX Claim 27; Page: 190pp; English.
XX
XX The invention relates to novel diagnostic and therapeutic polynucleotides
XX selected from one of the 2722 sequences defined in the specification. A
XX polynucleotide of the invention may have a use in gene therapy. The human
XX diagnostic and therapeutic polynucleotides (dittp) or polypeptides may be
XX used to diagnose a particular condition, disease or disorder associated
XX with human molecules, e.g. cell proliferative disorders,
XX autoimmune/inflammatory disorder, developmental disorder, endocrine
XX disorder, neurological disorders, gastrointestinal disorders, or
XX infections caused by virus, bacteria, fungi or parasite. The dittp
XX molecules may also be used in genetic mapping, in identifying individuals
XX from minute biological samples, in detecting single nucleotide
XX polymorphisms, as molecular weight markers, and for somatic or germline
XX gene therapy. The present sequence represents a dittp protein of the
XX invention. Note: The sequence data for this patent is not represented in
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at www.wipo.int/pct/en/sequences/listing.htm


```

XX Sequence 665 AA,
SO Query Match 100.0%; Score 86; DB 4; Length 665;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSWGKEDLIWELL 17
DB 270 VVARSWGKEDLIWELL 286

RESULT 11
ABP72820
ID ABP72820 standard; protein; 679 AA.
AC ABP72820;
XX
XX
XX 11-AUG-2003 (first entry)
XX
XX Human transferrin (mature polypeptide).
XX
XX Human; transferrin; neuroprotective; cerebroprotective; vasotropic;
XX antiparkinsonian; nootropic; anti-HIV; antiaesthetic; antiallergic;
XX cytostatic; immunosuppressive; antiatherosclerotic; cardiac;
XX gynaecological; immunostimulant; antinaemic; haemostatic;
XX antiinflammatory; dermatological; antibacterial; virucide; antiparasitic;
XX fungicide; hepatotropic; antirheumatic; antiarthritic; antigout;
XX traquilizer; vulnery; antidiabetic; nephrotropic; antipyretic;
XX gastrointestinal; gene therapy; transgenic animal.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Binding-site 63
XX /note= "Iron binding site"
XX Region 94..96
XX /note= "Hinge region"
XX Binding-site 95
XX /note= "Iron binding site"
XX Binding-site 120
XX /note= "Carbonate ion binding site"
XX Binding-site 124
XX /note= "Carbonate ion binding site"
XX Binding-site 126
XX /note= "Carbonate ion binding site"
XX Binding-site 127
XX /note= "Carbonate ion binding site"
XX Binding-site 188
XX /note= "Iron binding site"
XX Region 245..247
XX /note= "Hinge region"
XX Binding-site 249
XX /note= "Iron binding site"
XX Region 316..318
XX /note= "Hinge region"
XX Binding-site 392
XX /note= "Iron binding site"
XX Modified-site 413
XX /note= "N-glycosylated"
XX Region 425..427
XX /note= "Hinge region"
XX Binding-site 426
XX /note= "Iron binding site"
XX Binding-site 452
XX /note= "Carbonate ion binding site"
XX Binding-site 456
XX /note= "Carbonate ion binding site"
XX Binding-site 458
XX /note= "Carbonate ion binding site"
XX Binding-site 459
XX /note= "Carbonate ion binding site"
XX Binding-site 514

```

```

FT Binding-site 517 /note= "Iron binding site"
FT Region 581..582 /note= "Iron binding site"
FT Binding-site 585 /note= "Hinge region"
FT Modified-site 611 /note= "Iron binding site"
FT Region 652..658 /note= "N-glycosylated"
FT /note= "Hinge region"
XX
XX MO2003020746-A1.
XX
XX 13-MAR-2003.
XX
XX 30-AUG-2002; 2002WC-US027637.
XX
XX 30-AUG-2001; 2001US-0315745P.
XX
XX 30-NOV-2001; 2001US-0334059P.
XX
XX (BIOR-) BIOREXIS PHARM CORP.
XX
XX Prior CP;
XX
XX WPI; 2003-332916/31.
XX
XX New fusion protein, useful in the diagnosis and treatment of diseases or
XX disorders relating to the respiratory, cardiovascular and digestive
XX systems, comprises a transferrin protein fused to a therapeutic protein.
XX
XX Disclosure; Page 280-281, 298pp; English.
XX
XX The present sequence is the protein sequence of human transferrin (Tf),
XX minus the signal peptide. The invention relates to modified Tf fusion
XX proteins comprising at least one therapeutic protein, polypeptide or
XX peptide, in which the Tf portion is engineered to extend the serum half-
XX life or bioavailability of the molecule. The modified Tf fusion protein
XX preferably comprises a human Tf moiety that has been modified to reduce
XX or prevent glycosylation, iron binding and/or transferrin receptor
XX binding, having at least one amino acid substitution, deletion or
XX addition in the hinge region, or at residues Asp-63, Gly-65, Tyr-95, Tyr-
XX 188, Lys-206, His-207, His-249, Asp-392, Tyr-426, Tyr-514, Tyr-517, His-
XX 585, Thr-120, Arg-124, Ala-126, Gly-127, Thr-452, Arg-456, Ala-458 and
XX Gly-459, or a mutation which prevents glycosylation at Asn-413 or Asn-611
XX (all claimed). Nucleic acids encoding such fusion proteins, vectors, host
XX cells and transgenic animals which produce the fusion protein in their
XX serum or milk are also claimed. The modified fusion protein is useful for
XX treating a disease or disease symptom, or for delivering a therapeutic
XX agent complexed to the ferric iron of transferrin to the inside of a cell
XX or across the blood-brain barrier. The modified fusion protein, or a
XX nucleic acid encoding it, can be used in the diagnosis, prognosis,
XX prevention and/or treatment of diseases and/or disorders of the
XX endocrine, nervous, immune, respiratory, cardiovascular, reproductive and
XX digestive systems, diseases and/or disorders relating to the blood or to
XX cell proliferation, inflammatory conditions, and to treat viral, fungal,
XX bacterial or parasitic infection
XX
XX Sequence 679 AA;
SQ Query Match 100.0%; Score 86; DB 6; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSWGKEDLIWELL 17
DB 251 VVARSWGKEDLIWELL 267

RESULT 12
ADH89360
ID ADH89360 standard; protein; 679 AA.
XX

```


PR 30-AUG-2002; 2002US-0406977P.
PR 10-MAR-2003; 2003US-00384060.
PR 09-JUL-2003; 2003US-0485404P.
XX
XX
XX (BIORE-) BIOREXIS PHARM CORP.
PI Prior CP, Turner AJ, Sadeghi H,
XX N-PSDB; ADL70730.
DR WPI, 2004-239175/22.
XX
XX Novel library containing several fusion proteins each of which comprises
PT first transferrin polypeptide fused to at least one second peptide,
PT useful for screening for transferrin fusion protein having the particular
PT activity.
XX
XX Claim 44; SEQ ID NO 3; 243pp; English.
XX
XX The present invention relates to a library (I) of modified fusion
CC proteins of transferrin (Tf) and therapeutic proteins with increased
CC serum half-life or serum stability. Preferred fusion proteins include
CC those modified so that the Tf moiety exhibits no or reduced
CC glycosylation, iron binding and/or Tf receptor binding. The transferrin
CC fusion proteins are useful for treating, preventing or ameliorating
CC disorders or diseases of endocrine system, nervous system, immune system,
CC respiratory system, cardiovascular system, diseases and/or disorders
CC relating to cell proliferation, and/or diseases or disorders relating to
CC blood. The modified fusion proteins are useful in diagnosis, prognosis,
CC prevention and/or treatment of autoimmune disorders; diseases and
CC disorders of hematopoietic cells (e.g., leukopenia, neutropenia, anaemia
CC and thrombocytopenia); allergic reactions such as allergic asthma,
CC anaphylaxis, IgE-mediated allergic reactions such as asthma, rhinitis and
CC eczema; inflammatory conditions e.g., inflammation associated with
CC infection (e.g., septic shock, sepsis), ischaemia-reperfusion injury,
CC hepatitis, Crohn's disease, multiple sclerosis, respiratory disorders
CC (asthma and allergy), gastrointestinal disorders (inflammatory bowel
CC disease), cancers (e.g., gastric, ovarian, lung, bladder), CNS disorders
CC (multiple sclerosis, stroke, traumatic brain injury, neurodegenerative
CC disorders such as Parkinson's disease, Alzheimer's disease), etc. The
CC fusion protein is also useful as an adjuvant to enhance antibacterial or
CC antifungal immune responses, antiparasitic immune responses, etc. The
CC fusion protein is also useful for creating monoclonal gammopathy of
CC undetermined significance (MGUS), Waldenström's disease, plasmacytomas,
CC adult respiratory distress syndrome, for stimulating wound repair, for
CC preventing or treating infections of joints, bones, skin, etc. The fusion
CC protein is also useful for treating or preventing thrombosis, myocardial
CC infarction, cancers, thrombocytopenia, sickle cell anaemia,
CC glomerulonephritis, cardiac arrest, edema, pulmonary embolism,
CC atherosclerosis, etc. The present sequence is human Tf mature protein,
CC used to make the modified Tf fusion proteins of the invention.
XX
SQ Sequence 679 AA;
Query Match 100.0%; Score 86; DB 8; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VVARSWGKEDLIWELL 17
DB 251 VVARSWGKEDLIWELL 267
RESULT 15
ADL24413
ID ADL24413 standard; protein; 679 AA.
XX
XX ADL24413,
AC
XX
XX
DT 03-JUN-2004 (first entry)
XX
XX Human transferrin protein #2.
DE
XX
XX human; transferrin; oral delivery; glycosylation; cancer;

KW cardiovascular disease; gastrointestinal disease;
KW neurodegenerative disease; inflammatory disease; autoimmune disease;
KW diabetes; respiratory disease; multiple sclerosis; metabolic disease.
XX
XX Homo sapiens.
OS
XX
XX MO2004019872-A2.
PN
XX 11-MAR-2004.
PD
XX 28-AUG-2003; 2003WO-US026778.
PF
XX
XX 30-AUG-2002; 2002US-0406977P.
PR 04-MAR-2003; 2003US-00378094.
PR 08-APR-2003; 2003US-0460829P.
XX
XX (BIORE-) BIOREXIS PHARM CORP.
PA
XX
XX PI Prior CP, Sadeghi H, Turner A;
XX WPI, 2004-239108/22.
DR
XX
XX Pharmaceutical composition useful for treating diabetes, obesity,
PT multiple sclerosis, comprising transferrin protein exhibiting reduced
PT glycosylation and fused to therapeutic protein or peptide.
XX
XX disclosure; Page 325-327; 356pp; English.
PS
XX
XX The present invention relates to a pharmaceutical composition formulated
CC for oral, nasal or pulmonary delivery, comprising a transferrin (Tf)
CC protein exhibiting reduced glycosylation and fused to a therapeutic
CC protein or peptide. The composition is effective to treat a human
CC disease, preferably chronic human disease. The chronic disease is chosen
CC from viral disease, cancer, metabolic disease, obesity, autoimmune
CC disease, inflammatory disease, allergy, graft-vs.-host disease, systemic
CC microbial infection, anaemia, cardiovascular disease, neurodegenerative
CC disease, disorder of haematopoietic cells, diseases of the endocrine
CC system or reproductive systems, gastrointestinal disease, respiratory
CC disease, diabetes and multiple sclerosis. The present sequence is a
CC polypeptide shown in the exemplification of the invention.
XX
SQ Sequence 679 AA;
Query Match 100.0%; Score 86; DB 8; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VVARSWGKEDLIWELL 17
DB 251 VVARSWGKEDLIWELL 267
Search completed: November 1, 2005, 12:48:51
Job time : 100.25 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:37:09 ; Search time 25 Seconds
(without alignments)
50.761 Million cell updates/sec

Title: US-10-612-162A-1

Sequence: 1 VVARSNGKEDLIWELL 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/backfill1a1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	696	6 5262177-4	Patent No. 5262177
2	86	100.0	696	6 5262177-4	Sequence 2, Appl
3	86	100.0	698	2 US-08-175-158A-2	Sequence 2, Appl
4	86	100.0	698	4 US-09-439-740-2	Sequence 2, Appl
5	86	100.0	1074	2 US-08-470-058-2	Sequence 2, Appl
6	86	100.0	1074	3 US-09-037-188-2	Sequence 2, Appl
7	86	100.0	1074	2 US-09-285-310-2	Sequence 2, Appl
8	86	100.0	1410	3 US-08-470-058-4	Sequence 4, Appl
9	86	100.0	1410	3 US-09-037-188-4	Sequence 4, Appl
10	86	100.0	1410	3 US-09-285-310-4	Sequence 4, Appl
11	71	82.6	708	1 US-08-145-681-4	Sequence 4, Appl
12	71	82.6	708	1 US-08-453-703-4	Sequence 4, Appl
13	71	82.6	708	2 US-08-456-106-4	Sequence 4, Appl
14	71	82.6	708	3 US-08-456-108-4	Sequence 4, Appl
15	71	82.6	708	3 US-09-265-577-4	Sequence 4, Appl
16	71	82.6	708	4 US-09-633-739-4	Sequence 4, Appl
17	67	77.9	697	3 US-09-724-864-54	Sequence 4, Appl
18	66	76.7	694	3 US-08-154-019-2	Sequence 2, Appl
19	66	76.7	694	4 US-09-421-632-2	Sequence 2, Appl
20	66	76.7	705	4 US-08-655-640-2	Sequence 2, Appl
21	66	76.7	705	2 US-08-655-640-2	Sequence 2, Appl
22	66	76.7	709	1 US-08-154-019-2	Sequence 2, Appl
23	66	76.7	709	1 US-08-461-333-2	Sequence 2, Appl
24	66	76.7	709	3 US-08-464-167-2	Sequence 2, Appl
25	66	76.7	709	3 US-09-158-313-2	Sequence 2, Appl
26	66	76.7	709	3 US-08-476-798-2	Sequence 2, Appl
27	66	76.7	709	3 US-08-476-798-2	Sequence 2, Appl

28	66	76.7	711	1 US-08-145-681-2	Sequence 2, Appl
29	66	76.7	711	1 US-08-250-308-2	Sequence 2, Appl
30	66	76.7	711	1 US-08-154-019-4	Sequence 4, Appl
31	66	76.7	711	1 US-08-461-333-4	Sequence 4, Appl
32	66	76.7	711	1 US-08-453-703-2	Sequence 2, Appl
33	66	76.7	711	2 US-08-456-106-2	Sequence 2, Appl
34	66	76.7	711	3 US-08-464-167-4	Sequence 4, Appl
35	66	76.7	711	3 US-09-158-313-4	Sequence 4, Appl
36	66	76.7	711	3 US-08-456-108-2	Sequence 2, Appl
37	66	76.7	711	3 US-08-476-798-4	Sequence 4, Appl
38	66	76.7	711	3 US-09-265-577-2	Sequence 2, Appl
39	66	76.7	711	4 US-09-633-739-2	Sequence 2, Appl
40	66	76.7	711	5 PCT-US93-03614-2	Sequence 2, Appl
41	65	75.6	703	1 US-08-145-681-6	Sequence 6, Appl
42	65	75.6	703	1 US-08-453-703-6	Sequence 6, Appl
43	65	75.6	703	2 US-08-456-106-6	Sequence 6, Appl
44	65	75.6	703	3 US-08-456-108-6	Sequence 6, Appl
45	65	75.6	703	3 US-09-265-577-6	Sequence 6, Appl

ALIGNMENTS

```
RESULT 1
5262177-4
; Patent No. 5262177
; APPLICANT: BROWN, J. JOSEPH P.; ESTLIN, CHARLES D.; PLOWMAN, GREGORY
; D.; HELSTROM, KARL E.; ROSE, TIMOTHY M.; HELSTROM, INGEGERD;
; PURCHIO, ANTHONY F.; HU, SHU-LOK; PENNATHUR, SRIDHAR
; TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HHUMAN
; MELANOMA-ASSOCIATED ANTIGEN
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/7230
; FILING DATE: 27-JAN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 827,313
; FILING DATE: 07-FEB-1986
; SEQ ID NO:4
; LENGTH: 696
5262177-4

Query Match      100.0%; Score 86; DB 6; Length 696;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVARSNGKEDLIWELL 17
Db      270 VVARSNGKEDLIWELL 286

RESULT 2
5262177-4
; Patent No. 5262177
; APPLICANT: BROWN, J. JOSEPH P.; ESTLIN, CHARLES D.; PLOWMAN, GREGORY
; D.; HELSTROM, KARL E.; ROSE, TIMOTHY M.; HELSTROM, INGEGERD;
; PURCHIO, ANTHONY F.; HU, SHU-LOK; PENNATHUR, SRIDHAR
; TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HHUMAN
; MELANOMA-ASSOCIATED ANTIGEN
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/7230
; FILING DATE: 27-JAN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 827,313
; FILING DATE: 07-FEB-1986
; SEQ ID NO:4
; LENGTH: 696
5262177-4

Query Match      100.0%; Score 86; DB 6; Length 696;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


QY 1 VVARSNGKEDLIWELL 17
| | | | | | | | | | | | | | | | | | | | | |
DB 270 VVARSNGKEDLIWELL 286

RESULT 3
US-08-175-158A-2
; Sequence 2, Application US/08175158A
; Patent No. 5986067
; GENERAL INFORMATION:
; APPLICANT: FUNK, Walter D.
; APPLICANT: MACGILLIVRAY, Ross T.A.
; APPLICANT: MASON, Anne B.
; APPLICANT: WOODMORTH, Robert C.
; TITLE OF INVENTION: RECOMBINANT TRANSFERRINS, TRANSFERRIN HALF-
; TITLE OF INVENTION: MOLECULES AND MUTANTS THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/175,158A
; FILING DATE: 28-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/832,029
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Decont, Giulio A.
; REGISTRATION NUMBER: 31,503
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: UVI-005CP2
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 698 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-175-158A-2

Query Match 100.0%; Score 86; DB 2; Length 698;
Best Local Similarity 100.0%; Pred. NO. 1.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSNGKEDLIWELL 17
| | | | | | | | | | | | | | | | | | | | | |
DB 270 VVARSNGKEDLIWELL 286

RESULT 4
US-09-439-740-2
; Sequence 2, Application US/09439740
; Patent No. 6825037
; GENERAL INFORMATION:
; APPLICANT: FUNK, Walter D.
; APPLICANT: MACGILLIVRAY, Ross T.A.
; APPLICANT: MASON, Anne B.
; APPLICANT: WOODMORTH, Robert C.
; TITLE OF INVENTION: RECOMBINANT TRANSFERRINS, TRANSFERRIN HALF-
; TITLE OF INVENTION: MOLECULES AND MUTANTS THEREOF
; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/439,740
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/175,158
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Decont, Giulio A.
; REGISTRATION NUMBER: 31,503
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 698 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-439-740-2

Query Match 100.0%; Score 86; DB 4; Length 698;
Best Local Similarity 100.0%; Pred. NO. 1.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSNGKEDLIWELL 17
| | | | | | | | | | | | | | | | | | | | | |
DB 270 VVARSNGKEDLIWELL 286

RESULT 5
US-08-470-058-2
; Sequence 2, Application US/08470058
; Patent No. 5817789
; GENERAL INFORMATION:
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Lemont, Jeffrey F.
; TITLE OF INVENTION: Chimeric Proteins For Use in Transport
; TITLE OF INVENTION: of a Selected Substance Into Cells
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamillon, Brook, Smith & Reynolds, P.C.
; STREET: Two Millicia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,058
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: TK193-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-058-2

Query Match 100.0%; Score 86; DB 2; Length 1074;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
|||||
646 VVARSMGKEDLIWELL 662

Db 646 VVARSMGKEDLIWELL 662

RESULT 6
US-09-037-188-2
Sequence 2, Application US/09037188
Patent No. 6027921
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,188
FILING DATE: 02-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-037-188-2

Query Match 100.0%; Score 86; DB 3; Length 1074;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
|||||

Db 646 VVARSMGKEDLIWELL 662

RESULT 7
US-09-285-310-2
Sequence 2, Application US/09285310
Patent No. 6262026
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,310
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/037,188
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-285-310-2

Query Match 100.0%; Score 86; DB 3; Length 1074;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
|||||

Db 646 VVARSMGKEDLIWELL 662

RESULT 8
US-08-470-058-4
Sequence 4, Application US/08470058
Patent No. 5817789
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
TITLE OF INVENTION: Chimeric Proteins For Use in Transport
TITLE OF INVENTION: of a Selected Substance Into Cells
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millita Drive
CITY: Lexington
STATE: MA
COUNTRY: USA

```

;
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,058
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: TKT93-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1410 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
;
US-08-470-058-4

```

```

Query Match      100.0%; Score 86; DB 2; Length 1410;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
Qy      1 VVARSWGKEDLIWELL 17
Db      982 VVARSWGKEDLIWELL 998

```

```

RESULT 9
US-09-037-188-4
; Sequence 4, Application US/09037188
; Patent No. 6027921
; GENERAL INFORMATION:
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Lemont, Jeffrey F.
; APPLICANT: Concino, Michael F.
; TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
; TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/037,188
; FILING DATE: 02-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Ph.D., J.D., Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 07236/009002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1410 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
;
US-09-037-188-4

```

```

Query Match      100.0%; Score 86; DB 3; Length 1410;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
Qy      1 VVARSWGKEDLIWELL 17
Db      982 VVARSWGKEDLIWELL 998

```

```

RESULT 10
US-09-285-310-4
; Sequence 4, Application US/09285310
; Patent No. 6262026
; GENERAL INFORMATION:
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Lemont, Jeffrey F.
; APPLICANT: Concino, Michael F.
; TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
; TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,310
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/037,188
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Ph.D., J.D., Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 07236/009002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1410 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
;
US-09-285-310-4

```

```

Query Match      100.0%; Score 86; DB 3; Length 1410;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
Qy      1 VVARSWGKEDLIWELL 17
Db      982 VVARSWGKEDLIWELL 998

```

```

RESULT 11
US-08-145-681-4
; Sequence 4, Application US/08145681

```

```
/ Patent No. 5571691
/ GENERAL INFORMATION:
/ APPLICANT: Conneely, Orla M.
/ APPLICANT: Heaton, Denis R.
/ APPLICANT: O'Malley, Bert W.
/ APPLICANT: May, Gregory S.
/ TITLE OF INVENTION: Production of Recombinant Lactoferrin
/ TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
/ TITLE OF INVENTION: Various Organisms
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Baker & Botts, L.L.P.
/ STREET: 910 Louisiana St
/ CITY: Houston
/ STATE: Texas
/ COUNTRY: USA
/ ZIP: 77002
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Releasee #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/145,681
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McGregor, Martin L.
/ REGISTRATION NUMBER: 29,329
/ REFERENCE/DOCKET NUMBER: 19928-0125
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 713/229/1874
/ TELEFAX: 713/229/1522
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 708 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: YES
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Bos taurus
/ US-08-145-681-4

Query Match      82.6%; Score 71; DB 1; Length 708;
Best Local Similarity 82.4%; Pred. No. 0.0006;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 VVARSWGKEDLIWELL 17
DB      274 VVARSYDGKEDLIWKLL 290

RESULT 12
US-08-453-703-4
/ Sequence 4, Application US/08453703
/ Patent No. 5766939
/ GENERAL INFORMATION:
/ APPLICANT: Conneely, Orla M.
/ APPLICANT: Heaton, Denis R.
/ APPLICANT: O'Malley, Bert W.
/ APPLICANT: May, Gregory S.
/ TITLE OF INVENTION: Production of Recombinant Lactoferrin
/ TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
```

```
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Releasee #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/453,703
/ FILING DATE: Concurrently herewith
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/145,681
/ FILING DATE: October 28, 1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Albert P. Halluin
/ REGISTRATION NUMBER: 25,227
/ REFERENCE/DOCKET NUMBER: 8206-024
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-854-3660
/ TELEFAX: 415-854-3694
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 708 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: YES
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Bos taurus
/ US-08-453-703-4

Query Match      82.6%; Score 71; DB 1; Length 708;
Best Local Similarity 82.4%; Pred. No. 0.0006;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 VVARSWGKEDLIWELL 17
DB      274 VVARSYDGKEDLIWKLL 290

RESULT 13
US-08-456-106-4
/ Sequence 4, Application US/08456106
/ Patent No. 5849881
/ GENERAL INFORMATION:
/ APPLICANT: Conneely, Orla M.
/ APPLICANT: Heaton, Denis R.
/ APPLICANT: O'Malley, Bert W.
/ APPLICANT: May, Gregory S.
/ TITLE OF INVENTION: Production of Recombinant Lactoferrin
/ TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Releasee #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/456,106
/ FILING DATE: Concurrently herewith
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/145,681
/ FILING DATE: October 28, 1993
```

ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halliuh
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8206-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bos taurus
US-08-456-106-4

Query Match 82.6%; Score 71; DB 2; Length 708;
Best Local Similarity 82.4%; Pred. No. 0.0006;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VVARSWGKEDLIWELL 17
||||:|||||:
Db 274 VVARSVDGKEDLIWKL 290

RESULT 14
US-08-456-108-4
Sequence 4, Application US/08456108
Patent No. 6100054
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Headon, Denis R.
APPLICANT: O'Malley, Bert W.
APPLICANT: May, Gregory S.
TITLE OF INVENTION: Production of Recombinant Lactoferrin
TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
TITLE OF INVENTION: Various Organisms
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,108
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/145,681
FILING DATE: October 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halliuh
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8206-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bos taurus
US-08-456-108-4

Query Match 82.6%; Score 71; DB 3; Length 708;
Best Local Similarity 82.4%; Pred. No. 0.0006;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VVARSWGKEDLIWELL 17
||||:|||||:
Db 274 VVARSVDGKEDLIWKL 290

RESULT 15
US-09-265-577-4
Sequence 4, Application US/09265577
Patent No. 6228614
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Headon, Denis R.
APPLICANT: O'Malley, Bert W.
APPLICANT: May, Gregory S.
TITLE OF INVENTION: PRODUCTION OF RECOMBINANT LACTOFERRIN
TITLE OF INVENTION: AND LACTOFERRIN POLYPEPTIDES USING cDNA SEQUENCES IN VARIOUS
TITLE OF INVENTION: ORGANISMS
FILE REFERENCE: 01380023US01
CURRENT APPLICATION NUMBER: US/09/265,577
CURRENT FILING DATE: 1999-03-09
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 708
TYPE: PRT
ORGANISM: Bos taurus
US-09-265-577-4

Query Match 82.6%; Score 71; DB 3; Length 708;
Best Local Similarity 82.4%; Pred. No. 0.0006;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VVARSWGKEDLIWELL 17
||||:|||||:
Db 274 VVARSVDGKEDLIWKL 290

Search completed: November 1, 2005, 12:57:29
Job time : 26 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:54:52, Search time 86 Seconds

(without alignments)
82,636 Million cell updates/sec

Title: US-10-612-162a-1

Sequence: 86
1 VVARSWGKEDLIWELL 17Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 1865214

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	17	US-10-612-162-1	Sequence 1, Appli
2	86	100.0	220	US-10-384-060-76	Sequence 76, Appli
3	86	100.0	679	US-10-378-094-3	Sequence 3, Appli
4	86	100.0	679	US-10-384-060-3	Sequence 3, Appli
5	86	100.0	679	US-10-231-494-3	Sequence 3, Appli
6	86	100.0	679	US-10-429-488-4	Sequence 4, Appli
7	86	100.0	679	US-10-429-497-4	Sequence 4, Appli
8	86	100.0	679	US-10-429-515-4	Sequence 4, Appli
9	86	100.0	679	US-10-429-598-4	Sequence 4, Appli
10	86	100.0	679	US-10-429-635-4	Sequence 4, Appli
11	86	100.0	679	US-10-429-653-4	Sequence 4, Appli

12	86	100.0	679	US-10-429-659-4	Sequence 4, Appli
13	86	100.0	679	US-10-429-661-4	Sequence 4, Appli
14	86	100.0	679	US-10-429-660-4	Sequence 4, Appli
15	86	100.0	679	US-10-429-662-4	Sequence 4, Appli
16	86	100.0	679	US-10-429-655-4	Sequence 4, Appli
17	86	100.0	679	US-10-429-654-4	Sequence 4, Appli
18	86	100.0	698	US-09-935-642-6	Sequence 6, Appli
19	86	100.0	698	US-10-378-094-2	Sequence 2, Appli
20	86	100.0	698	US-10-384-060-2	Sequence 2, Appli
21	86	100.0	698	US-10-231-494-2	Sequence 2, Appli
22	86	100.0	698	US-10-383-201-10	Sequence 10, Appli
23	86	100.0	698	US-10-383-201-14	Sequence 14, Appli
24	86	100.0	698	US-10-887-711-2	Sequence 2, Appli
25	86	100.0	698	US-10-513-523-3	Sequence 3, Appli
26	86	100.0	1074	US-09-753-385-2	Sequence 2, Appli
27	86	100.0	1410	US-09-753-385-4	Sequence 2, Appli
28	86	100.0	1410	US-10-473-127-805	Sequence 805, App
29	86	100.0	1418	US-10-473-127-804	Sequence 804, App
30	76	88.4	704	US-10-513-523-4	Sequence 8, Appli
31	71	82.6	708	US-10-169-297-8	Sequence 8, Appli
32	71	82.6	708	US-10-620-256-4	Sequence 4, Appli
33	71	82.6	708	US-10-513-523-2	Sequence 2, Appli
34	69	80.2	22	US-10-801-990-183	Sequence 183, App
35	66	76.7	100	US-09-864-408A-5324	Sequence 5324, App
36	66	76.7	333	US-10-408-765A-241	Sequence 241, App
37	66	76.7	359	US-10-169-297-49	Sequence 49, Appli
38	66	76.7	690	US-10-076-816-4	Sequence 4, Appli
39	66	76.7	690	US-10-077-381-4	Sequence 4, Appli
40	66	76.7	690	US-10-639-835-4	Sequence 4, Appli
41	66	76.7	694	US-10-023-056-2	Sequence 2, Appli
42	66	76.7	695	US-10-316-253-273	Sequence 273, App
43	66	76.7	698	US-10-316-253-275	Sequence 275, App
44	66	76.7	698	US-10-205-331-55	Sequence 55, Appli
45	66	76.7	709	US-10-170-221-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-612-162-1
; Sequence 1, Application US/10612162
; Publication No. US2004001415A1
; GENERAL INFORMATION:
; APPLICANT: Dade Behring Marburg GmbH
; TITLE OF INVENTION: Carbohydrate deficient transferrin (CDT)-specific
; FILE REFERENCE: 2002/0001
; CURRENT APPLICATION NUMBER: US/10/612,162
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 10230550.1
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 03011334.4
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-162-1

Query Match 100.0%; Score 86; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVARSWGKEDLIWELL 17
Db 1 VVARSWGKEDLIWELL 17
RESULT 2
US-10-384-060-76

Sequence 76, Application US/10384060
Publication No. US20030226155A1
GENERAL INFORMATION:
APPLICANT: SADEGH, Homayoun
APPLICANT: TURNER, Christopher P.
TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
FILE REFERENCE: 54710-5004-US
CURRENT APPLICATION NUMBER: US/10/384,060
CURRENT FILING DATE: 2003-03-10
PRIOR APPLICATION NUMBER: US 10/231,494
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 60/334,059
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 60/315,745
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US 60/406,977
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.2
SEQ ID NO 76
LENGTH: 220
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: mtf sequence in PREX0080
US-10-384-060-76

Query Match 100.0%; Score 86; DB 15; Length 220;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSNGKEDLIWELL 17
|||||
DB 183 VVARSNGKEDLIWELL 199

RESULT 3
US-10-378-094-3
Sequence 3, Application US/10378094
Publication No. US20030221201A1
GENERAL INFORMATION:
APPLICANT: PRIOR, Christopher P.
APPLICANT: LAI, Char-Huei
APPLICANT: SADEGH, Homayoun
APPLICANT: TURNER, Andrew
TITLE OF INVENTION: MODIFIED TRANSFERRIN FUSION PROTEINS
FILE REFERENCE: 54710-5001-01-US
CURRENT APPLICATION NUMBER: US/10/378,094
CURRENT FILING DATE: 2003-03-04
PRIOR APPLICATION NUMBER: US 10/231,494
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 60/334,059
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 60/315,745
PRIOR FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 679
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
OTHER INFORMATION: Mature Transferrin Protein
US-10-378-094-3

Query Match 100.0%; Score 86; DB 15; Length 679;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSNGKEDLIWELL 17
|||||

DB 251 VVARSNGKEDLIWELL 267

RESULT 4
US-10-384-060-3
Sequence 3, Application US/10384060
Publication No. US20030226155A1
GENERAL INFORMATION:
APPLICANT: SADEGH, Homayoun
APPLICANT: TURNER, Christopher P.
TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
FILE REFERENCE: 54710-5004-US
CURRENT APPLICATION NUMBER: US/10/384,060
CURRENT FILING DATE: 2003-03-10
PRIOR APPLICATION NUMBER: US 10/231,494
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 60/334,059
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 60/315,745
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US 60/406,977
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 679
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
OTHER INFORMATION: Mature Transferrin Protein
US-10-384-060-3

Query Match 100.0%; Score 86; DB 15; Length 679;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSNGKEDLIWELL 17
|||||
DB 251 VVARSNGKEDLIWELL 267

RESULT 5
US-10-231-494-3
Sequence 3, Application US/10231494
Publication No. US20040023334A1
GENERAL INFORMATION:
APPLICANT: Prior, Christopher P.
TITLE OF INVENTION: Modified Transferrin Fusion Proteins
FILE REFERENCE: 54710-5001-US
CURRENT APPLICATION NUMBER: US/10/231,494
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 60/315,745
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US 60/334,059
PRIOR FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 679
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Mature transferrin protein
US-10-231-494-3

Query Match 100.0%; Score 86; DB 15; Length 679;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSNGKEDLIWELL 17
|||||

Db 251 VVARSMGKEDLIWELL 267

RESULT 6
US-10-429-482-4

; Sequence 4, Application US/10429482
; Publication No. US20040219097A1

; GENERAL INFORMATION:

; APPLICANT: Sandhu, Jasbir

; TITLE OF INVENTION: Composition Useful For The Diagnosis, Imaging and Treatment Of Tu

; FILE REFERENCE: 2537.000001

; CURRENT APPLICATION NUMBER: US/10/429,482

; CURRENT FILING DATE: 2003-05-02

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 679

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-429-482-4

Query Match 100.0%; Score 86; DB 16; Length 679;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17

Db 251 VVARSMGKEDLIWELL 267

RESULT 7
US-10-429-497-4

; Sequence 4, Application US/10429497
; Publication No. US20040219098A1

; GENERAL INFORMATION:

; APPLICANT: Sandhu, Jasbir

; TITLE OF INVENTION: Methode For The Treatment of Tumors

; FILE REFERENCE: 2537.000006

; CURRENT APPLICATION NUMBER: US/10/429,497

; CURRENT FILING DATE: 2003-05-02

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 679

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-429-497-4

Query Match 100.0%; Score 86; DB 16; Length 679;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17

Db 251 VVARSMGKEDLIWELL 267

RESULT 8
US-10-429-515-4

; Sequence 4, Application US/10429515
; Publication No. US20040219099A1

; GENERAL INFORMATION:

; APPLICANT: Sandhu, Jasbir

; TITLE OF INVENTION: Methode For The Treatment Of Tumors

; FILE REFERENCE: 2537.000005

; CURRENT APPLICATION NUMBER: US/10/429,515

; CURRENT FILING DATE: 2003-05-02

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 679

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-429-515-4

Query Match 100.0%; Score 86; DB 16; Length 679;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17

Db 251 VVARSMGKEDLIWELL 267

RESULT 9
US-10-429-598-4

; Sequence 4, Application US/10429598
; Publication No. US20040219100A1

; GENERAL INFORMATION:

; APPLICANT: Sandhu, Jasbir

; TITLE OF INVENTION: Composition Useful For The Treatment of Tumors

; FILE REFERENCE: 2537.000003

; CURRENT APPLICATION NUMBER: US/10/429,598

; CURRENT FILING DATE: 2003-05-02

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 679

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-429-598-4

Query Match 100.0%; Score 86; DB 16; Length 679;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17

Db 251 VVARSMGKEDLIWELL 267

RESULT 10
US-10-429-635-4

; Sequence 4, Application US/10429635
; Publication No. US20040219101A1

; GENERAL INFORMATION:

; APPLICANT: Sandhu, Jasbir

; TITLE OF INVENTION: Composition Useful For Treatment Of Tumors

; FILE REFERENCE: 2537.000007

; CURRENT APPLICATION NUMBER: US/10/429,635

; CURRENT FILING DATE: 2003-05-02

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 679

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-429-635-4

Query Match 100.0%; Score 86; DB 16; Length 679;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17

Db 251 VVARSMGKEDLIWELL 267

RESULT 11
US-10-429-653-4

; Sequence 4, Application US/10429653
; Publication No. US20040219102A1

; GENERAL INFORMATION:

; APPLICANT: Sandhu, Jasbir

; TITLE OF INVENTION: Compositions For Drug Delivery

; FILE REFERENCE: 2537.000009

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

Query Match	100.0%;	Score 86;	DB 16;	Length 679;
Best Local Similarity	100.0%;	Pred. No. 9.6e-06;		
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

	QY	1 VVARSMGGKEDLIWELL 17
	Dd	251 VVARSMMGCKEDLIWELL 267

```

RESULT 12
US-10-429-659-4
; Sequence 4, Application US/10429659
; Publication No. US20040219103a1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods Useful For The Diagnosis, Imaging and Treatment Of Tumors
; FILE REFERENCE: 2537.000004
; CURRENT APPLICATION NUMBER: US/10/429,659
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-659-4

```

Query Match	100.0%;	Score 86;	DB 16;	Length 679;
Best Local Similarity	100.0%;	Pred. No. 9.6e-06;		
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

```

QY      1 VVARSMGKEDLIWELL 17
        |||||
Db      251 VVARSMGKEDLIWELL 267

```

```

RESULT 13
US-10-429-661-4
; Sequence 4, Application US/10429661
; Publication No. US20040219104A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For Treatment Of Tumors
; FILE REFERENCE: 2537.000008
; CURRENT APPLICATION NUMBER: US/10/429,661
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-429-661-4

```

Query Match	100.0%;	Score 86;	DB 16;	Length 679;
Best Local Similarity	100.0%;	Pred. No. 9.6e-06;		
Matches	17;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

```
QY      1 VVARSMGKEDLIWELL 17
        |||||
Db      251 VVARSMGKEDLIWELL 267
```

```

RESULT 14
US-10-429-660-4
; Sequence 4, Application US/10429660
; Publication No. US20040220084A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For Nucleic Acid Delivery
; FILE REFERENCE: 2537.000012
; CURRENT APPLICATION NUMBER: US/10/429,660
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-429-660-4

```

Query Match	100.0%;	Score 86;	DB 16;	Length 679;
Best Local Similarity	100.0%;	Pred. No. 9.6e-06;		
Matches 17; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

```
QY      1 VVARSMGKEDLIWELL 17  
        |||||  
Db     251 VVARSMGKEDLIWELL 267
```

```

RESULT 15-662-4
US-10-429-662-4
; Sequence 4, Application US/10429662
; Publication No. US20040220085A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Compositions For Nucleic Acid Delivery
; FILE REFERENCE: 2537,000010
; CURRENT APPLICATION NUMBER: US/10/429,662
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-662-4

```

Query Match	100.0%;	Score 86;	DB 16;	Length 679;
Best Local Similarity	100.0%;	Pred. No. 9.6e-06;		
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

```

QY      1 VVARSMGKEDLIWELL 17
        |||||
Db      251 VVARSMGKEDLIWELL 267

```

Search completed: November 1, 2005, 13:26:06
Job time : 88 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:35:39 / Search time 17.25 Seconds

(without alignments)
94.822 Million cell updates/sec

Title: US-10-612-162a-1

Perfect score: 86

Sequence: 1 VVARSWGKEDLIWELL 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

1: PIR 79:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	698	1	TFHNP
2	75	87.2	694	1	TFHNP
3	75	87.2	704	2	TFHNP
4	71	82.6	708	1	TFHNP
5	70	81.4	708	2	TFHNP
6	68	79.1	706	2	TFHNP
7	66	76.7	695	2	TFHNP
8	66	76.7	711	1	TFHNP
9	65	75.6	696	1	TFHNP
10	65	75.6	703	2	TFHNP
11	55	64.0	707	1	TFHNP
12	52	60.5	311	2	TFHNP
13	49.5	57.6	459	2	TFHNP
14	47.5	55.2	510	2	TFHNP
15	45	52.3	2958	2	TFHNP
16	44	51.2	386	2	TFHNP
17	44	51.2	885	2	TFHNP
18	43	50.0	210	1	TFHNP
19	43	50.0	439	2	TFHNP
20	43	50.0	2340	2	TFHNP
21	42	48.8	164	2	TFHNP
22	42	48.8	882	2	TFHNP
23	42	48.8	970	2	TFHNP
24	42	48.8	995	2	TFHNP
25	41	47.7	99	2	TFHNP
26	41	47.7	324	2	TFHNP
27	41	47.7	326	2	TFHNP
28	41	47.7	346	2	TFHNP
29	41	47.7	451	2	TFHNP

ALIGNMENTS

30	41	47.7	452	2	E71154	hypothetical prote
31	41	47.7	559	2	A99237	hypothetical prote
32	41	47.7	559	2	UC3616	group II chaperon
33	41	47.7	560	2	S59859	rosellatome alpha
34	41	47.7	853	2	A95269	probable sensory t
35	41	47.7	1502	2	T42216	multidrug resistanc
36	41	47.7	1677	2	T46095	hypothetical prote
37	41	47.7	1938	1	S06005	myosin alpha heavy
38	40.5	47.1	201	2	S75047	drga protein - Syn
39	40	46.5	98	2	T14691	hypothetical prote
40	40	46.5	103	2	A10259	hypothetical phage
41	40	46.5	136	2	T15031	hypothetical prote
42	40	46.5	169	2	AD1293	hypothetical prote
43	40	46.5	307	2	D36868	copd homolog - Xan
44	40	46.5	374	2	D81937	probable ribosomal
45	40	46.5	403	2	H83477	conserved hypochet

RESULT 1

transferrin precursor (validated) - human

N:Alternate names: siderophilin

C:Species: Homo sapiens (man)

C>Date: 15-Oct-1982 #sequence, revision 30-Sep-1993 #text change 09-Jul-2004

C/Accession: A20981; A92417; A94044; A29090; A32739; I51959; I61133; I54011; I68160; A0

R/Yang, F.; Lum, J.B.; McGill, J.R.; Moore, C.M.; Naylor, S.L.; van Bragt, P.H.; Baldwin

Proc. Natl. Acad. Sci. U.S.A. 81, 2752-2756, 1984

A>Title: Human transferrin: cDNA characterization and chromosomal localization.

A/Reference number: A20981; NCBI:84194084; PMID:6585826

A/Contents: Variant C

A/Accession: A20981

A/Molecule type: mRNA

A/Residues: 1-698 <YAN>

A/Cross-references: UNIPROT:P02787; EMBL:M12530; NID:G339452; PIDN:AAA61140.1; PID:G339

A/Note: The authors translated the codon CAA for residue 203 as Glu

R/MacGillivray, R.T.A.; Mendes, E.; Shevale, J.G.; Sinha, S.K.; Linebeck-Zinn, J.; Brew,

U. Biol. Chem. 258, 3543-3553, 1983

A>Title: The primary structure of human serum transferrin. The structures of seven cyan

A/Reference number: A92417; NCBI:83160878; PMID:6833213

A/Accession: A92417

A/Molecule type: protein

A/Residues: 20-263, 'E', 265-328, 'N', 330-379, 'SD', 382-435, 'D', 437-557, 'T', 559-560, 'P', 562

A/Note: The sequence shown is the predominant electrophoretic genetic variant (C or T/C)

R/Park, I.; Schaeffer, E.; Sidoli, A.; Baralle, F.E.; Cohen, G.N.; Zakin, M.M.

Proc. Natl. Acad. Sci. U.S.A. 82, 3149-3153, 1985

A>Title: Organization of the human transferrin gene: direct evidence that it originated

A/Reference number: A94044; NCBI:85216459; PMID:3858612

A/Accession: A94044

A/Molecule type: DNA

A/Residues: 73-263, 'E', 265-328, 'N', 330-562 <PAR>

A/Cross-references: EMBL:M1361

R/Radian, G.S.; Korinek, B.W.; Bowman, B.H.; Yang, F.

Gene 49, 167-175, 1986

A>Title: The human transferrin gene: 5' region contains conserved sequences which match

A/Reference number: A29090; NCBI:87192006; PMID:3106157

A/Accession: A29090

A/Molecule type: DNA

A/Residues: 1-72; 291-300 <ADR>

A/Cross-references: EMBL:M15673

R/Juzan, G.; Frain, M.; Park, I.; Beemond, C.; Maessen, G.; Trepac, J.S.; Zakin, M.M.; K

Biochem. Biophys. Res. Commun. 119, 273-281, 1984

A>Title: Molecular cloning and sequence analysis of cDNA for human transferrin.

A/Reference number: A32739; NCBI:84153910; PMID:6322780

A/Accession: A32739

A/Molecule type: mRNA

A/Residues: 422-690, 'G', 692-698 <UZA>

A/Cross-references: EMBL:M12525; NID:G339468; PIDN:AAA61142.1; PID:G339469

R/MacGillivray, R.T.A.; Mendes, E.; Sinha, S.K.; Sutton, M.R.; Linebeck-Zinn, J.; Brew,

Proc. Natl. Acad. Sci. U.S.A. 79, 2504-2508, 1982

A>Title: Human transferrin: cDNA characterization and chromosomal localization.

A/Reference number: A20981; NCBI:84194084; PMID:6585826

A/Contents: Variant C

A/Accession: A20981

A/Molecule type: mRNA

A>Title: The complete amino acid sequence of human serum transferrin.
 A:Reference number: A93911; MUID:82232166; PMID:6953407
 A:Contents: annotation; disulfide bonds
 R:Herzenberg, C.L.; Larson, J.L.; Arnold, B.; Roatbeck, P.R.
 Ann. N. Y. Acad. Sci. 646, 140-154, 1991
 A>Title: A cloned gene for human transferrin.
 A:Reference number: 151959; MUID:92231399; PMID:1809186
 A:Accession: 151959
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-698 <RES>
 A:Cross-references: GB:S95936; NID:9248647; PIDN:AA822049.1; PID:9248648
 R:Duguid, J.R.; Bonmont, C.W.; Liu, N.G.; Tourtelotte, W.W.
 Proc. Natl. Acad. Sci. U.S.A. 86, 7260-7264, 1989
 A>Title: Changes in brain gene expression shared by scrapie and Alzheimer disease.
 A:Reference number: 148174; MUID:89386721; PMID:2780570
 A:Accession: 163133
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 636-696 <RE2>
 A:Cross-references: GB:M26641; NID:9339988; PIDN:AAA61233.1; PID:9339989
 R:Schaeffer, E.; Lucero, M.A.; Jeltch, J.M.; Py, M.C.; Levin, M.J.; Chambon, P.; Cohen, Gene 56, 109-116, 1987
 A>Title: Complete structure of the human transferrin gene. Comparison with analogous chi
 A:Reference number: 154011; MUID:88056305; PMID:3678832
 A:Accession: 154011
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-72 <RE3>
 A:Cross-references: GB:M17611; NID:9339480; PIDN:AAA61147.1; PID:9339485
 A:Accession: 168160
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 564-698 <RR4>
 A:Cross-references: GB:M17614; NID:9339483; PIDN:AAA61148.1; PID:9339486
 A:Comment: Each of the two repetitive domains binds a ferric ion and a bicarbonate anion
 C:Comment: Each of the two repetitive domains binds a ferric ion and a bicarbonate anion
 C:Gene: GDB:TF
 A:Cross-references: GDB:120432; OMIM:190000
 A:Map position: 3621-3621
 A:Intons: 15/1; 72/3; 119/1; 166/1; 212/2; 231/1; 290/3; 350/1; 401/3; 433/1; 444/1; 49
 C:Function:
 A:Description: binds iron for delivery into cells
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein; iron transport; metal binding; plasma
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-698/Product: transferrin #status experimental <MAT>
 F:20-350/Domain: transferrin repeat homology <TRH2>
 F:356-686/Domain: transferrin repeat homology <TRH2>
 F:28-67,38-58,137-213,156-350,177-193,180-196,190-198,246-260,358-615,364-396,374-387,42
 F:432,630/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 100.0%; Score 86; DB 1; Length 698;
 Best Local Similarity 100.0%; Pred. NO. 1.6e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VVARSNGKEDLIWELL 17
 |||||
 DB 270 VVARSNGKEDLIWELL 286

RESULT 2
 TFRBP
 transferrin precursor - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
 C:Accession: S16246; A61259; G61573; S00335; S02694; A25504; S14853
 R:Banfield, D.K.; Chow, B.K.C.; Funk, W.D.; Robertson, K.A.; Umels, T.M.; Woodworth, R.
 Biochim. Biophys. Acta 1089, 262-265, 1991
 A>Title: The nucleotide sequence of rabbit liver transferrin cDNA.
 A:Reference number: S16246; MUID:91274362; PMID:2054387
 A:Accession: S16246
 A:Molecule type: mRNA

A:Residues: 1-694 <BAN>
 A:Cross-references: EMBL:X59533; NID:91750; PIDN:CAA41424.1; PID:91751
 R:Pierpaoli, W.; Dalli'Ata, A.; Yi, C.; Neri, P.; Santucci, A.; Choay, J.
 Cell. Immunol. 134, 225-234, 1991
 A>Title: Iron carrier proteins facilitate engraftment of allogeneic bone marrow and endu
 A:Reference number: A61239; MUID:91191584; PMID:2013104
 A:Accession: A61239
 A:Molecule type: protein
 A:Residues: 19-36 <PIR>
 R:Chung, M.C.M.; Chan, S.L.; Shintzu, S.
 Int. J. Biochem. 23, 609-616, 1991
 A>Title: Purification of transferrins and lactoferrin using DEAE Affi-Gel Blue.
 A:Reference number: A61573; MUID:91293379; PMID:2065820
 A:Accession: C61573
 A:Molecule type: protein
 A:Residues: 19-26, 'X', 28-36, 'X', 38-53 <CHU>
 R:Godovac-Zimmermann, J.
 Biol. Chem. Hoppe-Seyler 369, 93-96, 1988
 A>Title: Isolation, characterization and N-terminal amino-acid sequence of rabbit transf
 A:Reference number: S00335; MUID:88209278; PMID:3365331
 A:Accession: S00335
 A:Molecule type: protein
 A:Residues: 19-45, 'S', 47-48, 'Y', 50 <GOD>
 R:Evans, R.W.; Aitken, A.; Patel, K.J.
 FEBS Lett. 238, 39-42, 1988
 A>Title: Evidence for a single glycan moiety in rabbit serum transferrin and location of
 A:Reference number: S02694; MUID:89005676; PMID:3169252
 A:Accession: S02694
 A:Molecule type: protein
 A:Residues: 482-515, 'V', 517-544 <EVA>
 A>Note: 516-116 was also found
 R:Heaphy, S.; Williams, J.
 Biochem. J. 205, 611-617, 1982
 A>Title: The preparation and partial characterization of N-terminal and C-terminal iron-
 A:Reference number: A26504; MUID:83074540; PMID:6816218
 A:Accession: A26504
 A:Molecule type: protein
 A:Residues: 19-24, 'N', 26, 'X', 28-29, 'S' <HEA>
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein; iron transport; metal binding; plasma
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-694/Product: transferrin #status experimental <MAT>
 F:19-349/Domain: transferrin repeat homology <TRH1>
 F:355-682/Domain: transferrin repeat homology <TRH2>
 F:27-66,37-57,136-212,155-349,176-192,179-195,189-197,245-259,357-611,363-395,373-386,42
 F:508/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 87.2%; Score 75; DB 1; Length 694;
 Best Local Similarity 88.2%; Pred. NO. 0.00012;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 VVARSNGKEDLIWELL 17
 |||||
 DB 269 VVARSNGKEDLIWELL 285

RESULT 3
 147228
 carbonic anhydrase II inhibitor (transferrin homology) precursor - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
 C:Accession: 147228
 R:Roush, E.D.; Fierke, C.A.
 Biochemistry 31, 12536-12542, 1992
 A>Title: Purification and characterization of a carbonic anhydrase II inhibitor from por
 A:Reference number: 147228; MUID:93099129; PMID:1463741
 A:Accession: 147228
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-704 <ROU>
 A:Cross-references: UNIPROT:Q29545; EMBL:U36916; NID:91016329; PIDN:AA858956.1; PID:9101
 A:Gene: pICA

C/Superfamily: transferrin; transferrin repeat homology
 C/Keywords: duplication
 F:20-350/Domain: transferrin repeat homology <TRH1>
 Query Match 87.2%; Score 75; DB 2; Length 704;
 Best Local Similarity 88.2%; Pred. No. 0.00013;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VVARSMGKEDLIWELL 17
 |||||:|||||
 Db 270 VVARSDGKEDLIWELL 286

RESULT 4
 lactotransferrin precursor - bovine
 N/Alternate names: lactoferrin
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 09-Jul-2004
 C/Accession: I45919, S14674, S14110, S18517, J10595, S13057, S18518, S13881, P10148, S21
 R/Bang, J.C.; Burns, D.K.; Wang, F.; Pan, Y.
 FASEB J. 6, 233, 1991
 A/Title: Cloning of a 80-kD advanced glycosylation end product (AGE) binding protein frc
 A/Reference number: I45919
 A/Accession: I45919
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-708 <TSA>
 A/Cross-references: UNIPROT:P24627; GB:L08604; NID:G13269; PIDN:AAA30609.1; PID:G163270
 R/Pierce, A.
 submitted to the EMBL Data Library, November 1990
 A/Reference number: S14674
 A/Accession: S14674
 A/Molecule type: mRNA
 A/Residues: 1-144, 'V', 146-163, 'P', 166-339, 'A', 341-438, 'Y', 440-513, 'R', 515-708 <PI1>
 A/Cross-references: EMBL:X57084; NID:G505; PIDN:CAA40366.1; PID:G506
 R/Pierce, A.; Colavizza, D.; Benalissa, M.; Maes, P.; Tartar, A.; Montreuil, J.; Spik, G.
 Eur. J. Biochem. 196, 177-184, 1991
 A/Title: Molecular cloning and sequence analysis of bovine lactotransferrin.
 A/Reference number: S14110; MUID:9160550; PMID:2001696
 A/Accession: S14110
 A/Molecule type: mRNA
 A/Residues: 3-144, 'V', 146-339, 'A', 341-438, 'Y', 440-513, 'R', 515-708 <PI2>
 A/Cross-references: EMBL:X57084
 A/Accession: S18517
 A/Molecule type: protein
 A/Residues: 20-35;82-114;148-163, 'P', 166-178, 'V', 'P', 183-190;205-212;230-239;304-339;59
 R/Goodman, R.E.; Schanbacher, F.L.
 Biochem. Biophys. Res. Commun. 180, 75-84, 1991
 A/Title: Bovine lactoferrin mRNA: sequence, analysis, and expression in the mammary gland
 A/Reference number: J10595; MUID:92028986; PMID:1718281
 A/Accession: J10595
 A/Molecule type: mRNA
 A/Residues: 1-65, 'P', 68-296, 'S', 298-339, 'A', 341-708 <GOO>
 A/Cross-references: GB:M63502
 R/Goodman, R.E.; Schanbacher, F.L.
 Biochem. Biophys. Res. Commun. 180, 75-84, 1991
 A/Title: The authors translated the codon CCG for residue 66 as Arg and TCT for residue 2
 Nucleic Acids Res. 18, 7167, 1990
 A/Title: cDNA and protein sequence of bovine lactoferrin.
 A/Reference number: S13097; MUID:91088328; PMID:2263492
 A/Accession: S13097
 A/Molecule type: mRNA
 A/Residues: 28-33, 'DS', 36-38, 'P', 40-708 <MEA>
 A/Cross-references: EMBL:X54801
 A/Accession: S18518
 A/Molecule type: protein
 A/Residues: 20-47;59-66;132-139;256-277;278,305-332;343-351;361-363;586,587-589;598-619
 R/Read, P.E.
 submitted to the EMBL Data Library, October 1990
 A/Reference number: S13881
 A/Molecule type: mRNA
 A/Residues: 28-38, 'P', 40-86, 'C', 88-708 <ME3>

A/Cross-references: EMBL:X54801
 R/Rejman, J.U.; Hegarty, H.M.; Hurley, W.L.
 Comp. Biochem. Physiol. B 93, 929-934, 1989
 A/Title: Purification and characterization of bovine lactoferrin from secretions of the
 A/Reference number: P10148; MUID:90011466; PMID:2805645
 A/Accession: P10148
 A/Molecule type: protein
 A/Residues: 20-27, 'X', 29-37, 'X', 39-54, 'X', 56-59 <REJ>
 R/Beilamy, W.; Takae, M.; Yamuchi, K.; Wakabayashi, H.; Kawase, K.; Tomita, M.
 Biochim. Biophys. Acta 1121, 130-136, 1992
 A/Title: Identification of the bactericidal domain of lactoferrin.
 A/Reference number: S21756; MUID:92287941; PMID:1599934
 A/Accession: S21756
 A/Molecule type: protein
 A/Residues: 36-60 <BEL>
 R/Shimazaki, K.; Tanaka, T.; Kon, H.; Oota, K.; Kawaguchi, A.; Maki, Y.; Sato, T.
 J. Dairy Sci. 76, 946-955, 1993
 A/Title: Separation and characterization of the C-terminal half molecule of bovine lact
 A/Reference number: A56659; MUID:93253156; PMID:8486845
 A/Accession: A56659
 A/Molecule type: protein
 A/Residues: 20-25;302-308;359-366, 'X', 368-376, 'X', 378 <SHI>
 C/Superfamily: transferrin; transferrin repeat homology
 C/Keywords: duplication; glycoprotein; iron; iron binding; metalloprotein; milk
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-708/Product: lactotransferrin #status experimental <MAT>
 F:20-35/Domain: transferrin repeat homology <TRH1>
 F:36-60/Region: antimicrobial
 F:359-696/Domain: transferrin repeat homology <TRH2>
 F:26-64;134-217, 176-192, 179-200, 189-202, 250-264, 367-399, 377-390, 424-703, 444-666, 476-551
 P:38-55/Disulfide bonds: #status predicted
 F:79,111,211,272/Binding site: iron (Asp, Tyr, Tyr, His) #status experimental
 F:140/Binding site: carbonate (Arg) #status experimental
 F:252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:414,452,545,614/Binding site: iron (Asp, Tyr, Tyr, His) #status experimental
 F:482/Binding site: carbonate (Arg) #status experimental

Query Match 82.6%; Score 71; DB 1; Length 708;
 Best Local Similarity 82.4%; Pred. No. 0.00061;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 VVARSMGKEDLIWELL 17
 |||||:|||||
 Db 274 VVARSDGKEDLIWELL 290

RESULT 5
 lactoferrin - goat
 J102323
 C/Species: Capra aegagrus hircus (domestic goat)
 C/Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text change 07-May-1999
 C/Accession: J102323
 R/Le Provost, F.; Nocard, M.; Guerin, G.; Martin, P.
 Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
 A/Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locu
 A/Reference number: J102323; MUID:94380047; PMID:8093048
 A/Accession: J102323
 A/Molecule type: mRNA
 A/Residues: 1-708 <LEP>
 A/Superfamily: transferrin; transferrin repeat homology
 C/Keywords: duplication; glycoprotein
 F:359-696/Domain: transferrin repeat homology
 F:252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 81.4%; Score 70; DB 2; Length 708;
 Best Local Similarity 82.4%; Pred. No. 0.00091;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 VVARSMGKEDLIWELL 17
 |||||:|||||
 Db 274 VVARSDGKEDLIWELL 290

```

RESULT 6
transferrin precursor - horse
N:Alternate names: growth-promoting factor
C:Species: Equus caballus (domestic horse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S33761; S02145
R:Carpenier, M.A.; Broad, T.E.
Biochim. Biophys. Acta 1173, 230-232, 1993
A:Title: The cDNA sequence of horse transferrin.
A:Reference number: S33761; MUID:93277958; PMID:8504171
A:Accession: S33761
A:Molecule type: mRNA
A:Status: preliminary
A:Cross-references: UNIPROT:P27425; EMBL:ME9020; NID:g164242; PIDN:AAA30958.1; PID:g1642
A:Experimental source: liver; developmental stage adult
R:Yoshinari, K.; Yuasa, K.; Iga, F.; Minura, A.
Biochim. Biophys. Acta 1010, 28-34, 1989
A:Title: A growth-promoting factor for human myeloid leukemia cells from horse serum ide
A:Reference number: S02145; MUID:89076897; PMID:2909248
A:Accession: S02145
A:Molecule type: protein
A:Residues: 20-35, 'X', 37, 'X', 39-40, 'X', 43-44 <YOS>
C:Complex: monomer
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; glycoprotein; iron transport; metal binding; plasma
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-706/Product: transferrin #status experimental <NAT>
F:358-694/Domain: transferrin repeat homology <TRH2>
F:26-64, 36-55, 134-215, 174-190, 187-198, 248-262, 360-623, 366-398, 376-389, 423-701, 44

Query Match          79.1%; Score 68; DB 2; Length 706;
Best Local Similarity 82.4%; Pred. No. 0.002;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 VVARSMGKEDLIWELL 17
Db      272 VVARSVDGKEDLIWGL 288

RESULT 7
S49163
transferrin precursor - rat
N:Alternate names: lung-derived growth factor; siderophilin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S49163; S54980; A30014; A4679; A53289; A30512; 152203
R:Escrivá, H.; Pierce, A.; Coddeville, B.; Gonzalez, F.; Benalissa, M.; Leger, D.; Wierus
submitted to the EMBL Data Library, January 1994
A:Description: Rat mammary gland transferrin: glycan structure, nucleotide sequence and
A:Reference number: S49163
A:Accession: S49163
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <ESC>
A:Cross-references: UNIPROT:P12346; UNIPROT:Q63602; EMBL:X77158; NID:g510195; PIDN:CAA54
R:Escrivá, H.; Pierce, A.; Coddeville, B.; Gonzalez, F.; Benalissa, M.; Leger, D.; Wierus
Biochem. J. 307, 47-55, 1995
A:Title: Rat mammary-gland transferrin: nucleotide sequence, phylogenetic analysis and g
A:Reference number: S54980; MUID:95234054; PMID:7717992
A:Accession: S54980
A:Molecule type: mRNA
A:Status: preliminary
A:Residues: 1-695 <ESC>
A:Cross-references: EMBL:X77158; NID:g510195; PIDN:CAA54403.1; PID:g510196
R:Hugueny, J.L.; Idzerda, R.L.; Haywood, L.; Lee, D.C.; McKnight, G.S.; Griswold, M.D.
Endocrinology 120, 332-340, 1987
A:Title: Transferrin messenger ribonucleic acid: molecular cloning and hormonal regulati
A:Reference number: A30014; MUID:87053639; PMID:3023031
A:Accession: A30014
A:Molecule type: mRNA
A:Residues: 518-687, 'D', 689-692, 'TA', 695 <HUG>
A:Cross-references: GB:M27966; NID:g207439; PIDN:AAA42267.1; PID:g207440

```

```

R:Schreiber, G.; Dryburgh, H.; Millerhip, A.; Matsuda, Y.; Inglis, A.; Phillips, J.; Ed
J. Biol. Chem. 254, 12013-12019, 1979
A:Title: The synthesis and secretion of rat transferrin.
A:Reference number: A14679; MUID:80049855; PMID:500689
A:Accession: A14679
A:Molecule type: protein
A:Residues: 20-47 <SCH>
R:Cavanaugh, P.G.; Nicolson, G.L.
J. Cell. Biochem. 47, 261-271, 1991
A:Title: Lung-derived growth factor that stimulates the growth of lung-metastasizing tum
A:Reference number: A53289; MUID:92165927; PMID:1791188
A:Accession: A53289
A:Status: preliminary
A:Molecule type: protein
A:Residues: 89, 'Y', 91, 'A', 93-99, 'V', 101-102, 'N', 233, 'AN', 236-243, 401-406, 'N', 408 <CAV>
A:Experimental source: lung
A:Note: sequence modified after extraction from NCBI backbone
A:Note: sequence extracted from NCBI backbone (NCBI:86115, NCBI:86116, NCBI:86114)
R:Purves, L.R.; Purves, M.; Linton, N.; Brandt, W.; Johnson, G.; Jacobs, P.
Biochim. Biophys. Acta 966, 318-327, 1988
A:Title: Properties of the transferrin associated with rat intestinal mucosa.
A:Reference number: A30512; MUID:88327006; PMID:304665
A:Accession: A30512
A:Molecule type: protein
A:Residues: 20-30, 639-643, 'KD', 646, 'LXACD' <PUR>
R:Alfred, A.R.; Howlett, G.J.; Schreiber, G.
Biochem. Biophys. Res. Commun. 122, 960-965, 1984
A:Title: Synthesis of rat transferrin in Escherichia coli containing a recombinant bacte
A:Reference number: 152203; MUID:84307580; PMID:6233811
A:Accession: 152203
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 7-25, 'X', 27-56, 'A', 58-64, 267-295 <RES>
A:Cross-references: GB:M6113; NID:g207437; PIDN:AAA42266.1; PID:g207438
C:Genetics:
A:Gene: TF
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication
F:20-348/Domain: transferrin repeat homology <TRH1>

Query Match          76.7%; Score 66; DB 2; Length 695;
Best Local Similarity 76.5%; Pred. No. 0.0043;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 VVARSMGKEDLIWELL 17
Db      270 VVARSVDGKEDLIWGL 286

RESULT 8
TFHUL
lactotransferrin precursor [validated] - human
N:Alternate names: lactoferrin
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 21-Nov-1997 #text_change 08-Dec-2000
C:Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A31000; S74
R:Cho, Y.
submitted to the EMBL Data Library, March 1994
A:Reference number: G06820
A:Accession: G01394
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-711 <CHO>
A:Cross-references: EMBL:U07643; NID:g467236; PIDN:AAB60324.1; PID:g467237
R:Rey, M.W.; Moloshuk, S.L.; deBoer, H.A.; Pieper, F.R.
Nucleic Acids Res. 18, 5288, 1990
A:Title: Complete nucleotide sequence of human mammary gland lactoferrin.
A:Reference number: S11228; MUID:90384839; PMID:2402455
A:Accession: S11228
A:Molecule type: mRNA
A:Residues: 1-148, 'T', 150-422, 'C', 424-711 <REY>
A:Cross-references: EMBL:X5361; NID:g34415; PIDN:CAA37914.1; PID:g34416
R:Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Pannella, T.

```

Mol. Endocrinol. 6, 1969-1981, 1992
 A>Title: Differential molecular mechanism of the estrogen action that regulates lactoferrin
 A/Reference number: A45401; PMID:9312571; PMID:1480183
 A/Accession: A45401
 A/Molecule type: DNA
 A/Residues: 1-15 <TRN>
 A/Cross-references: GB:852659; NID:9263311; PIDN:AAB24877.1; PID:9263312
 A/Experimental source: placenta
 A/Note: sequence extracted from NCBI backbone (NCBIP:122202)
 R/Powell, M.O.; Ogden, U.E.
 Nucleic Acids Res. 18, 4013, 1990
 A>Title: Nucleotide sequence of human lactoferrin cDNA.
 A/Reference number: S10324; PMID:90326549; PMID:2374734
 A/Accession: S10324
 A/Molecule type: mRNA
 A/Residues: 3-711 <POW>
 A/Cross-references: EMBL:X52941; NID:934411; PIDN:CAA37116.1; PID:934412
 R/Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.
 Biochem. J. 276, 349-355, 1991
 A>Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.
 A/Reference number: S15853; PMID:91264786; PMID:2049066
 A/Accession: S15853
 A/Status: nucleic acid sequence not shown; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 20-31 <ST1>
 A/Accession: S20841
 A/Molecule type: protein
 A/Residues: 20-28, 'X', 30-31 <ST2>
 R/Rado, T.A.; Wei, X.; Benz Jr., E.J.
 Blood 70, 989-993, 1987
 A>Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA
 A/Reference number: S07160; PMID:88001031; PMID:3477300
 A/Accession: S07160
 A/Molecule type: mRNA
 A/Residues: 436-487, 'A', 489-711 <RAD>
 A/Cross-references: EMBL:M8642; NID:916815; PIDN:AAA8665.1; PID:9386855
 R/Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
 Cancer Res. 51, 3037-3043, 1991
 A>Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes
 A/Reference number: A61169; PMID:91235214; PMID:1674448
 A/Accession: A61169
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 3-701, 'SMKPVN' <PAN>
 A/Experimental source: normal breast tissue
 R/Metz-Boutique, M.H.; Jolles, U.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.; Eur. J. Biochem. 145, 659-666, 1984
 A>Title: Human lactotransferrin: amino acid sequence and structural comparisons with other
 A/Reference number: A31000; PMID:85076667; PMID:6510420
 A/Accession: A31000
 A/Molecule type: protein
 A/Residues: 20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-4
 A/Note: this is the final paper in a series
 R/Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norzkov, L.
 Eur. J. Biochem. 241, 303-308, 1996
 A>Title: Lactoferrin: similarity to diamine oxidase and purification by aminoheptyl affinity
 A/Reference number: S74119; PMID:97054624; PMID:8898921
 A/Accession: S74119
 A/Molecule type: protein
 A/Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>
 A/Experimental source: neutrophil granulocytes
 C/Genetics:
 A/Genes: GDB:ITP
 A/Cross-references: GDB:119368; OMIM:150210
 A/Map position: 3q21-3q23
 C/Superfamily: transferrin, transferrin repeat homology
 C/Keywords: duplication; glycoprotein; iron binding; milk
 F:1-13/Domains: signal sequence #status predicted <SIG>
 F:20-71/Product: lactotransferrin #status experimental <MAT>
 F:21-356/Domains: transferrin repeat homology <TRH1>
 F:360-699/Domains: transferrin repeat homology <TRH2>
 F:59-65, 39-55, 135-218, 177-193, 190-201, 251-265, 503-697, 595-609/disulfide bonds: #status
 F:157, 498/Binding site: carbohydrate (Agn) (covalent) #status experimental

F:368-400, 378-391, 425-706, 447-669, 479-554, 513-527, 524-537, 647-652/disulfide bonds: #sta
 Query Match 76.7%; Score 66; DB 1; Length 711;
 Best Local Similarity 76.5%; Pred. No. 0.0044;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 VVARSNGKEDLIWELL 17
 DB 275 VVARSNGKEDLIWELL 291
 RESULT 9
 S01384
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C/Accession: S01384; A60520; A61573
 R/Baldwin, G.S.; Weinstein, J.
 Nucleic Acids Res. 16, 8720, 1988
 A>Title: Nucleotide sequence of porcine liver transferrin.
 A/Reference number: S01384; PMID:88335629; PMID:3419934
 A/Accession: S01384
 A/Status: translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-696 <BAL>
 A/Cross-references: UNIPROT:P09571; EMBL:X12386; NID:92126; PIDN:CAA30943.1; PID:9833800
 A/Note: 308-Arg was also found
 R/Baldwin, G.S.; Baci, T.; Chandler, R.; Grego, B.; Pedersen, J.; Simpson, R.J.; Toh, T.
 Comp. Biochem. Physiol. B 95, 261-268, 1990
 A>Title: Isolation of transferrin from porcine gastric mucosa: comparison with porcine
 A/Reference number: A60520; PMID:90227903; PMID:2328566
 A/Accession: A60520
 A/Molecule type: protein
 A/Residues: 1-8, 'X', 10-11, 'X', 13-15 <BA2>
 A/Experimental source: gastric mucosa
 A/Note: the authors suggest transferrin from gastric mucosa may act in dietary iron uptake
 R/Chung, M.C.M.; Chan, S.L.; Shih, S.
 Int. J. Biochem. 23, 609-616, 1991
 A>Title: Purification of transferrins and lactoferrin using DEAE Affi-Gel Blue.
 A/Reference number: A61573; PMID:91293379; PMID:2065820
 A/Accession: A61573
 A/Molecule type: protein
 A/Residues: 1-8, 'X', 10-18, 'XE', <CHU>
 C/Superfamily: transferrin, transferrin repeat homology
 C/Keywords: duplication; glycoprotein; iron transport; plasma
 F:1-656/Product: transferrin #status predicted <MAT>
 F:1-335/Domains: transferrin repeat homology <TRH1>
 Query Match 75.6%; Score 65; DB 1; Length 696;
 Best Local Similarity 76.5%; Pred. No. 0.0064;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 VVARSNGKEDLIWELL 17
 DB 255 VVARSVDGEDSIWELL 271
 RESULT 10
 A45543
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
 C/Accession: A45543; S24173
 R/Alexander, L.J.; Levine, W.B.; Teng, C.T.; Beattie, C.W.
 Anim. Genet. 23, 251-256, 1992
 A>Title: Cloning and sequencing of the porcine lactoferrin cDNA.
 A/Reference number: A45543; PMID:92367939; PMID:1503259
 A/Accession: A45543
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-703 <ALE>
 A/Cross-references: UNIPROT:P14632
 A/Experimental source: mammary gland

A>Note: sequence extracted from NCBI backbone (NCBIN:111151, NCBI:111153)
 R.Lydon, J.P.; O'Malley, B.R.; Sancedo, O.; Lee, T.; Headon, D.R.; Connely, O.M.
 Biochim. Biophys. Acta 1132, 97-99, 1993
 A>Title: Nucleotide and primary amino acid sequence of porcine lactoferrin.
 A:Reference number: S24173; MUID:92379101; PMID:1511016
 A:Accession: S24173
 A:Molecule type: mRNA
 A:Residues: 1-11, 'W', 'I', '52-84', 'G', '86-120', 'L', '121-130', 'I', '132-282', 'S', '284-571', 'Q',
 A:Cross-references: EMBL:M92089; NID:g164613; PIDN:AAA31102.1; PID:g164614
 A:Experimental source: mammary gland
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein; iron; iron binding; metalloprotein; milk
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-703/Product: lactoferrin #status predicted <MAT>
 F:20-350/Domain: transferrin repeat homology <TRH>
 F:354-691/Domain: transferrin repeat homology <TRH2>
 F:128-62,38-53,119-212,171-187,184-195,245-259,362-394,372-385,419-698,439-661,471-546,45
 F:77,107,206,267/Binding site: iron (Asp, Tyr, His) #status predicted
 F:135/Binding site: carbonate (Arg) #status predicted
 F:409,447,540,609/Binding site: iron (Asp, Tyr, Tyr, His) #status predicted
 F:477/Binding site: carbonate (Arg) #status predicted
 F:490/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 75.6%; Score 65; DB 2; Length 703;
 Best Local Similarity 76.5%; Pred. No. 0.0065;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VVARSNGKEDLIWEIL 17
 |||||:|||||
 DB 269 VVARSNGKENSWEIL 285

RESULT 11
 A28438
 Lactoferrin precursor - mouse
 N:Alternate names: lactotransferrin
 C:Species: Mus musculus (house mouse)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A28438; A41205
 R:Penetecost, B.T.; Teng, C.T.
 J. Biol. Chem. 262, 10134-10139, 1987
 A>Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secre
 A:Reference number: A92596; MUID:87280033; PMID:3611056
 A:Accession: A28438
 A:Molecule type: mRNA
 A:Residues: 3-707 <PEN>
 A:Cross-references: EMBL:J03298
 R:Lin, Y.; Teng, C.T.
 J. Biol. Chem. 266, 21880-21885, 1991
 A>Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
 A:Reference number: A41205; MUID:92042099; PMID:1939212
 A:Accession: A41205
 A:Molecule type: DNA
 A:Residues: 1-15 <LIU>
 A:Cross-references: GB:M74778
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-707/Product: lactotransferrin #status predicted <MAT>
 F:358-695/Domain: transferrin repeat homology <TRH2>
 F:494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 64.0%; Score 55; DB 1; Length 707;
 Best Local Similarity 64.7%; Pred. No. 0.33;
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 VVARSNGKEDLIWEIL 17
 |||||:|||||
 DB 273 VVRSSTNDKERAIWEIL 289

RESULT 12

A28446
 transferrin - mouse (fragments)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Jun-1988 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C:Accession: A28446; A33482; B28438
 R:Chen, L.H.; Bissell, M.J.
 J. Biol. Chem. 262, 17247-17250, 1987
 A>Title: Transferrin mRNA level in the mouse mammary gland is regulated by pregnancy and
 A:Reference number: A28446; MUID:88086992; PMID:3693348
 A:Accession: A28446
 A:Molecule type: mRNA
 A:Residues: 15-80; 81-141,217-251;252-301 <CHR>
 A:Cross-references: UNIPROT:Q92111
 A>Note: the authors translated the codon ACC for residue 61 as Tyr, TCC for residue 62 a
 R:Idzerda, R.L.; Behringer, R.R.; Theisen, M.; Huguenyik, J.I.; McKnight, G.S.; Brinster
 Mol. Cell. Biol. 9, 5154-5162, 1989
 A>Title: Expression from the transferrin gene promoter in transgenic mice.
 A:Reference number: A33482; MUID:90097932; PMID:2601714
 A:Accession: A33482
 A:Molecule type: DNA
 A:Residues: 1-14;302-311 <IDZ>
 A:Cross-references: GB:M30819; GB:M30820
 R:Penetecost, B.T.; Teng, C.T.
 J. Biol. Chem. 262, 10134-10139, 1987
 A>Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secre
 A:Reference number: A92596; MUID:87280033; PMID:3611056
 A:Accession: B28438
 A:Molecule type: mRNA
 A:Residues: 86-216 <PEN>
 A:Cross-references: GB:J03299; GB:J02737; NID:g198847; PIDN:AAA39438.1; PID:g198848
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication

Query Match 60.5%; Score 52; DB 2; Length 311;
 Best Local Similarity 90.0%; Pred. No. 0.44;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 GKEDLIWEIL 17
 |||||:|||||
 DB 81 GKEDLIWEIL 90

RESULT 13
 A75097
 hypothetical protein PAB1598 - Pyrococcus abyssi (strain Orsay)
 C:Species: Pyrococcus abyssi
 C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C:Accession: A75097
 R:Anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
 A:Reference number: A75001
 A:Accession: A75097
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-459 <XAN>
 A:Cross-references: UNIPROT:Q9UZH9; GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB5007
 A:Experimental source: strain Orsay
 C:Genetics:
 A:Gene: PAB1598
 C:Superfamily: Methanobacterium thermoautotrophicum conserved hypothetical protein MTH19

Query Match 57.6%; Score 49.5; DB 2; Length 459;
 Best Local Similarity 52.4%; Pred. No. 1.8;
 Matches 11; Conservative 3; Mismatches 2; Indels 5; Gaps 1;

QY 1 VVARSNGKEDLIWEIL 16
 |||||:|||||
 DB 428 IVARDVQKEDLIEDNSHIWIL 448

RESULT 14

G72464

THIS PAGE BLANK (USPTO)


```

AC Q9GL95;
BT 01-MAR-2001 (TRENBLREL. 16, Created)
DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Transferrin (Fragment).
OS Phocoenoides phocaena (Harbor porpoise).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Phocoenidae;
OC Phocoena.
OX NCBI_TaxID=9742;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20481910; PubMed=11027333; DOI=10.1073/pnas.97.21.11343;
RA Caspersen I., Valcarlos S., Waddell V.G., Balchowsky H., Van Belle D.,
RA Ding M., Fan C., Mohan L., Simoes-Lopes P.C., Bastida R., Meyer A.,
RA Stanhope W.J., Minkovitch M.C.;
RT "Independent adaptation to riverine habitats allowed survival of
RT ancient cetacean lineages."
RL Proc. Natl. Acad. Sci. U.S.A. 97:11343-11347(2000).
DR EMBL, AF041100; MAG32042.1; -.
DR HSSP; P09571; 1H76.
DR GO; GO:0005576; Cytochrome b; IEA.
DR GO; GO:0008199; Ferritin iron binding; IEA.
DR GO; GO:0006879; Pili on iron homeostasis; IEA.
DR GO; GO:0006826; Pili on iron transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin; 1.
DR PRINTS; PR00422; TRANSFERRIN.
FT NON_TER
FT 1
FT 81
FT NON_TER
SQ SEQUENCE 81 AA; 9379 MW; 785DE6D52445A45 CRC64;

Query Match 100.0%; Score 86; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 6; 4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
DB 39 VVARSMGKEDLIWELL 55

RESULT 3
ID TRPE_HUMAN STANDARD; PRT; 698 AA.
AC P02787; O43890; Q9NQB8; Q9UHV0;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Serotransferrin precursor (transferrin) (Siderophilin) (beta-1-metal
DE binding globulin) (PRO1400).
GN Name=TF;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS TF*B2; TF*CHI AND TF*D1.
RX MEDLINE=84194084; PubMed=6585826;
RA Yang F., Lum J.B., McGill J.R., Moore C.M., Naylor S.L.,
RA van Bregt P.H., Baldwin W.D., Bowman B.H.;
RT "Human transferrin: CDNA characterization and chromosomal
RT localization."
RL Proc. Natl. Acad. Sci. U.S.A. 81:2752-2756(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88056305; PubMed=3678832; DOI=10.1016/0378-1119(87)90163-6;
RA Schaeffer E., Lucero M.A., Jeltsch J.-M., Py M.-C., Levin M.J.,
RA Chanbon P., Cohen G.N., Zakim M.M.;
RT "Complete structure of the human transferrin gene. Comparison with
RT analogous chicken gene and human pseudogene."
RL Gene 56:109-116(1987).
RN [3]
RP SEQUENCE FROM N.A.

```

```

RC TISSUE=Liver;
RX MEDLINE=92223139; PubMed=1809186;
RA Herberberger C.L., Larson J.L., Arnold B., Rostock P.R., Jr.;
RA Williams P., Dehoff B., Dunn P., O'Neal K.L., Riemen M.W., Rice P.A.;
RT "A cloned gene for human transferrin."
RL Ann. N. Y. Acad. Sci. 646:140-154(1991).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT ATRANSFERRINEMIA PRO-477.
RX MEDLINE=20563920; PubMed=1110675;
RA Beutler E., Gelbart T., Lee P.L., Trevino R., Fernandez M.A.,
RA Fairbanks V.P.;
RT "Molecular characterization of a case of atransferrinemia."
RL Blood 96:4071-4074(2000).
RN [5]
RP SEQUENCE FROM N.A.
RX Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
RA Ahearn M.O., Kulaneck S.A., Rajkumar N., Toch E.J., Yi Q.,
RA Nickerson D.A.;
RT "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
RT FHCR, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (MAY-2003) to the EMBL/Genbank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M., Utell T.B., Toshyuk S., Carlni P., Prange C.,
RA Raha S.S., Loughlan N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.T., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP SEQUENCE OF 99-698 FROM N.A.
RC TISSUE=Fetal liver;
RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M.,
RA He P.;
RT "Functional prediction of the coding sequences of 33 new genes deduced
RT by analysis of cDNA clones from human fetal liver."
RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
RN [8]
RP SEQUENCE OF 422-698 FROM N.A.
RX MEDLINE=84153910; PubMed=6322780;
RA Uzan G., Frain M., Park I., Besmond C., Maessen G., Trepas J.S.,
RA Zakim M.M., Kahn A.;
RT "Molecular cloning and sequence analysis of cDNA for human
RT transferrin."
RL Biochem. Biophys. Res. Commun. 119:273-281(1984).
RN [9]
RP SEQUENCE OF 20-698.
RX MEDLINE=83160878; PubMed=6833213;
RA McGilivray R.T.A., Mendez E., Shewale J.G., Sinha S.K.,
RA Linback-Zins J., Brew K.;
RT "The primary structure of human serum transferrin. The structures of
RT structure."
RL J. Biol. Chem. 258:3543-3553(1983).
RN [10]
RP SEQUENCE OF 73-698 FROM N.A.
RX MEDLINE=85216459; PubMed=3858812;

```

RA Park I., Schaeffer E., Sidoli A., Baralle F.E., Cohen G.N.,
 RA Zakin M.M.,
 RT "Origination of the human transferrin gene: direct evidence that it
 RT originated by gene duplication.",
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3149-3153 (1985).
 RN [11]
 RP SEQUENCE OF 1-14 FROM N.A.
 RX MEDLINE=87066744; PubMed=3786138;
 RA Lucero M.A., Schaeffer E., Cohen G.N., Zakin M.M.,
 RT "The 5' region of the human transferrin gene: structure and potential
 RT regulatory sites.",
 RN Nucleic Acids Res. 14:8692-8692 (1986).
 RN [12]
 RP SEQUENCE OF 1-72 AND 291-300 FROM N.A.
 RX MEDLINE=87192006; PubMed=3106157; DOI=10.1016/0378-1119(86)90277-5;
 RA Adrian G.S., Korinek B.W., Bowman B.H., Yang F.,
 RT "The human transferrin gene: 5' region contains conserved sequences
 RT which match the control elements regulated by heavy metals,
 RT glucocorticoids and acute phase reaction.",
 RL Gene 49:167-175 (1986).
 RN [13]
 RP SEQUENCE OF 45-72 FROM N.A.
 RX MEDLINE=20392111; PubMed=10931525;
 RA DOI=10.1002/1097-4547(200008)51:4<388::AID-JNRS>3.0.CO;2-Q;
 RA de Arriba Zepa G.A., Saleh M.-C., Fernandez P.M., Guillou F.,
 RA Espinosa de los Monteros A., de Vellis J., Zakin M.M., Baron B.,
 RT "Alternative splicing prevents transferrin secretion during
 RT differentiation of a human oligodendrocyte cell line.",
 RL J. Neurosci. Res. 61:388-395 (2000).
 RN [14]
 RP SEQUENCE OF 564-624 FROM N.A., AND VARIANT TF+C2.
 RC TISSUE=Brain;
 RX MEDLINE=97418135; PubMed=9272172;
 RA Namekata K., Oyama F., Imagawa M., Ihara Y.,
 RT "Human transferrin (TF): a single mutation at codon 570 determines TF
 RT C1 or TF C2 variant.",
 RL Hum. Genet. 100:457-458 (1997).
 RN [15]
 RP SEQUENCE OF 564-624 FROM N.A.
 RA Teuchida S., Ikemoto S., Kajii E.,
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [16]
 RP SEQUENCE OF 636-696 FROM N.A.
 RX MEDLINE=89386721; PubMed=2789570;
 RA Duguid J.R., Bohmont C.W., Liu N.G., Tourtellotte W.W.,
 RT "Changes in brain gene expression shared by scrapie and Alzheimer
 RT disease.",
 RL Proc. Natl. Acad. Sci. U.S.A. 86:7260-7264 (1989).
 RN [17]
 RP SEQUENCE OF 263-266; 454-458; 531-538 AND 589-595.
 RC TISSUE=Heart;
 RX MEDLINE=96007936; PubMed=7498159;
 RA Kovalyov L.I., Sheshkin S.S., Efimochkin A.S., Kovalyova M.A.,
 RA Ereshova E.S., Egorov T.A., Musalyanov A.K.,
 RT "The major protein expression profile and two-dimensional protein
 RT database of human heart.",
 RL Electrophoresis 16:1160-1169 (1995).
 RN [18]
 RP DISULFIDE BONDS.
 RX MEDLINE=8222216; PubMed=6953407;
 RA McGillivray R.T.A., Mendez E., Simha S.K., Sutton M.R.,
 RA Lineback-Zins J., Brew K.,
 RT "The complete amino acid sequence of human serum transferrin.",
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2504-2508 (1982).
 RN [19]
 RP MUTAGENESIS.
 RX MEDLINE=92031536; PubMed=1932003;
 RA Woodworth R.C., Mason A.B., Funk W.D., McGillivray R.T.A.,
 RT "Expression and initial characterization of five site-directed mutants
 RT of the N-terminal half-molecule of human transferrin.",
 RL Biochemistry 30:10824-10829 (1991).
 RN [20]
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 22-350.

RX MEDLINE=98272665; PubMed=9609685; DOI=10.1021/b39803551;
 RA McGillivray R.T.A., Moore S.A., Chen J., Anderson B.F., Baker H.,
 RA Luo Y., Bewley M.C., Smith C.A., Murphy M.E.P., Wang Y., Mason A.B.,
 RA Woodworth R.C., Brayer G.D., Baker E.N.,
 RT "Two high-resolution crystal structures of the recombinant N-lobe of
 RT human transferrin reveal a structural change implicated in iron
 RT release.",
 RL Biochemistry 37:7919-7928 (1998).
 RN [21]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-350.
 RX MEDLINE=98434369; PubMed=9760232; DOI=10.1021/b19812064;
 RA Jeffrey P.D., Bewley M.C., McGillivray R.T.A., Mason A.B.,
 RA Woodworth R.C., Baker E.N.,
 RT "Ligand-induced conformational change in transferrin: crystal
 RT structure of the open form of the N-terminal half-molecule of human
 RT transferrin.",
 RL Biochemistry 37:13978-13986 (1998).
 RN [22]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 23-352.
 RX MEDLINE=99155227; PubMed=10029548; DOI=10.1021/b19824543;
 RA Bewley M.C., Tam B.M., Grewal J., He S., Shewry S., Murphy M.E.P.,
 RA Mason A.B., Woodworth R.C., Baker E.N., McGillivray R.T.A.,
 RT "X-ray crystallography and mass spectroscopy reveal that the N-lobe of
 RT human transferrin expressed in *Pichia pastoris* is folded correctly but

Query Match 100.0%; Score 86; DB 1; Length 698;
 Best Local Similarity 100.0%; Pred. No. 5.8e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVARSMGKEDLIWELL 17
 DB 270 VVARSMGKEDLIWELL 286

RESULT 4
 O9GL91
 ID O9GL91 PRELIMINARY; PRT; 81 AA.
 AC O9GL91;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Transferrin (Fragment).
 OS Ziphilus cavirostris (Goose-beaked whale).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Ziphiidae;
 OC Ziphius.
 OX NCBI_TaxID=9760;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20481910; PubMed=11027333; DOI=10.1073/pnas.97.21.11343;
 RA Cassens I., Vicario S., Maddell V.G., Balchowsky H., Van Belle D.,
 RA Ding W., Fan C., Mohan L., Simoes-Lopes P.C., Bastida R., Meyer A.,
 RA Stanhope M.J., Milinkovitch M.C.,
 RT "Independent adaptation to riverine habitats allowed survival of
 RT ancient cetacean lineages.",
 RL Proc. Natl. Acad. Sci. U.S.A. 97:11343-11347 (2000).
 DR EMBL; AF304104; AAG32046.1; -.
 DR HSSP; P02787; IABE.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008199; F:feric iron binding; IEA.
 DR GO; GO:0006879; P:iron ion homeostasis; IEA.
 DR GO; GO:0006826; P:iron ion transport; IEA.
 DR InterPro; IPR001156; Peptidase_S60.
 DR Pfam; PF00405; Transferrin; I.
 DR PRINTS; PR00422; TRANSFERRIN.
 FT NON_TER 1
 FT TER 81
 SO SEQUENCE 81 AA; 9243 MW; D6EE22B822C983B3 CRC64;

Query Match 95.3%; Score 82; DB 2; Length 81;
 Best Local Similarity 94.1%; Pred. No. 3.2e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 VVARSMGKEDLIWELL 17
DB 39 VVARSVGKEDLIWELL 55

RESULT 5
O9GL92 PRELIMINARY; PRT; 81 AA.
ID O9GL92;
AC O9GL92;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE Transferrin (Fragment).
OS Mesopodon peruvianus (Peruvian beaked whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Ziphiidae;
OC Mesopodon.
OX NCBI_TaxID=27617;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20481910; PubMed=11027333; DOI=10.1073/pnas.97.21.11343;
RA Casens I., Vicario S., Maddell V.G., Balchowsky H., Van Belle D.,
RA Ding W., Fan C., Mohan L., Simoes-Lopes P.C., Bastida R., Meyer A.,
RA Stanhope M.J., Mlinkovitch M.C.;
RT "Independent adaptation to riverine habitats allowed survival of
RT ancient cetacean lineages."
RL Proc. Natl. Acad. Sci. U.S.A. 97:11343-11347(2000).
DR EMBL; AF304103; AAC32045.1; -.
DR HSSP; P02787; IUOF.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin; 1.
DR PRINTS; PR00422; TRANSFERRIN.
FT NON_TER 1
SQ SEQUENCE 81 AA; 9138 MW; 1DC9418BF5FAC3 CRC64;

Query Match
Best Local Similarity 95.3%; Score 82; DB 2; Length 81;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
DB 39 VVARSVGKEDLIWELL 55

RESULT 6
O9GL94 PRELIMINARY; PRT; 81 AA.
ID O9GL94;
AC O9GL94;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE Transferrin (Fragment).
OS Inia geoffrensis (Amazon dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Iniidae;
OC Inia.
OX NCBI_TaxID=9725;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20481910; PubMed=11027333; DOI=10.1073/pnas.97.21.11343;
RA Casens I., Vicario S., Maddell V.G., Balchowsky H., Van Belle D.,
RA Ding W., Fan C., Mohan L., Simoes-Lopes P.C., Bastida R., Meyer A.,
RA Stanhope M.J., Mlinkovitch M.C.;
RT "Independent adaptation to riverine habitats allowed survival of
RT ancient cetacean lineages."
RL Proc. Natl. Acad. Sci. U.S.A. 97:11343-11347(2000).
DR EMBL; AF304101; AAC32043.1; -.
DR HSSP; P19134; IJNF.

```

```

DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin; 1.
DR PRINTS; PR00422; TRANSFERRIN.
FT NON_TER 1
SQ SEQUENCE 81 AA; 9220 MW; 49BD4339D3F1B52A CRC64;

Query Match
Best Local Similarity 93.0%; Score 80; DB 2; Length 81;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
DB 39 VVARSVGKEDLIWELL 55

RESULT 7
O9GL93 PRELIMINARY; PRT; 81 AA.
ID O9GL93;
AC O9GL93;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE Transferrin (Fragment).
OS Physeter catodon (Sperm whale) (Physeter macrocephalus).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Physeteridae; Physeter.
OX NCBI_TaxID=9755;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20481910; PubMed=11027333; DOI=10.1073/pnas.97.21.11343;
RA Casens I., Vicario S., Maddell V.G., Balchowsky H., Van Belle D.,
RA Ding W., Fan C., Mohan L., Simoes-Lopes P.C., Bastida R., Meyer A.,
RA Stanhope M.J., Mlinkovitch M.C.;
RT "Independent adaptation to riverine habitats allowed survival of
RT ancient cetacean lineages."
RL Proc. Natl. Acad. Sci. U.S.A. 97:11343-11347(2000).
DR EMBL; AF304102; AAC32044.1; -.
DR HSSP; P19134; IJNF.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin; 1.
DR PRINTS; PR00422; TRANSFERRIN.
FT NON_TER 1
SQ SEQUENCE 81 AA; 9219 MW; 8B9DEA2153941BA6 CRC64;

Query Match
Best Local Similarity 91.9%; Score 79; DB 2; Length 81;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
DB 39 VVARSMGKEDLIWELL 55

RESULT 8
TRFE_BOVIN STANDARD; PRT; 704 AA.
ID TRFE_BOVIN;
AC Q29443;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-UNL-2004 (Rel. 44, Last annotation update)
DE Serritransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal
binding globulin).

```


RC TISSUE=Plasma;
RX MEDLINE=89026775; PubMed=3179277;
RA Bailey S., Evans R.W., Garrate R.C., Gorinsky B., Hasnain S.,
RA Horeburg C., Jhoti H., Lindley P.F., Mydin A., Sarra R., Watson J.L.;
RT "Molecular structure of serum transferrin at 3.3-A resolution.";
RL Biochemistry 27:5804-5812(1988).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS)
RA Sarra R., Garrate R.C., Gorinsky B., Jhoti H., Lindley P.F.;
RT "High-resolution X-ray studies on rabbit serum transferrin:
RT preliminary structure analysis of the N-terminal half-molecule at 2.3-
RT A resolution.";
RL Acta Crystallogr. B 46:763-771(1990).
CC -I- FUNCTION: Transferrins are iron binding transport proteins which
CC can bind two atoms of ferric iron in association with the binding
CC of an anion, usually bicarbonate. It is responsible for the
CC transport of iron from sites of absorption and hence degradation to
CC those of storage and utilization. Serum transferrin may also have
CC a further role in stimulating cell proliferation.
CC -I- SUBUNIT: Monomer.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -I- DOMAIN: Composed of two homologous domains.
CC -I- SIMILARITY: Belongs to the transferrin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC
DR EMBL, X58533; CAA1424.1; -.
DR EMBL, AF031625; AAB94136.1; -.
DR EMBL, AF031611; AAB94136.1; JOINED.
DR EMBL, AF031612; AAB94136.1; JOINED.
DR EMBL, AF031613; AAB94136.1; JOINED.
DR EMBL, AF031614; AAB94136.1; JOINED.
DR EMBL, AF031615; AAB94136.1; JOINED.
DR EMBL, AF031616; AAB94136.1; JOINED.
DR EMBL, AF031617; AAB94136.1; JOINED.
DR EMBL, AF031618; AAB94136.1; JOINED.
DR EMBL, AF031619; AAB94136.1; JOINED.
DR EMBL, AF031620; AAB94136.1; JOINED.
DR EMBL, AF031621; AAB94136.1; JOINED.
DR EMBL, AF031622; AAB94136.1; JOINED.
DR EMBL, AF031623; AAB94136.1; JOINED.
DR EMBL, AF031624; AAB94136.1; JOINED.
DR PDB, 1UNF; X-ray; A=20-695.
DR PDB, 1TFD; X-ray; A=20-323.
DR InterPro: IPR001156; Peptidase_S60.
DR Pfam: PF00405; Transferrin; 2.
DR PRINTS: PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW 3D-structure; Direct protein sequencing; Glycoprotein; Iron transport;
KW Metal-binding; Repeat; Signal; Transport.
KW SIGNAL
FT CHAIN 1 19
FT REPEAT 20 695 Serotransferrin.
FT REPEAT 356 695 1.
FT REPEAT 356 695 2.
FT DISULFID 28 67
FT DISULFID 38 58
FT DISULFID 137 213
FT DISULFID 156 350
FT DISULFID 177 193
FT DISULFID 180 196
FT DISULFID 190 198
FT DISULFID 246 260
FT DISULFID 358 612

FT DISULFID 364 396
FT DISULFID 374 387
FT DISULFID 421 690
FT DISULFID 436 653
FT DISULFID 468 539
FT DISULFID 492 681
FT DISULFID 502 516
FT DISULFID 513 522
FT DISULFID 579 593
FT DISULFID 631 609
FT CARBOHYD 509 536
FT METAL 82 82
FT METAL 114 114
FT METAL 207 207
FT METAL 268 268
FT METAL 411 411
FT METAL 444 444
FT METAL 533 533
FT METAL 601 601
FT BINDING 139 139
FT BINDING 143 143
FT BINDING 145 145
FT BINDING 146 146
FT BINDING 470 470
FT BINDING 474 474
FT BINDING 476 476
FT BINDING 477 477
FT VARIANT 517 517
FT CONFLICT 7 7
FT CONFLICT 47 47
FT CONFLICT 50 50
FT STRAND 24 30
FT HELIX 31 48
FT TURN 51 52
FT STRAND 55 61
FT HELIX 64 72
FT TURN 73 74
FT STRAND 78 81
FT HELIX 83 90
FT TURN 92 94
FT STRAND 96 104
FT STRAND 111 111
FT STRAND 113 121
FT TURN 122 123
FT HELIX 128 130
FT TURN 132 133
FT STRAND 136 138
FT TURN 141 142
FT TURN 144 147
FT HELIX 148 154
FT HELIX 155 157
FT HELIX 165 172
FT STRAND 176 177
FT TURN 179 180
FT TURN 183 185
FT HELIX 187 190
FT TURN 191 192
FT TURN 194 195
FT TURN 200 201
FT TURN 203 204
FT HELIX 206 215
FT TURN 216 217
FT STRAND 221 225
FT TURN 226 227
FT HELIX 232 232
FT HELIX 236 239
FT TURN 240 241
FT STRAND 242 245
FT TURN 247 248
FT STRAND 251 253
FT HELIX 254 256
FT TURN 257 258
FT STRAND 263 266

N-linked (GlcNAc. . .).
Iron 1.
Iron 1.
Iron 1.
Iron 1.
Iron 2.
Iron 2.
Iron 2.
Carbonate 1.
Carbonate 1 (via amide nitrogen).
Carbonate 1 (via amide nitrogen).
Carbonate 2.
Carbonate 2.
Carbonate 2 (via amide nitrogen).
Carbonate 2 (via amide nitrogen).
V -> I. (in Ref. 1).
Missing
K -> S (in Ref. 3).
P -> Y (in Ref. 3).

```

FT STRAND 269 273
FT HELIX 279 293
FT TURN 303 304
FT TURN 307 308
FT TURN 316 317
FT STRAND 320 323
FT TURN 326 327
FT HELIX 330 334
FT HELIX 335 346
FT TURN 347 348

Query Match 87.2%; Score 75; DB 1; Length 695;
Best Local Similarity 88.2%; Pred. No. 0.00047;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VVARSWGKEDLIWELL 17
Db 270 VVARSVDGKEDLIWELL 286

RESULT 10
ICA_PIG STANDARD; PRT; 704 AA.
ID ICA_PIG
AC Q29545;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Inhibitor of carbonic anhydrase precursor.
GN Name=ICA;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sue.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RA MEDLINE:97254619; PubMed:9100029; DOI=10.1021/bi9627424;
RA Muebbers M.W., Roush E.D., Decastro C.M., Fierke C.A.;
RT "Cloning, sequencing, and recombinant expression of the porcine
RT inhibitor of carbonic anhydrase: a novel member of the transferrin
RT family."
RN Biochemistry 36:4327-4336(1997).
RN [2]
RA CHARACTERIZATION.
RP MEDLINE:93099129; PubMed:1463741;
RA Roush E.D., Fierke C.A.;
RT "Purification and characterization of a carbonic anhydrase II
RT inhibitor from porcine plasma."
RN Biochemistry 31:12536-12542(1992).
CC -1- FUNCTION: Specifically binds and inhibits carbonic anhydrase II
CC with nanomolar affinity.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Plasma.
CC -1- DOMAIN: Composed of two homologous domains.
CC -1- PTM: N-glycosylated.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL: U36916; AAB58956.1; -.
CC PIR: I47228; I47228.
CC HSSP: P09571; 1H76.
CC InterPro: IPR001156; Peptidase_S60.
CC Pfam: PF00405; Transferrin_2.
CC PRINTS: PR00422; TRANSFERRIN.
CC SMART: SM00094; TR_FER_2.
CC PROSITE: PS00205; TRANSFERRIN_1; 2.

```

```

DR PROSITE: PS00206; TRANSFERRIN_2; 1.
DR PROSITE: PS00207; TRANSFERRIN_3; 2.
KW Direct protein sequencing; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 19
FT CHAIN 20 704
FT REPEAT 20 351
FT REPEAT 352 704
FT DISULFID 28 67
FT DISULFID 38 58
FT DISULFID 137 213
FT DISULFID 172 188
FT DISULFID 175 196
FT DISULFID 185 198
FT DISULFID 246 260
FT DISULFID 360 392
FT DISULFID 370 383
FT DISULFID 417 699
FT DISULFID 440 662
FT DISULFID 472 549
FT DISULFID 496 690
FT DISULFID 506 520
FT DISULFID 517 532
FT DISULFID 589 603
FT CARBOHYD 491 491
SQ SEQUENCE 704 AA; 77634 MW; 16B80E5191E336 CRC64;

Query Match 87.2%; Score 75; DB 1; Length 704;
Best Local Similarity 88.2%; Pred. No. 0.00048;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VVARSWGKEDLIWELL 17
Db 270 VVARSVDGKEDLIWELL 286

RESULT 11
QTSX8 PRELIMINARY; PRT; 694 AA.
ID QTSX8
AC QTSX8;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Transferrin.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE: Liver;
RA Rinaudo J.A.S., Gerin J.L.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC bind ferric iron in association with the binding of an anion,
CC usually bicarbonate (By similarity).
CC -1- DOMAIN: Composed of two homologous domains (By similarity).
CC -1- SIMILARITY: Belongs to the transferrin family.
CC EMBL: AY288100; AAP37129.1; -.
CC HSSP: P19134; 1UNF.
CC GO: GO:0005576; Cytoplasm; IEA.
CC GO: GO:0008199; Ferric iron binding; IEA.
CC GO: GO:0006879; Pitron ion homeostasis; IEA.
CC GO: GO:0006826; Pitron ion transport; IEA.
CC GO: GO:0006810; Pitron ion transport; IEA.
CC InterPro: IPR001156; Peptidase_S60.
CC Pfam: PF00405; Transferrin_2.
CC SMART: SM00094; TR_FER_2.
CC PROSITE: PS00205; TRANSFERRIN_1; 2.
CC PROSITE: PS00206; TRANSFERRIN_2; 2.
CC PROSITE: PS00207; TRANSFERRIN_3; 2.
CC Itron transport; Metal-binding; Transport.
SQ SEQUENCE 694 AA; 76466 MW; 40053F7DC1CFCAB7 CRC64;

```

Query Match 83.7%; Score 72; DB 2; Length 694;
 Best Local Similarity 82.4%; Pred. No. 0.0016;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 1 VVARGMGKEDLIWELL 17
 270 VVARTVDGKEDLIWELL 286

RESULT 12
 TRFL CAMDR STANDARD; PRT; 708 AA.

AC O9TUM0; Q9WZ55; 16-OCT-2001 (Rel. 40. Created)
 DT 16-OCT-2001 (Rel. 40. Last sequence update)
 DT 25-OCT-2004 (Rel. 45. Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN Name=LTF;
 OS Camelus dromedarius (Dromedary) (Arabian camel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 NCBI_TaxId=9838;
 RX SEQUENCE FROM N.A.
 RC STRAIN=Somali; TISSUE=Lactating mammary gland;
 RA Kappeler S.R., Ackermann M., Farah Z., Puhon Z.;
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin";
 RL Int. Dairy J. 9:481-486(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
 RT Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Transferrins are iron binding transport proteins which
 can bind two atoms of ferric iron in association with the binding
 of an anion, usually bicarbonate (By similarity).
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: Composed of two homologous domains.
 CC -1- SIMILARITY: Belongs to the transferrin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/) or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL, AJ131674; CAB53387.1; -;
 DR EMBL, AF165879; AA63241.1; -;
 DR PDB, 1DTZ; X-ray; A=20-708.
 DR InterPro, IPR001156; Peptidase_S60.
 DR Pfam, PF00405; Transferrin; 2.
 DR PRINTS, PR00422; TRANSFERRIN.
 DR SMART, SM00094; TR_FER; 2.
 DR PROSITE, PS00205; TRANSFERRIN_1; 2.
 DR PROSITE, PS00206; TRANSFERRIN_2; 2.
 DR PROSITE, PS00207; TRANSFERRIN_3; 2.
 DR 3D-structure, Glycoprotein; Iron transport; Metal-binding; Repeat;
 KW Signal; Transport.
 FT SIGNAL 1 19 By similarity.
 FT CHAIN 20 708 Lactotransferrin.
 FT REPEAT 20 363 1.
 FT REPEAT 364 708 2.
 FT DISULFID 28 64 By similarity.
 FT DISULFID 38 55 By similarity.
 FT DISULFID 134 217 By similarity.
 FT DISULFID 176 192 By similarity.
 FT DISULFID 189 200 By similarity.
 FT DISULFID 250 264 By similarity.

FT DISULFID 367 399 By similarity.
 FT DISULFID 377 390 By similarity.
 FT DISULFID 424 703 By similarity.
 FT DISULFID 444 666 By similarity.
 FT DISULFID 476 551 By similarity.
 FT DISULFID 500 694 By similarity.
 FT DISULFID 510 524 By similarity.
 FT DISULFID 521 534 By similarity.
 FT DISULFID 592 606 By similarity.
 FT DISULFID 644 649 By similarity.
 FT METAL 79 79 Iron 1 (By similarity).
 FT METAL 111 111 Iron 1 (By similarity).
 FT METAL 211 211 Iron 1 (By similarity).
 FT METAL 272 272 Iron 1 (By similarity).
 FT METAL 414 414 Iron 2 (By similarity).
 FT METAL 452 452 Iron 2 (By similarity).
 FT METAL 545 545 Iron 2 (By similarity).
 FT METAL 614 614 Iron 2 (By similarity).
 FT BINDING 136 136 Carbonate 1 (By similarity).
 FT BINDING 140 140 Carbonate 1 (By similarity).
 FT BINDING 142 142 Carbonate 1 (via amide nitrogen) (By similarity).
 FT BINDING 143 143 Carbonate 1 (via amide nitrogen) (By similarity).
 FT BINDING 478 478 Carbonate 2 (By similarity).
 FT BINDING 482 482 Carbonate 2 (By similarity).
 FT BINDING 484 484 Carbonate 2 (via amide nitrogen) (By similarity).
 FT BINDING 485 485 Carbonate 2 (via amide nitrogen) (By similarity).
 FT CARBOHYD 252 252 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 385 385 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 537 537 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 594 594 N-linked (GlcNAc...) (potential).
 FT CONFLICT 261 261 F -> S (in Ref. 2).
 FT CONFLICT 304 304 G -> A (in Ref. 2).
 FT CONFLICT 330 330 S -> P (in Ref. 2).
 FT CONFLICT 492 494 LLS -> PLF (in Ref. 2).
 FT CONFLICT 506 506 L -> F (in Ref. 2).
 FT CONFLICT 609 609 A -> P (in Ref. 2).
 FT CONFLICT 642 642 R -> Q (in Ref. 2).
 FT STRAND 25 29
 FT HELIX 32 46
 FT TURN 47 49
 FT STRAND 53 57
 FT HELIX 61 69
 FT TURN 70 71
 FT STRAND 75 77
 FT HELIX 80 87
 FT TURN 89 91
 FT STRAND 93 99
 FT STRAND 101 101
 FT STRAND 108 108
 FT STRAND 110 118
 FT HELIX 125 127
 FT TURN 129 130
 FT STRAND 132 135
 FT TURN 138 139
 FT TURN 141 144
 FT HELIX 145 150
 FT TURN 151 151
 FT HELIX 152 154
 FT TURN 155 155
 FT TURN 160 161
 FT HELIX 164 171
 FT STRAND 174 176
 FT TURN 178 179
 FT TURN 182 184
 FT HELIX 186 189
 FT TURN 190 191
 FT HELIX 196 198
 FT TURN 199 200
 FT TURN 204 205

```
FT TURN 207 208
PT HELIX 210 219
PT STRAND 225 229
PT TURN 230 231
PT HELIX 232 236
PT HELIX 240 243
PT TURN 244 245
PT STRAND 246 250
PT TURN 251 253
PT STRAND 254 256
PT HELIX 258 260
PT TURN 261 263
PT STRAND 267 270
PT STRAND 273 277
PT TURN 279 280
PT HELIX 283 297
PT TURN 299 300
PT TURN 321 322
PT STRAND 326 328
PT TURN 331 332
PT HELIX 335 339
PT HELIX 341 348
PT TURN 349 351
PT HELIX 354 362
PT STRAND 364 369
PT HELIX 371 384
PT TURN 385 386
PT STRAND 388 393
PT HELIX 396 404
PT TURN 405 406
PT STRAND 410 413
PT HELIX 415 422
PT TURN 423 425
PT STRAND 427 434
PT TURN 437 438
PT TURN 444 446
PT STRAND 453 459
PT TURN 467 472
PT STRAND 474 477
PT TURN 480 481
PT TURN 483 493
PT TURN 502 503
PT STRAND 508 510
PT TURN 512 513
PT TURN 516 517
PT TURN 519 520
PT STRAND 521 521
PT STRAND 527 527
PT TURN 528 530
PT STRAND 531 531
PT TURN 538 539
PT TURN 541 542
PT HELIX 544 553
PT TURN 554 555
PT STRAND 559 563
PT HELIX 564 567
PT TURN 568 569
PT TURN 579 580
PT TURN 586 587
PT STRAND 588 589
PT TURN 593 594
PT HELIX 600 605
PT STRAND 610 610
PT STRAND 615 618
PT TURN 620 622
PT HELIX 623 637
```

Query Match 83.7%; Score 72; DB 1; Length 708;

Best Local Similarity 82.4%; Pred. No. 0.0016; 1; Indels 0; Gaps 0;

Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSGKEDLIWELL 17

|||||:|||||:|

DB 274 VVARSGKEDLIWKL 290

RESULT 13

ID 06LC78 PRELIMINARY; PRT; 117 AA.

AC 06LC78; 05-JUL-2004 (TREMblrel. 27, Created)

DT 05-JUL-2004 (TREMblrel. 27, last sequence update)

DE 05-JUL-2004 (TREMblrel. 27, last annotation update)

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1] SEQUENCE FROM N.A.

RC STRAIN=Holstein;

RA Noble M.S., Hurley W.L.; Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Transferrins are iron binding transport proteins which bind ferric iron in association with the binding of an anion, usually bicarbonate (By similarity).

CC -1- SIMILARITY: Belongs to the transferrin family.

CC EMBL; U82254; AAB62030.1; -.

DR HSSP; Q29477; IWL.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0008199; F:ferric iron binding; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0006879; P:iron ion homeostasis; IEA.

DR GO; GO:0006826; P:iron ion transport; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR002197; HTH_Fla.

DR Pfam; PF00405; Transferrin; 1.

DR PRINTS; PR01590; HTHFRS.

DR SMART; SM00094; TR_FER; 1.

DR PROSITE; PS00207; TRANSFERRIN_3; 1.

KW Iron transport; Metal-binding; Transport.

FT NON_TER 1 1

FT NON_TER 117 117

SQ SEQUENCE 117 AA; 13206 MW; FD344261BD056BE6 CRC64;

Query Match 82.6%; Score 71; DB 2; Length 117;

Best Local Similarity 82.4%; Pred. No. 0.00038; 1; Indels 0; Gaps 0;

Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSGKEDLIWELL 17

DB 39 VVARSVGKEDLIWKL 55

RESULT 14

ID 06LBN7 PRELIMINARY; PRT; 681 AA.

AC 06LBN7; 05-JUL-2004 (TREMblrel. 27, Created)

DT 05-JUL-2004 (TREMblrel. 27, last sequence update)

DE 05-JUL-2004 (TREMblrel. 27, last annotation update)

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1] SEQUENCE FROM N.A.

RC TISSUE=Mammary;

RX MEDLINE=9108328; PubMed=2263492;

RA Mead P.E., Tweedie J.W.;

```

RT "cDNA and protein sequence of bovine lactoferrin."
RT Nucleic Acids Res. 18:7167-7167(1990).
RU [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary;
RA Tweedie J.;
RU Submitted (JAN-1991) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC bind ferric iron in association with the binding of an anion,
CC usually bicarbonate (By similarity).
CC -1- DOMAIN: Composed of two homologous domains (By similarity).
CC -1- SIMILARITY: Belongs to the transferrin family.
DR EMBL; X54801; CAA38572.1; -.
DR HSP; 029477; JMW1.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR01156; Peptidase_S60.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_PRR; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
DR Iron transport; Metal-binding; Transport.
KW NON TER
FT CHAIN 1 681 Bovine lactoferrin.
SQ SEQUENCE 681 AA; 75181 MW; 4927DE88144D99BA CRC64;

```

Query Match 82.6%; Score 71; DB 2; Length 681;
Best Local Similarity 82.4%; Pred. No. 0.0023;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 VVARGMGKEDLIWELL 17
    |||||:|||||:|
Db 247 VVARSVDGKEDLIWKL 263

```

RESULT 15

TRFL_BOVIN	STANDARD;	PRT;	708 AA.
ID	P24627; Q29629; Q9MZ73;		
AC	01-MAR-1992 (Rel. 21, Created)		
DT	01-OCT-1993 (Rel. 27, Last sequence update)		
DR	25-OCT-2004 (Rel. 45, Last annotation update)		
DE	Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferricin B (Lfcin B)]		
GN	Name=Lrf;		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovinae; Bos		
OK	NCBI_TaxId=9913;		
RN	(1)		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Submaxillary gland;		
RX	MEDLINE=91160550; PubMed=2001696;		
RA	Pierce A., Colavizza D., Benaisa M., Mee P., Tartar A.,		
RA	Montreuil J., Spik G.,		
RT	"Molecular cloning and sequence analysis of bovine lactotransferrin."		
RL	Eur. J. Biochem. 196;177-184(1991).		
RN	(2)		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=92028986; PubMed=1718281;		
RA	Goodman R.E., Schanbacher F.L.;		
RA	"Bovine lactoferrin mRNA: sequence, analysis, and expression in the		
RT	mammary gland."		
RL	Biochem. Biophys. Res. Commun. 180;75-84(1991).		
RN	(3)		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Lung;		
RA	Tsang T.C., Burns D.K., Wang F., Pan Y.C.E., Schmidt A.M., Stern D.;		

```

RT "Cloning of a 80-kD advanced glycosylation end product (AGE) binding
RT protein from bovine lung."
RT FASEB J. 6:233-233(1991).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood, and Mammary gland;
RX MEDLINE=9426164; PubMed=8206385; DOI=10.1016/0378-1119(94)90108-2;
RA Seyfert H.-M., Tuckorick A., Interthal H., Koczan D., Hobom G.
RT "Structure of the bovine lactoferrin-encoding gene and its promoter."
RL Gene 143:265-269(1994).
RN [5]
RP SEQUENCE FROM N.A.
RA Nakamura I., Shinazaki K., Yagi Y., Watanabe A.
RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
RN [6]
RP SEQUENCE OF 20-59.
RX MEDLINE=90031466; PubMed=2805645;
RA Rejman J.U., Hegarty H.M., Hurley W.L.
RT "Purification and characterization of bovine lactoferrin from
RT secretions of the involuting mammary gland: identification of multiple
RT molecular weight forms."
RL Comp. Biochem. Physiol. 93B:929-934(1989).
RN [7]
RP FUNCTION OF LACTOFERRICIN.
RX PubMed=8980754;
RA Hoek K.S., Milne J.M., Griewe P.A., Dionysius D.A., Smith R.
RT "Antibacterial activity in bovine lactoferrin-derived peptides."
RL Antimicrob. Agents Chemother. 41:54-59(1997).
RN [8]
RP ANTIMICROBIAL ACTIVITY.
RX PubMed=14650542;
RA Kurita T., Pyorala S., Saloniemi H., Kaartinen L.
RT "Antibacterial effect of bovine lactoferrin against udder pathogens."
RL Acta Vet. Scand. 44:35-42(2003).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=98062367; PubMed=9398529; DOI=10.1006/jmbi.1997.1386;
RA Moore S.A., Anderson B.F., Groom C.R., Haridas M., Baker E.N.
RT "Three-dimensional structure of dimeric bovine lactoferrin at 2.8-A
RT resolution."
RL J. Mol. Biol. 274:222-236(1997).
RN [10]
RP STRUCTURE BY NMR OF 36-60.
RX MEDLINE=98190007; PubMed=9521752; DOI=10.1021/bi972323m;
RA Hwang P.M., Zhou N., Shan X., Arrowmith C.H., Vogel H.J.
RT "Three-dimensional solution structure of lactoferricin B, an
RT antimicrobial peptide derived from bovine lactoferrin."
RL Biochemistry 37:4288-4298(1998).
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC can bind two atoms of ferric iron in association with the binding
CC of an anion, usually bicarbonate.
CC -1- FUNCTION: Lactotransferrin has antimicrobial activity. The most
CC effective inhibitory activity was seen against E.coli and
CC P.aeruginosa.
CC -1- FUNCTION: Lactoferricin B is an antimicrobial peptide. Inhibits
CC the growth of Gram-negative and Gram-positive bacteria.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: Composed of two homologous domains.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X57084; CAA40366.1; -.
DR EMBL; M63502; AAA30617.1; -.
DR EMBL; U08604; AAA30609.1; -.
DR EMBL; U19933; AAA21722.1; -.

```

DR EMBL; L19983; AAA21722.1; JOINED.
 DR EMBL; L19983; AAA21722.1; JOINED.
 DR EMBL; L19984; AAA21722.1; JOINED.
 DR EMBL; L19985; AAA21722.1; JOINED.
 DR EMBL; L19986; AAA21722.1; JOINED.
 DR EMBL; L19986; AAA21722.1; JOINED.
 DR EMBL; L19989; AAA21722.1; JOINED.
 DR EMBL; L19991; AAA21722.1; JOINED.
 DR EMBL; L19992; AAA21722.1; JOINED.
 DR EMBL; AB046664; BAB03470.1; -.
 DR PIR; I45919; TFEOL.
 DR PDB; 1BLF; X-ray; @=20-708.
 DR PDB; 1LFC; NMR; @=36-60.
 DR PDB; 1NKC; X-ray; A=361-708.
 DR GlycoSuiteDB; P24627; -.
 DR InterPro; IPR001156; Peptidase_S60.
 DR Pfam; PF00405; Transferrin_2.
 DR PRINTS; PRO0422; TRANSFERRIN.
 DR SMART; SM00094; TR_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN_1; 2.
 DR PROSITE; PS00206; TRANSFERRIN_2; 2.
 DR PROSITE; PS00207; TRANSFERRIN_3; 2.
 DR 3D-structure; Antibiotic; Direct protein sequencing; Glycoprotein;
 KM Iron transport; Metal-binding; Repeat; Signal; Transport.
 PT SIGNAL 1 19
 FT CHAIN 20 708 Lactotransferrin.
 FT PEPTIDE 36 60 Lactoferricin B.
 FT REPEAT 20 363 1.
 FT REPEAT 364 708 2.
 FT DISULFID 28 64 By similarity.
 FT DISULFID 38 55 By similarity.
 FT DISULFID 134 217 By similarity.
 FT DISULFID 176 192 By similarity.
 FT DISULFID 189 200 By similarity.
 FT DISULFID 250 264 By similarity.
 FT DISULFID 367 399 By similarity.
 FT DISULFID 377 390 By similarity.
 FT DISULFID 424 703 By similarity.
 FT DISULFID 444 666 By similarity.
 FT DISULFID 476 551 By similarity.
 FT DISULFID 500 694 By similarity.
 FT DISULFID 510 524 By similarity.
 FT DISULFID 521 534 By similarity.
 FT DISULFID 592 606 By similarity.
 FT DISULFID 644 649 By similarity.
 FT METAL 79 79 Iron 1.
 FT METAL 111 111 Iron 1.
 FT METAL 211 211 Iron 1.
 FT METAL 272 272 Iron 1.
 FT METAL 414 414 Iron 2.
 FT METAL 452 452 Iron 2.
 FT METAL 545 545 Iron 2.
 FT METAL 614 614 Iron 2.
 FT BINDING 136 136 Carbonate 1.
 FT BINDING 140 140 Carbonate 1 (via amide nitrogen).
 FT BINDING 142 142 Carbonate 1 (via amide nitrogen).
 FT BINDING 143 143 Carbonate 1 (via amide nitrogen).
 FT BINDING 178 178 Carbonate 2.
 FT BINDING 482 482 Carbonate 2 (via amide nitrogen).
 FT BINDING 484 484 Carbonate 2 (via amide nitrogen).
 FT BINDING 485 485 Carbonate 2 (via amide nitrogen).
 FT CARBOHYD 252 252 N-linked (GlcNAc...).
 FT CARBOHYD 387 387 /FTid=CAR_000186.
 FT CARBOHYD 495 495 N-linked (GlcNAc...).
 FT CARBOHYD 495 495 N-linked (GlcNAc...).
 FT CARBOHYD 564 564 /FTid=CAR_000197.
 FT CARBOHYD 564 564 N-linked (GlcNAc...).
 FT CARBOHYD 564 564 /FTid=CAR_000198.
 FT CARBOHYD 564 564 E-> A (in Ref. 4).
 FT CARBOHYD 63 63 RA-> PG (in Ref. 2).
 FT CARBOHYD 66 67 I-> V (in Ref. 1 and 4).
 FT CARBOHYD 145 145 LQ-> PP (in Ref. 1).
 FT CARBOHYD 164 164

FT CONFLICT 264 264 C -> Y (in Ref. 4).
 FT CONFLICT 273 273 A -> P (in Ref. 4).
 FT CONFLICT 281 281 G -> A (in Ref. 4).
 FT CONFLICT 291 291 S -> R (in Ref. 4).
 FT CONFLICT 297 297 F -> S (in Ref. 2).
 FT CONFLICT 340 340 G -> A (in Ref. 1).
 FT CONFLICT 418 418 I -> V (in Ref. 4).
 FT CONFLICT 439 439 H -> Y (in Ref. 4).
 FT CONFLICT 459 459 K -> R (in Ref. 1).
 FT CONFLICT 514 514 A -> R (in Ref. 1).
 FT CONFLICT 632 632 H -> R (in Ref. 5).
 FT STRAND 25 29
 FT HELIX 32 45
 FT HELIX 46 48
 FT STRAND 53 57
 FT HELIX 61 69
 FT TURN 70 71
 FT STRAND 75 78
 FT HELIX 80 87
 FT TURN 89 91
 FT STRAND 93 102
 FT STRAND 107 108

Query Match 82.6%; Score 71; DB 1; Length 708;
 Best Local Similarity 82.4%; Pred. No. 0.0024; 1; Indels 0; Gaps 0;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 VVARSMGKEDLIWELL 17
 Db 274 VVARSVGKEDLIWKL 290

Search completed: November 1, 2005, 12:54:29
 Job time : 85.25 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

CM protein - protein search, using sw model

Run on: November 1, 2005, 12:56:01 ; Search time 162 Seconds
(without alignments)

40,586 Million cell updates/sec

Title: US-10-612-162a-1

Sequence: 1 VVARSMSGKEDLIWELL 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 664154

Minimum DB seq length: 0
Maximum DB seq length: 17

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	17	8	ADG46075
2	70	81.4	13	8	ADG46088
3	69	80.2	13	8	ADG46089
4	43	50.0	17	8	ADRI5903
5	43	50.0	17	8	ADRI5963
6	43	50.0	17	8	ADSI3216
7	35	40.7	13	2	AAR49486
8	35	40.7	13	2	AAR47038
9	35	40.7	15	2	AAR49426
10	35	39.5	15	6	ABR30177
11	33	38.4	9	8	ADRI9363
12	33	38.4	13	5	ABP63629
13	33	38.4	13	5	ABP63628
14	33	38.4	13	5	ABP63627
15	33	38.4	13	5	ABP63627
16	33	38.4	13	5	AAE27219
17	33	38.4	13	5	AAE27218
18	33	38.4	13	5	AAE27220
19	32	37.2	10	7	ADLI7482
20	32	37.2	14	4	ABBS6643
21	32	37.2	15	6	ABR33637
22	32	37.2	15	6	ABR33654
23	32	37.2	15	6	ABR33753
24	32	37.2	15	6	ABR33660
25	32	37.2	15	8	ADRE8334

26	31	36.0	6	8	AD085220	AD085220 Milk proc
27	31	36.0	6	8	AD067999	Ad067999 TNP-alpha
28	31	36.0	9	4	AA099695	AA099695 ERA bindi
29	31	36.0	9	4	AA099702	AA099702 ERA bindi
30	31	36.0	15	7	ADM75931	Adm75931 Human MHC
31	31	36.0	9	7	AD066590	Ad066590 Human MHC
32	30	34.9	9	7	AD067321	Ad067321 Human MHC
33	30	34.9	9	7	AD067560	Ad067560 Human MHC
34	30	34.9	9	7	AD067775	Ad067775 Human MHC
35	30	34.9	9	7	AD069001	Ad069001 Human MHC
36	30	34.9	9	7	AD066352	Ad066352 Human MHC
37	30	34.9	9	7	AD066836	Ad066836 Human MHC
38	30	34.9	9	7	AD067558	Ad067558 Human MHC
39	30	34.9	9	7	AD066106	Ad066106 Human MHC
40	30	34.9	9	7	AD066111	Ad066111 Human MHC
41	30	34.9	9	7	AD068044	Ad068044 Human MHC
42	30	34.9	9	7	AD066593	Ad066593 Human MHC
43	30	34.9	9	7	AD067316	Ad067316 Human MHC
44	30	34.9	9	7	AD068899	Ad068899 Human MHC
45	30	34.9	9	7	AD066345	Ad066345 Human MHC

ALIGNMENTS

RESULT 1
ID ADG46075 standard; peptide, 17 AA.
XX
AC ADG46075;
DT 25-MAR-2004 (first entry)
XX
DE Human CDT peptide fragment #1.
XX
KW antibody; carbohydrate-deficient transferrin; CDT;
KW non-glycosylated transferrin; alcoholism; alcoholic; diagnosis; human.
XX
OS Homo sapiens.
XX
PN EP1378521-A1.
XX
PD 07-JAN-2004.
XX
PF 19-MAY-2003; 2003EP-00011334.
XX
PR 05-JUL-2002; 2002DE-01030550.
XX
PA (DADE-) DADE BEHRING MAREBURG GMBH.
XX
PI Althaus H;
XX
DR WPI; 2004-073743/08.
XX
PT New antibody specific for carbohydrate-deficient transferrin, useful for
PT diagnosis of alcoholism, can bind its target in solution, eliminating
PT need for immobilization.
XX
PS Claim 4; SEQ ID NO 1; 21pp; German.
XX
CC This invention describes a novel antibody that, in aqueous solution,
CC binds selectively to carbohydrate-deficient transferrin (CDT) without
CC having to bind CDT to a solid phase. The invention also describes an
CC antibody that binds selectively to CDT at regions containing the
CC sequences VVARSMSGKEDLIWELL, TTEDSIKTIWNGEADAMSIDGAF, SKLSMSGSLNISEPN and
CC YEKLYGEYVAV (ADG46075-ADG46078) and an immunoassay for detecting CDT
CC using the antibodies of the invention. The antibodies of the invention
CC are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
CC antibodies are obtained by immunisation with non-glycosylated
CC transferrin, or a fragment, then generation of hybridomas by standard
CC fusion of spleen and myeloma cells. Hybridomas are then selected for
CC production of antibodies that specifically bind CDT from the aqueous
CC phase. The antibodies are useful for diagnosis of alcoholism, CDT, which

CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
 CC alcohols. The antibodies allow direct detection of CDT in solution,
 CC eliminating the need for immobilizing it on a solid phase (as required
 CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
 CC fragments used in the method of the invention.

XX Sequence 17 AA;

Query Match 100.0%; Score 86; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.8e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSWGKEDLIWEIL 17
 |||||
 DB 1 VVARSWGKEDLIWEIL 17

RESULT 2
 ADG46088

ID ADG46088 standard; peptide; 13 AA.

XX ADG46088;

XX 25-MAR-2004 (first entry)

XX Human CDT peptide fragment #14.

XX antibody; carbohydrate-deficient transferrin; CDT;
 KW non-glycosylated transferrin; alcoholic; diagnosis; human.

XX Homo sapiens.

XX EPI378521-A1.

XX 07-JAN-2004.

XX 19-MAY-2003; 2003EP-00011334.

XX 05-JUL-2002; 2002DE-01030550.

XX (DADE-) DADE BEHRING MARBURG GMBH.

XX Althaus H;

XX WPI; 2004-073743/08.

XX New antibody specific for carbohydrate-deficient transferrin, useful for
 PT diagnosis of alcoholism, can bind its target in solution, eliminating
 PT need for immobilization.

XX Example 7; Page 15; 21pp; German.

XX This invention describes a novel antibody that, in aqueous solution,
 CC binds selectively to carbohydrate-deficient transferrin (CDT) without
 CC having to bind CDT to a solid phase. The invention also describes an
 CC antibody that binds selectively to CDT at regions containing the
 CC sequences VVARSWGKEDLIWEIL, TTEDSIKIMGEADAMSLDGF, SKUSMSGGLNLSBN and
 CC YEKYLGEYVAV (ADG46075-ADG46078) and an immunoassay for detecting CDT
 CC using the antibodies of the invention. The antibodies of the invention
 CC are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
 CC antibodies are obtained by immunisation with non-glycosylated
 CC transferrin, or a fragment, then generation of hybridomas by standard
 CC fusion of spleen and myeloma cells. Hybridomas are then selected for
 CC production of antibodies that specifically bind CDT from the aqueous
 CC phase. The antibodies are useful for diagnosis of alcoholism, CDT, which
 CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
 CC alcohols. The antibodies allow direct detection of CDT in solution,
 CC eliminating the need for immobilizing it on a solid phase (as required
 CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
 CC fragments used in the method of the invention.

XX Sequence 13 AA;

Query Match 81.4%; Score 70; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 9.9e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ARSWGKEDLIWE 15
 |||||
 DB 1 ARSWGKEDLIWE 13

RESULT 3
 ADG46089

ID ADG46089 standard; peptide; 13 AA.

XX ADG46089;

XX 25-MAR-2004 (first entry)

XX Human CDT peptide fragment #15.

XX antibody; carbohydrate-deficient transferrin; CDT;
 KW non-glycosylated transferrin; alcoholic; diagnosis; human.

XX Homo sapiens.

XX EPI378521-A1.

XX 07-JAN-2004.

XX 19-MAY-2003; 2003EP-00011334.

XX 05-JUL-2002; 2002DE-01030550.

XX (DADE-) DADE BEHRING MARBURG GMBH.

XX Althaus H;

XX WPI; 2004-073743/08.

XX New antibody specific for carbohydrate-deficient transferrin, useful for
 PT diagnosis of alcoholism, can bind its target in solution, eliminating
 PT need for immobilization.

XX Example 7; Page 15; 21pp; German.

XX This invention describes a novel antibody that, in aqueous solution,
 CC binds selectively to carbohydrate-deficient transferrin (CDT) without
 CC having to bind CDT to a solid phase. The invention also describes an
 CC antibody that binds selectively to CDT at regions containing the
 CC sequences VVARSWGKEDLIWEIL, TTEDSIKIMGEADAMSLDGF, SKUSMSGGLNLSBN and
 CC YEKYLGEYVAV (ADG46075-ADG46078) and an immunoassay for detecting CDT
 CC using the antibodies of the invention. The antibodies of the invention
 CC are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
 CC antibodies are obtained by immunisation with non-glycosylated
 CC transferrin, or a fragment, then generation of hybridomas by standard
 CC fusion of spleen and myeloma cells. Hybridomas are then selected for
 CC production of antibodies that specifically bind CDT from the aqueous
 CC phase. The antibodies are useful for diagnosis of alcoholism, CDT, which
 CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
 CC alcohols. The antibodies allow direct detection of CDT in solution,
 CC eliminating the need for immobilizing it on a solid phase (as required
 CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
 CC fragments used in the method of the invention.

XX Sequence 13 AA;

Query Match 80.2%; Score 69; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SMGKEDLIWEIL 17
 |||||
 DB 1 SMGKEDLIWEIL 13

RESULT 4
ADRI5903
ID ADRI5903 standard; peptide; 17 AA.
XX
AC ADRI5903;
XX
DT 04-NOV-2004 (first entry)
XX
DE Transferrin peptide fragment #61.
XX
KM glycosylation; proteolytic enzyme; proteolysis; detection; transferrin.
XX
OS Synthetic.
XX
PN WO2004070389-A1.
XX
PD 19-AUG-2004.
XX
PF 06-FEB-2004; 2004WO-GB000480.
XX
PR 06-FEB-2003; 2003GB-00002740.
XX
PA (AXIS-) AXIS-SHIELD ASA.
XX
PI Rye PD;
XX
DR WPI; 2004-625547/60.
XX
XX
PT Assay for differentiating protein isoforms to determine their
PT concentrations in sample e.g. blood, involves contacting the sample with
PT proteolytic enzyme to produce peptide fragment by proteolysis followed by
PT detecting.
XX
XX
PS Disclosure; Page 15; 30pp; English.
XX
CC The present invention describes an assay for a protein having at least
CC two isoforms with different glycosylation patterns. The assay involves
CC contacting a sample containing the protein with a proteolytic enzyme,
CC followed by detecting the content or relative content of at least one
CC peptide fragment produced by proteolysis. Also described is a kit for the
CC assay method comprising the proteolytic enzyme and a substrate bound
CC specific binding partner (SI) for at least 2 of the isoforms of the
CC proteins. The method can be used for assaying isoforms of proteins
CC according to their glycosylation pattern to determine their concentration
CC or relative concentration in the sample or material (e.g. blood). The
CC method avoids use of antibodies for distinguishing between glycosylated
CC isoforms of the proteins. The present sequence represents a transferrin
CC peptide fragment which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 17 AA;
XX
Query Match 50.0%; Score 43; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.5; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 EDLIWELL 17
DB 1 EDLIWELL 8
XX
RESULT 5
ADRI5963
ID ADRI5963 standard; peptide; 17 AA.
XX
AC ADRI5963;
XX
DT 04-NOV-2004 (first entry)
XX
DE Transferrin peptide fragment #121.
XX
KM glycosylation; proteolytic enzyme; proteolysis; detection; transferrin.
XX

XX
OS Synthetic.
XX
PN WO2004070389-A1.
XX
PD 19-AUG-2004.
XX
PF 06-FEB-2004; 2004WO-GB000480.
XX
PR 06-FEB-2003; 2003GB-00002740.
XX
PA (AXIS-) AXIS-SHIELD ASA.
XX
PI Rye PD;
XX
DR WPI; 2004-625547/60.
XX
PT Assay for differentiating protein isoforms to determine their
PT concentrations in sample e.g. blood, involves contacting the sample with
PT proteolytic enzyme to produce peptide fragment by proteolysis followed by
PT detecting.
XX
XX
PS Disclosure; Page 17; 30pp; English.
XX
CC The present invention describes an assay for a protein having at least
CC two isoforms with different glycosylation patterns. The assay involves
CC contacting a sample containing the protein with a proteolytic enzyme,
CC followed by detecting the content or relative content of at least one
CC peptide fragment produced by proteolysis. Also described is a kit for the
CC assay method comprising the proteolytic enzyme and a substrate bound
CC specific binding partner (SI) for at least 2 of the isoforms of the
CC proteins. The method can be used for assaying isoforms of proteins
CC according to their glycosylation pattern to determine their concentration
CC or relative concentration in the sample or material (e.g. blood). The
CC method avoids use of antibodies for distinguishing between glycosylated
CC isoforms of the proteins. The present sequence represents a transferrin
CC peptide fragment which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 17 AA;
XX
Query Match 50.0%; Score 43; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.5; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 EDLIWELL 17
DB 1 EDLIWELL 8
XX
RESULT 6
ADSI3216
ID ADSI3216 standard; peptide; 17 AA.
XX
AC ADSI3216;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human rheumatoid arthritis marker peptide - SEQ ID 7.
XX
KM rheumatoid arthritis; marker; antiinflammatory; antiarthritic.
XX
OS Homo sapiens.
XX
PN WO2004082617-A2.
XX
PD 30-SEP-2004.
XX
PF 15-MAR-2004; 2004WO-US007880.
XX
PR 14-MAR-2003; 2003US-0455037P.
XX
PA (SURR-) SURROWED INC.
XX

```

XX XX Kantor AB, Becker CH, Schulman H;
PI XX
XX XX WPI; 2004-690929/67.
DR XX
XX XX New isolated marker for rheumatoid arthritis, useful in preparing a
PT XX composition for diagnosing or treating rheumatoid arthritis.
XX PS
XX PS Claim 1, SEQ ID NO 7, 184pp; English.
XX
CC The invention relates to a novel isolated marker for rheumatoid arthritis
CC selected from one of many (around 400) markers defined in the
CC specification. Rheumatoid arthritis is a chronic inflammatory disorder of
CC the small joints which is estimated to affect 2.1 million people in the
CC United States alone. Current approaches to treat the disease include the
CC use of non-steroidal antiinflammatory drugs (NSAIDs), which may reduce
CC pain, swelling and inflammation, and disease-modifying anti-rheumatic
CC drugs (DMARDs), which act to slow the progression of the disease and
CC avoid further joint injury. These drugs are associated with a number of
CC serious side effects and the search for improved therapeutics is a
CC subject of active research. The marker of the invention demonstrates
CC antirheumatic activity and may be useful in preparing a composition for
CC diagnosing or treating rheumatoid arthritis. The current sequence is that
CC of a human rheumatoid arthritis marker peptide of the invention.
CC
SQ Sequence 17 AA;
Query Match 50.0%; Score 43; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.5; Mismatches 0; Gaps 0;
Matches 8; Conservative 0; Indels 0;
OY 10 EDLWEL 17
DB 1 EDLWEL 8
RESULT 7
AAR49486
ID AAR49486 standard; protein; 13 AA.
XX AC
XX AC AAR49486;
XX
XX 25-MAR-2003 (revised)
DT 16-SEP-1994 (first entry)
XX
XX Bovine transferrin position 261-273.
DE
XX
XX Naturally-occurring; immunomodulatory protein; human; therapy; class I;
XX major histocompatibility complex; class II; allotype; type I diabetes;
XX autoimmune disease; rheumatoid arthritis; T-cell-mediated response;
XX multiple sclerosis; transplant rejection; vaccine; MHC.
OS
XX Bos taurus.
XX
XX WO9404171-A1.
XX
XX 03-MAR-1994.
XX
XX 11-AUG-1993; 93WO-US007545.
XX
XX 11-AUG-1992; 92US-00925460.
XX
XX 15-JUN-1993; 93US-00077255.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Urban RG, Chicz RM, Vignali DA, Hedley ML, Stern LJ;
PI Strominger JL;
XX
XX WPI; 1994-082825/10.
DR
XX Novel immunomodulatory peptide(s) and nucleic acids - useful for
PT treatment of autoimmune diseases, transplant rejection and for
PT vaccination.

```

```

XX XX Disclosure; Page 49; 139pp; English.
PS XX
XX XX The sequences given in AAR49291-505 and AAR46981-7038 represent peptide
CC fragments of naturally-occurring immunomodulatory proteins. These
CC fragments are between 10-30 residues in length and bind to a human major
CC histocompatibility complex (MHC) class II allotype. These peptides may be
CC used for therapy of autoimmune diseases, such as type I diabetes,
CC rheumatoid arthritis and multiple sclerosis, and to reduce transplant
CC rejection. They may also be used for vaccination providing an exclusively
CC T-cell-mediated response, which can be class I or class-II based, or
CC both, depending on the length and character of the immunogenic peptides.
CC (updated on 25-MAR-2003 to correct PN field.) (updated on 25-MAR-2003 to
CC correct PR field.)
XX
SQ Sequence 13 AA;
Query Match 40.7%; Score 35; DB 2; Length 13;
Best Local Similarity 85.7%; Pred. No. 73;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 11 DLWEL 17
DB 1 DLWEL 7
RESULT 8
AAR47038
ID AAR47038 standard; protein; 15 AA.
XX AC
XX AC AAR47038;
XX
XX 25-MAR-2003 (revised)
DT 16-SEP-1994 (first entry)
XX
XX Bovine transferrin position 261-275.
DE
XX
XX Naturally-occurring; immunomodulatory protein; human; therapy; class I;
XX major histocompatibility complex; class II; allotype; type I diabetes;
XX autoimmune disease; rheumatoid arthritis; T-cell-mediated response;
XX multiple sclerosis; transplant rejection; vaccine; MHC.
XX
XX Bos taurus.
XX
XX WO9404171-A1.
XX
XX 03-MAR-1994.
XX
XX 11-AUG-1993; 93WO-US007545.
XX
XX 11-AUG-1992; 92US-00925460.
XX
XX 15-JUN-1993; 93US-00077255.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Urban RG, Chicz RM, Vignali DA, Hedley ML, Stern LJ;
PI Strominger JL;
XX
XX WPI; 1994-082825/10.
DR
XX Novel immunomodulatory peptide(s) and nucleic acids - useful for
PT treatment of autoimmune diseases, transplant rejection and for
PT vaccination.
XX
XX Disclosure; Page 49; 139pp; English.
XX
XX The sequences given in AAR49291-505 and AAR46981-7038 represent peptide
CC fragments of naturally-occurring immunomodulatory proteins. These
CC fragments are between 10-30 residues in length and bind to a human major
CC histocompatibility complex (MHC) class II allotype. These peptides may be
CC used for therapy of autoimmune diseases, such as type I diabetes,
CC rheumatoid arthritis and multiple sclerosis, and to reduce transplant
CC rejection. They may also be used for vaccination providing an exclusively

```

CC T-cell-mediated response, which can be class I or class-II based, or
 CC both, depending on the length and character of the immunogenic peptides.
 CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to
 CC correct PR field.)
 CC
 XX
 SQ Sequence 15 AA;

Query Match 40.7%; Score 35; DB 2; Length 15;
 Best Local Similarity 85.7%; Pred. No. 85;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 DLIWELL 17
 |:|||||
 Db 1 DVIWELL 7

RESULT 9
 AAR49426
 ID AAR49426 standard; protein; 15 AA.

AC AAR49426;
 DT 25-MAR-2003 (revised)
 DT 16-SEP-1994 (first entry)

XX Immunomodulatory peptide fragment #1.

XX Naturally-occurring; immunomodulatory protein; human; therapy; class I;
 KW major histocompatibility complex; class II; allotype; type I diabetes;
 KW autoimmune disease; rheumatoid arthritis; T-cell-mediated response;
 XX multiple sclerosis; transplant rejection; vaccine; MHC.

OS Homo sapiens.

PN WO9404171-A1.

XX 03-MAR-1994.

PD 11-AUG-1993; 93WO-US007545.

XX 11-AUG-1992; 92US-00925460.

PR 15-JUN-1993; 93US-00077255.

XX (HARD) HARVARD COLLEGE.

PI Urban RG, Chiciz RM, Vignani DA, Hedley ML, Stern LJ;
 PI Strominger JL;

XX WPI; 1994-082825/10.

XX Novel immunomodulatory peptide(s) and nucleic acids - useful for
 PT treatment of auto-immune diseases, transplant rejection and for
 PT vaccination.

XX Disclosure; Page 89; 139pp; English.

XX The sequences given in AAR49291-505 and AAR46981-7038 represent peptide
 CC fragments of naturally-occurring immunomodulatory proteins. These
 CC fragments are between 10-30 residues in length and bind to a human major
 CC histocompatibility complex (MHC) class II allotype. These peptides may be
 CC used for therapy of autoimmune diseases, such as type I diabetes,
 CC rheumatoid arthritis and multiple sclerosis, and to reduce transplant
 CC rejection. They may also be used for vaccination providing an exclusively
 CC T-cell-mediated response, which can be class I or class-II based, or
 CC both, depending on the length and character of the immunogenic peptides.
 CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to
 CC correct PR field.)
 CC
 XX

SQ Sequence 15 AA;

Query Match 40.7%; Score 35; DB 2; Length 15;
 Best Local Similarity 85.7%; Pred. No. 85;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 DLIWELL 17
 |:|||||
 Db 1 DVIWELL 7

RESULT 10

ID ABR30177
 ID ABR30177 standard; peptide; 15 AA.

AC ABR30177;

DT 19-MAY-2003 (first entry)

XX Human cancer-related protein 74P33 HLA peptide #3021.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.

OS Homo sapiens.

PN WO200283921-A2.

PD 24-OCT-2002.

PP 10-APR-2002; 2002WO-US011654.

XX 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.

XX Claim 13; Page 470; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 CC
 XX

SQ Sequence 15 AA;

Query Match 39.5%; Score 34; DB 6; Length 15;
 Best Local Similarity 41.7%; Pred. No. 13e+02;
 Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 4 RSMGKEDLIWE 15
 |:|||||
 Db 4 ROOGGAHQAWME 15

RESULT 11

ID ADR19363
 ID ADR19363 standard; peptide; 9 AA.

AC ADR19363;
XX
DT 04-NOV-2004 (first entry)
XX
DE TRPI derived human tryptic digest peptide, SEQ ID 25.
XX
XX Tissue damage; chronic; tissue repair-associated protein isoform; TRPI;
KW antitumor; vulnerability; chronic dermal ulcer; human; tryptic digest;
XX proteolysis; trypsin.
XX
OS Homo sapiens.
XX
PN WO2004069795-A2.
XX
PD 19-AUG-2004.
XX
PF 02-FEB-2004; 2004WO-US002881.
XX
PR 03-FEB-2003; 2003US-044600P.
XX
XX (PFIZ) PFIZER PROD INC.
PA (OXFO-) OXFORD GLAXOSCIENCES UK LTD.
XX
PI But R, Rumpel K, Williams-Jones BI, Herath HMA, Rohlf C;
PI Bruce JA, Patel TP;
XX
DR WPI; 2004-604404/58.
XX
XX
PT Diagnosing, or monitoring the effect of therapy of, chronic tissue damage
PT (e.g. chronic dermal ulcer) comprises detecting and/or quantifying tissue
PT Repair-Associated protein isoform in a sample (e.g. wound exudate) from
PT the subject.
XX
PS Claim 7; SEQ ID NO 25; 107pp; English.
XX
XX The invention relates to a novel method for assessing, screening,
CC diagnosing or prognosing chronic tissue damage in a subject, identifying
CC a subject at risk of developing chronic tissue damage, or monitoring the
CC effect of therapy administered to a subject having chronic tissue damage.
CC The method comprises detecting and/or quantifying in a biological sample
CC from the subject a tissue repair-associated protein isoform (TRPI), given
CC in the specification. The invention further comprises: an isolated or
CC recombinant TRPI selected from the proteins listed in the specification;
CC screening for or identifying an agent capable of modulating the
CC expression or activity of the TRPI or a TRPI-related polypeptide; a
CC pharmaceutical composition comprising the TRPI cited above or an active
CC agent that modulates the expression and/or activity of the TRPI or a TRPI
CC -related polypeptide, and a pharmaceutical carrier, vehicle or diluent;
CC and treating chronic tissue damage. The novel compositions have antitumor
CC and vulnerability activity. The composition and methods are useful for
CC diagnosing, preventing, prognosing and treating chronic tissue damage,
CC such as a chronic dermal ulcer. These may also be used for drug screening
CC or drug development, or for screening or identifying agents capable of
CC modulating the activity of TRPI or TRPI-related polypeptides. This
CC sequence represents a TRPI derived human tryptic digest peptide. The
CC peptide was produced by proteolysis using trypsin of a tissue repair-
CC associated protein isoform of the invention.
XX
SQ Sequence 9 AA;
Query Match 38.4%; Score 33; DB 8; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 10 EDLIWELL 17
DB 1 EDALWML 8

RESULT 12
ABP63629
ID ABP63629 standard; peptide; 13 AA.
XX

AC ABP63629;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human MHC class II binding peptide #50.
XX
XX Human; obesity; leptin; T-cell epitope; diabetes; high blood pressure;
KW cholesterol metabolism; MHC class II.
XX
XX
OS Homo sapiens.
XX
PN WO200262833-A2.
XX
PD 15-AUG-2002.
XX
PF 05-FEB-2002; 2002WO-EP001188.
XX
PR 06-FEB-2001; 2001EP-00102618.
XX
PR 19-FEB-2001; 2001EP-00103954.
XX
XX (MERE) MERCK PATENT CMBH.
PA
XX Carr FJ, Carter G, Jones T, Williams S, Hamilton A;
PI
PI WPI; 2002-643399/69.
XX
DR
XX
XX Modified forms of human obesity protein, for therapeutic use, in which
PT the immune characteristic is modified by means of reduced or removed
PT numbers of potential T-cell epitopes.
XX
PS Claim 6; Page 11; 32pp; English.
XX
XX The invention relates to a novel modified molecule with the biological
CC activity of human obesity protein (leptin) which is substantially non-
CC immunogenic or less immunogenic than any non-modified molecule with the
CC same biological activity when used in vivo. The immune characteristic of
CC the protein is modified by means of reduced/removed numbers of potential
CC T-cell epitopes. The modified proteins have therapeutic potential for the
CC treatment of diabetes, high blood pressure, and cholesterol metabolism.
CC The sequence represents a peptide of the invention contained in human
CC leptin with potential human MHC class II binding activity
XX
SQ Sequence 13 AA;
Query Match 38.4%; Score 33; DB 5; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 7 GSKEDLIWEL 16
DB 1 GSLQDMLWQL 10

RESULT 13
ABP63628
ID ABP63628 standard; peptide; 13 AA.
XX
XX
AC ABP63628;
XX
DT 05-NOV-2002 (first entry)
XX
XX
DE Human MHC class II binding peptide #49.
XX
XX Human; obesity; leptin; T-cell epitope; diabetes; high blood pressure;
KW cholesterol metabolism; MHC class II.
XX
XX
OS Homo sapiens.
XX
PN WO200262833-A2.
XX
PD 15-AUG-2002.
XX
PF 05-FEB-2002; 2002WO-EP001188.

```

XX 06-FEB-2001; 2001EP-00102618.
PR 19-FEB-2001; 2001EP-00103954.
XX (MERE ) MERCK PATENT GMBH.
XX PA Carr FJ, Carter G, Jones T, Williams S, Hamilton A;
XX PI WPI; 2002-643399/69.
XX DR
XX Modified forms of human obesity protein, for therapeutic use, in which
PT the immune characteristic is modified by means of reduced or removed
XX numbers of potential T-cell epitopes.
XX PS Claim 6; Page 11; 32pp; English.
XX
CC The invention relates to a novel modified molecule with the biological
CC activity of human obesity protein (leptin) which is substantially non-
CC immunogenic or less immunogenic than any non-modified molecule with the
CC same biological activity when used in vivo. The immune characteristic of
CC the protein is modified by means of reduced/removed numbers of potential
CC T-cell epitopes. The modified proteins have therapeutic potential for the
CC treatment of diabetes, high blood pressure, and cholesterol metabolism.
CC The sequence represents a peptide of the invention contained in human
CC leptin with potential human MHC class II binding activity
XX
SQ Sequence 13 AA;
XX
Query Match      38.4%; Score 33; DB 5; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 7 GGEKEDLIWEI 16
   | : : : : |
Db 2 GSLLQDMLWQL 11
XX
RESULT 14
ABP63627
ID ABP63627 standard; peptide; 13 AA.
XX
AC ABP63627;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human MHC class II binding peptide #48.
XX
KW Human; obesity; leptin; T-cell epitope; diabetes; high blood pressure;
KW cholesterol metabolism; MHC class II.
XX
OS Homo sapiens.
XX
PN WO200262833-A2.
XX
PD 15-AUG-2002.
XX
PR 05-FEB-2002; 2002WO-EP001188.
XX
PR 06-FEB-2001; 2001EP-00102618.
PR 19-FEB-2001; 2001EP-00103954.
XX
PA (MERE ) MERCK PATENT GMBH.
XX
PI Carr FJ, Carter G, Jones T, Williams S, Hamilton A;
XX
DR WPI; 2002-643399/69.
XX
PT Modified forms of human obesity protein, for therapeutic use, in which
PT the immune characteristic is modified by means of reduced or removed
XX numbers of potential T-cell epitopes.
XX PS Claim 6; Page 11; 32pp; English.
XX

```

```

CC The invention relates to a novel modified molecule with the biological
CC activity of human obesity protein (leptin) which is substantially non-
CC immunogenic or less immunogenic than any non-modified molecule with the
CC same biological activity when used in vivo. The immune characteristic of
CC the protein is modified by means of reduced/removed numbers of potential
CC T-cell epitopes. The modified proteins have therapeutic potential for the
CC treatment of diabetes, high blood pressure, and cholesterol metabolism.
CC The sequence represents a peptide of the invention contained in human
CC leptin with potential human MHC class II binding activity
XX
SQ Sequence 13 AA;
XX
Query Match      38.4%; Score 33; DB 5; Length 13;
Best Local Similarity 30.8%; Pred. No. 1.6e+02;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 3 ARSMGKEDLIWE 15
   | | : : : |
Db 1 SRLQGSLLQDMLWQ 13
XX
RESULT 15
AAE27219
ID AAE27219 standard; peptide; 13 AA.
XX
AC AAE27219;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human obesity protein (leptin) peptide #49.
XX
KW Human; fusion protein; immunological; major histocompatibility complex;
KW MHC; nausea; gastric upset; obesity protein; leptin.
XX
OS Homo sapiens.
XX
PN WO200266514-A2.
XX
PD 29-AUG-2002.
XX
PR 18-FEB-2002; 2002WO-EP001690.
XX
PR 19-FEB-2001; 2001EP-00103955.
PR 05-APR-2001; 2001EP-00108291.
XX
PA (MERE ) MERCK PATENT GMBH.
XX
PI Gillies S, Carr FJ, Jones T, Carter G, Hamilton A, Williams S;
PI Hanlon M, Watkins J, Baker M, Way JC;
XX
DR WPI; 2002-667054/71.
XX
XX New modified fusion protein with reduced immunogenicity, useful for
PT combining favorable properties of a composition, comprises an
PT immunoglobulin molecule linked to a non-immunoglobulin target
PT polypeptide.
XX
PS Example 2; Page 46; 92pp; English.
XX
XX The invention relates to an immunogenically modified fusion protein
CC derived from a parent fusion protein, comprising first and second
CC proteins/polypeptides, where the first protein is an immunoglobulin
CC molecule or its fragment and the second protein is non-immunoglobulin
CC molecule. The immunogenically modified fusion protein is useful in
CC combining known favourable properties of a composition or in creating new
CC properties of a composition which elicits biological or pharmacological
CC efficacy without having undesirable physiological effects such as nausea
CC or gastric upset. The present sequence is human obesity protein (leptin)
CC peptide with potential major histocompatibility complex (MHC) binding
CC activity. This sequence is used in the exemplification of the invention
XX
SQ Sequence 13 AA;
XX

```

Query Match 38.4%; Score 33; DB 5; length 13;
Best Local Similarity 40.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GGEKDLIMEL 16
| : : : : :
Db 2 GSLQDMLWQL 11

Search completed: November 1, 2005, 13:28:55
Job time : 165 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 13:26:23 ; Search time 41 Seconds

(Without alignments)
30,952 Million cell updates/sec

Title: US-10-612-162a-1

Perfect score: 86
Sequence: 1 VARSMSGKEDLIWELL 17Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 177072

Minimum DB seq length: 0
Maximum DB seq length: 17

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	40.7	13	2	US-08-480-190-196
2	35	40.7	13	2	US-08-488-379-196
3	35	40.7	13	4	US-08-475-399A-196
4	35	40.7	13	4	US-08-077-255A-196
5	35	40.7	13	5	PCT-US93-07545-196
6	35	40.7	15	2	US-08-480-190-136
7	35	40.7	15	2	US-08-488-379-136
8	35	40.7	15	4	US-08-475-399A-136
9	35	40.7	15	4	US-08-077-255A-136
10	35	40.7	15	5	PCT-US93-07545-136
11	35	40.7	16	2	US-08-480-190-273
12	35	40.7	16	4	US-08-488-379-273
13	35	40.7	16	4	US-08-475-399A-273
14	35	40.7	16	4	US-08-077-255A-273
15	35	40.7	16	5	PCT-US93-07545-273
16	30	34.9	10	2	US-08-735-253-5
17	30	34.9	10	2	US-08-735-253-11
18	29	33.7	10	1	US-07-802-667-17
19	28	32.6	5	1	US-07-802-667-20
20	28	32.6	6	5	US-08-269-257-6
21	28	32.6	6	5	PCT-US95-04171-6
22	28	32.6	12	1	US-08-241-054-33
23	28	32.6	12	1	US-08-390-156A-47
24	28	32.6	12	1	US-08-439-817-13
25	28	32.6	12	1	US-08-485-508-33
26	28	32.6	14	4	US-09-053-611-29
27	31.4	9	2	4	US-08-765-061-6

28	27	31.4	12	2	US-08-466-860-4	Sequence 4, Appl
29	27	31.4	12	3	US-08-472-040A-4	Sequence 4, Appl
30	27	31.4	12	3	US-08-276-776-4	Sequence 4, Appl
31	27	31.4	12	3	US-08-471-209-4	Sequence 4, Appl
32	27	31.4	15	4	US-09-255-501-146	Sequence 146, App
33	27	31.4	15	4	US-09-255-501-147	Sequence 147, App
34	27	31.4	15	4	US-09-255-501-148	Sequence 148, App
35	27	31.4	15	4	US-09-255-501-149	Sequence 149, App
36	27	31.4	15	4	US-09-060-872A-146	Sequence 146, App
37	27	31.4	15	4	US-09-060-872A-147	Sequence 147, App
38	27	31.4	15	4	US-09-060-872A-148	Sequence 148, App
39	27	31.4	15	4	US-09-060-872A-149	Sequence 149, App
40	27	31.4	15	4	US-09-500-135C-146	Sequence 146, App
41	27	31.4	15	4	US-09-500-135C-147	Sequence 147, App
42	27	31.4	15	4	US-09-500-135C-148	Sequence 148, App
43	27	31.4	15	4	US-09-500-135C-149	Sequence 149, App
44	26.5	30.8	11	1	US-08-471-058-3	Sequence 3, Appl
45	26.5	30.8	11	3	US-08-471-057-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-480-190-196
; Sequence 196, Application US/08480190
; Patent No. 5827516
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack U. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,190
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 196:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; US-08-480-190-196

Query Match 40.7%; Score 35; DB 2; Length 13;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DIWELL 17
|:|||||
Db 1 DIWELL 7

RESULT 2

US-08-488-379-196
; Sequence 196, Application US/08488379
; Patent No. 5880103
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,379
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 196:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-488-379-196

Query Match 40.7%; Score 35; DB 2; Length 13;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DIWELL 17
|:|||||
Db 1 DIWELL 7

RESULT 3

US-08-475-399A-196
; Sequence 196, Application US/08475399A
; Patent No. 6509033
; GENERAL INFORMATION:

APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
APPLICANT: Vignali, Dario A.A.
APPLICANT: Hedley, Mary L.
APPLICANT: Stern, Lawrence J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 276
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,399A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: 15-JUN-1993
APPLICATION NUMBER: 07/925,460
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frazer, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00246/168003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-507
TELEFAX: 617/542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO: 196:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-475-399A-196

Query Match 40.7%; Score 35; DB 4; Length 13;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DIWELL 17
|:|||||
Db 1 DIWELL 7

RESULT 4

US-08-077-255A-196
; Sequence 196, Application US/08077255A
; Patent No. 6696061
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,255A
FILING DATE: June 15, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 196:
SEQUENCE CHARACTERISTICS:
LENGTH: 13
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-077-255A-196

Query Match 40.7%; Score 35; DB 4; Length 13;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 DLWELL 17
Db 1 DWELL 7

RESULT 5
PCT-US93-07545-196
Sequence 196, Application PC/TUS9307545
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Darlo A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07545
FILING DATE: 19930811
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 196:
SEQUENCE CHARACTERISTICS:
LENGTH: 13
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US93-07545-196

Query Match 40.7%; Score 35; DB 5; Length 13;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 DLWELL 17
Db 1 DWELL 7

RESULT 6
US-08-480-190-136

Sequence 136, Application US/08480190
Patent No. 5827516

GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Darlo A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,190
FILING DATE:
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-480-190-136

Query Match 40.7%; Score 35; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DVIWELL 17
|:|||||
Db 1 DVIWELL 7

RESULT 7
US-08-488-379-136

; Sequence 136, Application US/08488379
; Patent No. 5680103

GENERAL INFORMATION:

; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 555X
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,379

FILING DATE:

; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993

; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992

ATTORNEY/AGENT INFORMATION:

; NAME: Clark, Paul T.

; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070

; TELEFAX: (617) 542-8906
; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 136:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 15

; TYPE: amino acid
; STRANDEDNESS:

; TOPOLOGY: linear
; US-08-488-379-136

Query Match

; Best Local Similarity 40.7%; Score 35; DB 2; Length 15;
; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DVIWELL 17
|:|||||
Db 1 DVIWELL 7

RESULT 8
US-08-475-399A-136

; Sequence 136, Application US/08475399A
; Patent No. 6509033

GENERAL INFORMATION:

; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; APPLICANT: Vignali, Dario A.A.
; APPLICANT: Hedley, Mary L.

; APPLICANT: Stern, Lawrence J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 276

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA

; COUNTRY: US
; ZIP: 02110-2804

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,399A
; FILING DATE: 07-JUN-1995

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255

; FILING DATE: 15-JUN-1993
; APPLICATION NUMBER: 07/925,460

; FILING DATE: 11-AUG-1992
; ATTORNEY/AGENT INFORMATION:

; NAME: Frazer, Janis K.
; REGISTRATION NUMBER: 34,819

; REFERENCE/DOCKET NUMBER: 00246/168003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-507

; TELEFAX: 617/542-890
; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 136:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; US-08-475-399A-136

Query Match

; Best Local Similarity 40.7%; Score 35; DB 4; Length 15;
; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DVIWELL 17
|:|||||
Db 1 DVIWELL 7

RESULT 9
US-08-077-255A-136

; Sequence 136, Application US/08077255A
; Patent No. 6696061

; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban

; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali

; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern

; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson

; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts

; COUNTRY: U.S.A.
; ZIP: 02110-2804

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 555X
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)

```

/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/077,255A
/ FILING DATE: June 15, 1993
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/925,460
/ FILING DATE: August 11, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 00246/168001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 136:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/
US-08-077-255A-136

Query Match          40.7%; Score 35; DB 4; Length 15;
Best local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      11 DLIWELL 17
Db      1 DVIWELL 7

RESULT 10
PCT-US93-07545-136
/ Sequence 136, Application PC/TUS9307545
/ GENERAL INFORMATION:
/ APPLICANT: Robert G. Urban
/ APPLICANT: Roman M. Chicz
/ APPLICANT: Dario A. A. Vignali
/ APPLICANT: Mary L. Hedley
/ APPLICANT: Lawrence J. Stern
/ APPLICANT: Jack L. Strominger
/ TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
/ NUMBER OF SEQUENCES: 273
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: U.S.A.
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 MB
/ COMPUTER: IBM PS/2 Model 502 or 55SX
/ OPERATING SYSTEM: MS-DOS (Version 5.0)
/ SOFTWARE: WordPerfect (Version 5.1)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/07545
/ FILING DATE: 19930811
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/925,460
/ FILING DATE: August 11, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 00246/168001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 136:
/ SEQUENCE CHARACTERISTICS:
```

```

/ LENGTH: 15
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/
PCT-US93-07545-136

Query Match          40.7%; Score 35; DB 5; Length 15;
Best local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      11 DLIWELL 17
Db      1 DVIWELL 7

RESULT 11
US-08-480-190-273
/ Sequence 273, Application US/08480190
/ Patent No. 5827516
/ GENERAL INFORMATION:
/ APPLICANT: Robert G. Urban
/ APPLICANT: Roman M. Chicz
/ APPLICANT: Dario A. A. Vignali
/ APPLICANT: Mary L. Hedley
/ APPLICANT: Lawrence J. Stern
/ APPLICANT: Jack L. Strominger
/ TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
/ NUMBER OF SEQUENCES: 274
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: U.S.A.
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 MB
/ COMPUTER: IBM PS/2 Model 502 or 55SX
/ OPERATING SYSTEM: MS-DOS (Version 5.0)
/ SOFTWARE: WordPerfect (Version 5.1)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/480,190
/ FILING DATE:
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/077,255
/ FILING DATE: June 15, 1993
/ APPLICATION NUMBER: 07/925,460
/ FILING DATE: August 11, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 00246/168001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 273:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/
US-08-480-190-273

Query Match          40.7%; Score 35; DB 2; Length 16;
Best local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      11 DLIWELL 17
Db      1 DVIWELL 7
```

RESULT 12
US-08-488-379-273
Sequence 273, Application US/08488379
Patent No. 5880103
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,379
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 273:
SEQUENCE CHARACTERISTICS:
LENGTH: 16
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-488-379-273

Query Match 40.7%; Score 35; DB 2; Length 16;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 DIWELL 17
|:|||||
Db 1 DIWELL 7

RESULT 13
US-08-475-399A-273
Sequence 273, Application US/08475399A
Patent No. 6509033
GENERAL INFORMATION:
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
APPLICANT: Vignali, Dario A. A.
APPLICANT: Hedley, Mary L.
APPLICANT: Stern, Lawrence J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 276

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,399A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: 15-JUN-1993
APPLICATION NUMBER: 07/925,460
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00246/168003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-507
TELEFAX: 617/542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO: 273:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-475-399A-273

Query Match 40.7%; Score 35; DB 4; Length 16;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 DIWELL 17
|:|||||
Db 1 DIWELL 7

RESULT 14
US-08-077-255A-273
Sequence 273, Application US/08077255A
Patent No. 6696061
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,255A
FILING DATE: June 15, 1993
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 273:
SEQUENCE CHARACTERISTICS:
LENGTH: 16
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-077-255A-273

Query Match 40.7%; Score 35; DB 4; Length 16;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 DLIWELL 17
DB 1 DLIWELL 7

RESULT 15
PCT-US93-07545-273
Sequence 273, Application PC/TUS9307545
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chic
APPLICANT: Darlo A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07545
FILING DATE: 19930811
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 273:
SEQUENCE CHARACTERISTICS:
LENGTH: 16
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

PCT-US93-07545-273

Query Match 40.7%; Score 35; DB 5; Length 16;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 DLIWELL 17
DB 1 DLIWELL 7

Search completed: November 1, 2005, 13:41:21
Job time : 42 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 13:31:57 ; Search time 164 Seconds

(Without alignments)
43.334 Million cell updates/sec

Title: US-10-612-162a-1

Perfect score: 86
Sequence: 1 VVARSWGKEDLIWELL 17Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 344634

Minimum DB seq length: 0
Maximum DB seq length: 17Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

```
1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep:*
20: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	17	US-10-612-162-1	Sequence 1, Appl
2	43	50.0	15	US-10-769-514-5	Sequence 5, Appl
3	43	50.0	17	US-10-801-990-7	Sequence 7, Appl
4	33	38.4	13	US-10-467-114-49	Sequence 49, Appl
5	33	38.4	13	US-10-467-114-51	Sequence 50, Appl
6	33	38.4	13	US-10-467-114-50	Sequence 51, Appl
7	33	38.4	13	US-10-468-370-52	Sequence 52, Appl
8	33	38.4	13	US-10-468-370-53	Sequence 53, Appl
9	33	38.4	13	US-10-468-370-54	Sequence 54, Appl
10	32	37.2	10	US-10-190-082-445	Sequence 445, App
11	32	37.2	16	US-10-813-638-1208	Sequence 1208, Ap

12	31	36.0	16	US-10-155-481B-17	Sequence 17, Appl
13	30	34.9	14	US-10-783-989-3	Sequence 3, Appl
14	30	34.9	15	US-09-907-965-494	Sequence 494, App
15	30	34.9	15	US-10-198-053-494	Sequence 494, App
16	30	34.9	17	US-10-860-790-494	Sequence 494, App
17	30	34.9	17	US-10-291-241-85	Sequence 85, Appl
18	29	33.7	7	US-10-714-564A-607	Sequence 607, App
19	29	33.7	13	US-10-467-114-52	Sequence 52, Appl
20	29	33.7	13	US-10-468-370-55	Sequence 55, Appl
21	29	33.7	15	US-10-695-155-131	Sequence 131, App
22	29	33.7	15	US-10-695-155-132	Sequence 132, App
23	28.5	33.1	17	US-10-356-257-295	Sequence 295, App
24	28	32.6	10	US-09-572-404B-2179	Sequence 2179, Ap
25	28	32.6	10	US-10-190-082-446	Sequence 446, App
26	28	32.6	14	US-10-215-755-13	Sequence 13, Appl
27	28	32.6	14	US-10-264-672-13	Sequence 13, Appl
28	28	32.6	14	US-10-383-999-13	Sequence 13, Appl
29	28	32.6	14	US-11-031-919-13	Sequence 13, Appl
30	28	32.6	15	US-09-853-253-17	Sequence 17, Appl
31	28	32.6	15	US-10-264-309-173	Sequence 173, App
32	28	32.6	15	US-10-921-371-17	Sequence 17, Appl
33	28	32.6	15	US-10-264-309-173	Sequence 173, App
34	28	32.6	16	US-09-853-253-15	Sequence 15, Appl
35	28	32.6	16	US-09-853-253-16	Sequence 16, Appl
36	28	32.6	16	US-10-808-187-1148	Sequence 1148, Ap
37	28	32.6	16	US-10-921-371-15	Sequence 15, Appl
38	28	32.6	16	US-10-921-371-16	Sequence 16, Appl
39	28	32.6	16	US-10-807-807-1148	Sequence 1148, Ap
40	28	32.6	17	US-09-853-253-14	Sequence 14, Appl
41	28	32.6	17	US-09-798-116-23	Sequence 23, Appl
42	28	31.4	17	US-10-921-371-14	Sequence 14, Appl
43	27	31.4	12	US-10-190-082-444	Sequence 444, App
44	27	31.4	12	US-10-504-726-33	Sequence 33, Appl
45	27	31.4	14	US-10-403-847-85	Sequence 85, Appl

ALIGNMENTS

```
RESULT 1
US-10-612-162-1
; Sequence 1, Application US/10612162
; Publication No. US20040014145A1
; GENERAL INFORMATION:
; APPLICANT: Dade Behring Marburg GmbH
; TITLE OF INVENTION: Carbohydrate deficient transferrin (CDT)-specific
; FILE REFERENCE: 2002/B001
; CURRENT APPLICATION NUMBER: US/10/612,162
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 10230550.1
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 03011334.4
; PRIOR FILING DATE: 2003-05-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-162-1
```

Query Match 100.0%; Score 86; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSWGKEDLIWELL 17
|||||
Db 1 VVARSWGKEDLIWELL 17

RESULT 2
US-10-769-514-5

```
; Sequence 5, Application US/10769514
; Publication No. US20040258695A1
; GENERAL INFORMATION:
; APPLICANT: Schryvers, Anthony
; TITLE OF INVENTION: Transferrin Binding Peptides and Uses Thereof
; FILE REFERENCE: 028722-001
; CURRENT APPLICATION NUMBER: US/10/769,514
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/444,113
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-514-5
```

```
Query Match          50.0%; Score 43; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 VVARSWGK 9
      |||||
Db      7 VVARSWGK 15
```

```
RESULT 3
US-10-801-990-7
; Sequence 7, Application US/10801990
; Publication No. US20050048574A1
; GENERAL INFORMATION:
; APPLICANT: Kantrow, Aaron B.
; APPLICANT: Schulman, Howard
; APPLICANT: Becker, Christopher
; TITLE OF INVENTION: BIOMARKERS FOR RHEUMATOID ARTHRITIS
; FILE REFERENCE: SURR.121
; CURRENT APPLICATION NUMBER: US/10/801,990
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US 60/455,037
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 7
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-801-990-7
```

```
Query Match          50.0%; Score 43; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      10 EDLIWELL 17
      |||||
Db      1 EDLIWELL 8
```

```
RESULT 4
US-10-467-114-49
; Sequence 49, Application US/10467114
; Publication No. US20040072219A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: MODIFIED LEPTIN WITH REDUCED
; FILE REFERENCE: MER-115
; CURRENT APPLICATION NUMBER: US/10/467,114
; CURRENT FILING DATE: 2003-08-05
```

```
; PRIOR APPLICATION NUMBER: EP 01102618.4
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: EP 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01188
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MCH class II binding epitope
US-10-467-114-49
```

```
Query Match          38.4%; Score 33; DB 15; Length 13;
Best Local Similarity 30.8%; Pred. No. 1.4e+02;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      3 ARSWGKEDLIWE 15
      |||:|:|:|
Db      1 SRLGSLQDMLWQ 13
```

```
RESULT 5
US-10-467-114-50
; Sequence 50, Application US/10467114
; Publication No. US20040072219A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: MODIFIED LEPTIN WITH REDUCED
; FILE REFERENCE: MER-115
; CURRENT APPLICATION NUMBER: US/10/467,114
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: EP 01102618.4
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: EP 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01188
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MCH class II binding epitope
US-10-467-114-50
```

```
Query Match          38.4%; Score 33; DB 15; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      7 GKGEDLIWE 16
      |:|:|:|
Db      2 GSLQDMLWQL 11
```

```
RESULT 6
US-10-467-114-51
; Sequence 51, Application US/10467114
; Publication No. US20040072219A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
```

```

; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: MODIFIED LEPTIN WITH REDUCED
; FILE REFERENCE: IMMUNOGENICITY
; CURRENT APPLICATION NUMBER: US/10/467,114
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: EP 01102618.4
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: EP 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01188
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PaetSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-467-114-51

Query Match      38.4%; Score 33; DB 15; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      7 GSKEDLIWEL 16
| : : : |
Db      1 GSIQDMLWQL 10

RESULT 7
US-10-468-370-52
; Sequence 52, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gallies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; FILE REFERENCE: IMMUNOGENICITY
; CURRENT APPLICATION NUMBER: US/10/468,370
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: PaetSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-370-52

Query Match      38.4%; Score 33; DB 15; Length 13;
Best Local Similarity 30.8%; Pred. No. 1.4e+02;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      3 ARSMGKEDLIWE 15
```

```

Db      1 SRLOGSLQDMLWQ 13

RESULT 8
US-10-468-370-53
; Sequence 53, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gallies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; FILE REFERENCE: IMMUNOGENICITY
; CURRENT APPLICATION NUMBER: US/10/468,370
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: PaetSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-370-53

Query Match      38.4%; Score 33; DB 15; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      7 GSKEDLIWEL 16
| : : : |
Db      2 GSIQDMLWQL 11

RESULT 9
US-10-468-370-54
; Sequence 54, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gallies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; FILE REFERENCE: IMMUNOGENICITY
; CURRENT APPLICATION NUMBER: US/10/468,370
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
```

```

; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FaSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-370-54

Query Match          38.4%; Score 33; DB 15; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 GKEDLIWEL 16
DB 1 GSLQDMLWQL 10

RESULT 10
US-10-190-082-445
; Sequence 445, Application US/10190082
; Publication No. US20030148264A1
; GENERAL INFORMATION:
; APPLICANT: Lasky, Lawrence A.
; APPLICANT: Sidhu, Sachdev S.
; APPLICANT: Held, Heike A.
; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS
; FILE REFERENCE: P1905R1
; CURRENT APPLICATION NUMBER: US/10/190,082
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/303,634
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 683
; SEQ ID NO 445
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-190-082-445

Query Match          37.2%; Score 32; DB 14; Length 10;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 KEDLIWEL 17
DB 1 KNSWELL 9

RESULT 11
US-10-813-638-1208
; Sequence 1208, Application US/10813638
; Publication No. US20040235026A1
; GENERAL INFORMATION:
; APPLICANT: Shinketo, Richard A.
; APPLICANT: Leach, Martin D.
; TITLE OF INVENTION: NUCLEIC ACIDS CONTAINING SINGLE NUCLEIC ACID POLYMORPHISMS AND ME
; FILE REFERENCE: 15966-599
; CURRENT APPLICATION NUMBER: US/10/813,638
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: 60/163,783
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1468
; SOFTWARE: CuraGen Patent Formatter Version 0.9
; SEQ ID NO 1208
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```

; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (7)...(0)
; OTHER INFORMATION: cSNP translation
US-10-813-638-1208

Query Match          37.2%; Score 32; DB 16; Length 14;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 DLIWEL 17
DB 1 DLIWTL 7

RESULT 12
US-10-155-481B-17
; Sequence 17, Application US/10155481B
; Publication No. US20030113711A1
; GENERAL INFORMATION:
; APPLICANT: Stuart, J.
; APPLICANT: Bramson, H.
; APPLICANT: Moyer, Mary
; APPLICANT: Blackburn, Kevin
; TITLE OF INVENTION: PROTEIN KINASE PEPTIDE SUBSTRATE DETERMINATION USING PEPTIDE
; FILE REFERENCE: Attorney Docket No. US20030113711A1 447-76, Glaxo ID PU4253
; CURRENT APPLICATION NUMBER: US/10/155,481B
; CURRENT FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-155-481B-17

Query Match          36.0%; Score 31; DB 14; Length 16;
Best Local Similarity 45.5%; Pred. No. 3.9e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GKEDLIWEL 17
DB 1 GMDIYFEFM 11

RESULT 13
US-10-783-989-3
; Sequence 3, Application US/10783989
; Publication No. US20050015821A1
; GENERAL INFORMATION:
; APPLICANT: GYNNÉ, RICHARD J.
; APPLICANT: HONG, NANCY AI-HUA
; APPLICANT: NEJMS, KEATIS A.
; APPLICANT: WU, HUA
; TITLE OF INVENTION: SENSIN POLYPEPTIDES, ENCODING NUCLEIC ACIDS, MUTATIONS,
; FILE REFERENCE: 022731-0402
; CURRENT APPLICATION NUMBER: US/10/783,989
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,964
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-783-989-3

Query Match          34.9%; Score 30; DB 17; Length 14;
```

Best Local Similarity 66.7%; Pred. No. 5e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db : || || || ||
4 KEDLIWEL 11

Search completed: November 1, 2005, 13:45:54
Job time : 165 secs

Qy 9 KEDLIWEL 17
||| |||
1 KEDLKWSSL 9

RESULT 14

US-09-907-969-494
; Sequence 494, Application US/09907969
; Publication No. US20030091580A1

GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E.

APPLICANT: Algate, Paul A.

APPLICANT: Fling, Steven P.

APPLICANT: Retter, Marc W.

APPLICANT: Fanger, Gary Richard

APPLICANT: Reed, Steven G.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Darrick

APPLICANT: Hill, Paul

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.462C8

CURRENT APPLICATION NUMBER: US/09/907,969

CURRENT FILING DATE: 2001-07-17

NUMBER OF SEQ ID NOS: 596

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 494

LENGTH: 15

TYPE: PRT

ORGANISM: Homo sapiens

US-09-907-969-494

Query Match 34.9%; Score 30; DB 10; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 KEDLIWEL 16
: || || || ||

Db 4 REOLYWEL 11

RESULT 15

US-10-198-053-494

; Sequence 494, Application US/10198053
; Publication No. US20030124140A1

GENERAL INFORMATION:

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Retter, Marc W.

APPLICANT: Fanger, Gary R.

APPLICANT: Hill, Paul

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.462C9

CURRENT APPLICATION NUMBER: US/10/198,053

CURRENT FILING DATE: 2002-07-17

NUMBER OF SEQ ID NOS: 624

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 494

LENGTH: 15

TYPE: PRT

ORGANISM: Homo sapiens

US-10-198-053-494

Query Match 34.9%; Score 30; DB 14; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 KEDLIWEL 16

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 13:17:07 ; Search time 38 Seconds
(Without alignment)
43.044 Million cell updates/sec

Title: US-10-612-162a-1

Perfect score: 86
Sequence: 1 VVARSMGCKEDLIWELL 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2991

Minimum DB seq length: 0
Maximum DB seq length: 17

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	33.7	11	2	S60294 tubulin 2 beta-3 c
2	25	29.1	14	2	PH1769 T cell receptor al
3	25	29.1	16	2	A20190 hypodermis B - ear
4	24	27.9	13	2	S47383 T-cell antigen rec
5	24	27.9	13	2	P00700 unidentified 6.3/4
6	24	27.9	15	4	I38031 hypotheoretical MNL/T
7	23	26.7	12	2	S69123 proton-translocati
8	23	26.7	12	2	PH1183 T-cell receptor al
9	23	26.7	14	2	PH1626 Ig H chain V-D-J r
10	23	26.7	15	2	S26527 T-cell receptor al
11	23	26.7	15	2	PH0782 T-cell receptor al
12	23	26.7	16	2	B60560 formyltetrahydrofo
13	23	26.7	17	2	B61334 trypsin (EC 3.4.21
14	22	25.6	9	1	YF66 thymic factor - pi
15	22	25.6	9	2	A60957 thymocyte growth p
16	22	25.6	10	2	PT0310 Ig heavy chain CRD
17	22	25.6	14	2	PH0800 T-cell receptor al
18	22	25.6	14	2	PH0801 T-cell receptor al
19	22	25.6	14	2	P49037 TCR delta chain V-
20	22	25.6	16	2	A48839 T-cell receptor al
21	22	25.6	16	2	A46236 transforming prote
22	22	25.6	16	2	A26393 annexin 36k chain
23	21	24.4	6	2	PT0730 T-cell receptor be
24	21	24.4	8	2	A21440 variant surface gl
25	21	24.4	9	2	B45020 probable minipolyp
26	21	24.4	10	2	PT0289 Ig heavy chain CRD
27	21	24.4	11	2	H54346 pyruvate synthase
28	21	24.4	11	2	S57575 T cell receptor V-
29	21	24.4	12	1	U06W2 utroctensin II - lon

30	21	24.4	12	2	S42765 utroctensin II - tel
31	21	24.4	14	2	PH1759 T cell receptor al
32	21	24.4	14	2	S58426 spermadhesin AMN h
33	21	24.4	14	2	PH1625 Ig H chain V-D-J r
34	21	24.4	14	2	PH1627 Ig H chain V-D-J r
35	21	24.4	14	2	PH0762 T-cell receptor be
36	21	24.4	15	2	S57201 basic proteinase I
37	21	24.4	17	2	B61321 histone H4 - chick
38	21	24.4	17	2	A61321 histone H4 - chick
39	20	23.3	9	2	PT0670 T-cell receptor be
40	20	23.3	10	2	PT0245 Ig heavy chain CRD
41	20	23.3	11	2	B49164 chromogranin-B - r
42	20	23.3	12	2	JS0423 utroctensin II-A pep
43	20	23.3	13	2	PH1636 Ig H chain V-D-J r
44	20	23.3	14	2	A35105 hypotheoretical prote
45	20	23.3	15	2	A45103 7 alpha-hydroxy-4-

ALIGNMENTS

RESULT 1
S60294
tubulin 2 beta-3 chain - fruit fly (Drosophila melanogaster) (fragment)
C/Species: Drosophila melanogaster
C/Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #ext_change 21-Jun-2002
C/Accession: S60294
R/Chapel, S.; Sobrier, M.L.; Montpied, P.; Micard, D.; Brubet, A.; Couderc, J.L.; Dastu-
Insect Mol. Biol. 2, 39-48, 1993
A/Title: In Drosophila Kc cells 20-OHE induction of the 60C beta-3 tubulin gene expressi
A/Reference number: S60292; PMID:97242543; PMID:9087542
A/Accession: S60294
A/Molecule type: mRNA
A/Residues: 1-11 <CHA>
A/Cross-references: EMBL:X60393
C/Genetics:
A/Gene: FlyBase:beta-Tub60D
A:Cross-references: FlyBase:FBgn003888

Query Match 33.7%; Score 29; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 VVARSMGCK 9
DB 4 VTRSSGCK 11

RESULT 2
PH1769
T cell receptor alpha chain V region (clone 2V alpha 7.2-4) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #ext_change 16-Jul-1999
C/Accession: PH1769
R/Forelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 176, 1-16, 1993
A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; PMID:93301585; PMID:8391057
A/Accession: PH1769
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-14 <FOR>

Query Match 29.1%; Score 25; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 66+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 SMGCKEDLIW 14
DB 4 SMDSNYQLIWI 13

```
RESULT 3
A20190
Hypodermin B - early cattle grub (fragment)
C:Species: Hypoderma lineatum (early cattle grub)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C:Accession: A20190
R:Lectrolaey, A.; Tong, N.T.; Kell, B.
Eur. J. Biochem. 134, 261-267, 1983
A:Title: Hypodermin B, a trypsin-related enzyme from the insect Hypoderma lineatum.
A:Reference number: A20190; MUID:83261874; PMID:6307690
A:Accession: A20190
A:Molecule type: protein
A:Residues: 1-16 <LEC>
A:Cross-references: UNIPROT:P35588

Query Match      29.1%; Score 25; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 6.9e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db      10 EDLWEL 16
        |||
        10 EDFPWEV 16

RESULT 4
S47383
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47383
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A*0201 restricted recognition of Influenza A is dominated by T c
A:Reference number: S47355
A:Accession: S47383
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z55709; NID:9527513; PIDN:CAA84778.1; PID:9527514
C:Keywords: T-cell receptor

Query Match      27.9%; Score 24; DB 2; Length 13;
Best Local Similarity 83.3%; Pred. No. 8.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 ASMSG 8
        |||
        2 ASMSG 7

Db

RESULT 5
P00700
unidentified 6.3/40K protein [imported] - rice (fragment)
C:Species: Oryza sativa (rice)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: P00700
R:Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A:Title: A rice protein library; a data-file of rice proteins separated by two-dimension
A:Reference number: P00696
A:Accession: P00700
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <KOM>
A:Cross-references: UNIPROT:Q7MLU1

Query Match      27.9%; Score 24; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 8.1e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      2 VARSMGKEDLI 13
        |||
        1 VAGAYGALDIL 12

Db
```

```
RESULT 6
I18031
Hypothetical MNI/TEL mutant fusion protein type II - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000
C:Accession: I18031
R:Bulls, A.; Sherr, S.; van Baal, S.; van Bezouw, S.; van der Plas, D.; Van Kessel, A.G.
Oncogene 10, 1511-1519, 1995
A:Title: Translocation (12;22) (p13;q11) in myeloproliferative disorders results in fusi
A:Reference number: I18031; MUID:95249265; PMID:7731705
A:Accession: I18031
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-15 <BUT>
A:Cross-references: EMBL:X85027; NID:9971465; PIDN:CA59400.1; PID:9971466
C:Comment: This sequence is the chimeric product of a translocation mutation.
C:Genetics:
A:Gene: MNI/ETV6; MNI/TEL
A:Map position: 22q11/12p13
C:Keywords: fusion protein

Query Match      27.9%; Score 24; DB 4; Length 15;
Best Local Similarity 57.1%; Pred. No. 9.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      11 DLWEL 17
        |||
        9 DVLWEL 15

Db

RESULT 7
S69123
proton-translocating transhydrogenase - Rhodospirillum rubrum (fragment)
C:Species: Rhodospirillum rubrum
C:Date: 10-Mar-1998 #sequence_revision 24-Apr-1998 #text_change 24-Apr-1998
C:Accession: S69123
R:Diggle, C.; Hutton, M.; Jones, G.R.; Thomas, C.M.; Jackson, J.B.
Eur. J. Biochem. 228, 719-726, 1995
A:Title: Properties of the soluble polypeptide of the proton-translocating transhydrogen
A:Reference number: S69123; MUID:95255277; PMID:7737169
A:Accession: S69123
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <DIG>

Query Match      26.7%; Score 23; DB 2; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.1e+03;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      11 DLWEL 16
        |||
        3 DVWVKV 8

Db

RESULT 8
PH1183
T-cell receptor alpha chain V region (Cw3/A8) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1183
R:Caetano, J.L.; Cerotini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wld
J. Exp. Med. 176, 439-447, 1992
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A:Reference number: S26512; MUID:92364546; PMID:1380061
A:Accession: PH1183
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>

Query Match      26.7%; Score 23; DB 2; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;

Db
```


Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ARSMG 8

Db 2 ALSMG 7

RESULT 9

PH1626

19 H chain V-D-J region (clone B-less 118) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C/Accession: PH1626

R/Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A/Reference number: PH1580; PMID:93301609; PMID:8315387

A/Accession: PH1626

A/Molecule type: DNA

A/Residues: 1-14 <LEV>

A/Experimental source: bone marrow pre-B lymphocyte

C/Keywords: Immunoglobulin

Query Match

Best Local Similarity 26.7%; Score 23; DB 2; Length 14;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 DLIW 14

Db 10 DLIW 13

RESULT 10

S26527

T-cell receptor alpha chain V region (clone Cw3/A8, A3/74.1) - mouse (fragment)

C/Species: Mus musculus (house mouse)

A/Variety: clone Cw3/A8; A3/74.1

C/Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999

C/Accession: S26527; PH1442

R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gounthier, H.; Barra, C.; Wild

J. Exp. Med. 176, 439-447, 1992

A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor

A/Reference number: S26512; PMID:92364546; PMID:1180061

A/Accession: S26527

A/Molecule type: mRNA

A/Residues: 1-15 <CAS>

A/Cross-references: EMBL:X67978

A/Experimental source: cytolytic T-lymphocyte, clone Cw3/A8

J. Exp. Med. 177, 811-820, 1993

A/Title: T cell receptor selection by and recognition of two class I major histocompatibility

A/Reference number: PH1430; PMID:93171821; PMID:8436911

A/Accession: PH1442

A/Molecule type: mRNA

A/Residues: 1-15 <CA2>

A/Experimental source: cytolytic T-lymphocyte

C/Suprafamily: Immunoglobulin V region; immunoglobulin homology

C/Keywords: T-cell receptor

Query Match

Best Local Similarity 26.7%; Score 23; DB 2; Length 15;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ARSMG 8

Db 2 ALSMG 7

RESULT 11

PH0782

T-cell receptor alpha chain (H3 V-alpha-10, TA57) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C/Accession: PH0782

R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A/Title: T cell receptor genes in a series of class I major histocompatibility complex-

allelic exclusion and antigen-specific repertoire.

A/Reference number: PH0746; PMID:9207846; PMID:1836010

A/Accession: PH0782

A/Molecule type: mRNA

A/Residues: 1-15 <CAS>

A/Cross-references: EMBL:X60883

A/Experimental source: T lymphocyte

A/Note: the authors translated the codon TTC for residue 6 as Leu

C/Keywords: T-cell receptor

Query Match

Best Local Similarity 26.7%; Score 23; DB 2; Length 15;

Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 GGEKDLIW 14

Db 7 GDNKSLIW 14

RESULT 12

B60560

formyltetrahydrofolate dehydrogenase (EC 1.5.1.6) / aldehyde dehydrogenase (NADP) (EC 1

C/Species: Homo sapiens (man)

C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

C/Accession: B60560

R/Johlin, F.C.; Swain, B.; Smith, C.; Tephly, T.R.

Mol. Pharmacol. 35, 745-750, 1989

A/Title: Studies on the mechanism of methanol poisoning: purification and comparison of

A/Reference number: A60560; PMID:89281457; PMID:2733692

A/Accession: B60560

A/Molecule type: protein

A/Residues: 1-16 <JOH>

A/Cross-references: UNIPROT:Q8TBP8

C/Keywords: multifunctional enzyme; NADP; oxidoreductase

Query Match

Best Local Similarity 26.7%; Score 23; DB 2; Length 16;

Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 VVARSMGKE 10

Db 5 VVGQSLFGGE 14

RESULT 13

B61334

trypsin (EC 3.4.21.4) 2 - starfish (Dermasterias imbricata) (fragment)

C/Species: Dermasterias imbricata

C/Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 09-Jul-2004

C/Accession: B61334

R/Betell, D.A.; Laskowski, Jr., M.

Biochemistry 19, 124-131, 1980

A/Title: Dermasterias imbricata trypsin 1: an enzyme which rapidly hydrolyzes the react

A/Reference number: A61334; PMID:80109692; PMID:7352972

A/Accession: B61334

A/Molecule type: protein

A/Residues: 1-17 <BET>

A/Cross-references: UNIPROT:Q7M432

C/Suprafamily: trypsin; trypsin homology

C/Keywords: hydrolase; protein digestion; serine proteinase

Query Match

Best Local Similarity 26.7%; Score 23; DB 2; Length 17;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 MGSGKE 10

Db 2 VGGKE 6

Job time : 40 secs

RESULT 14

YFPG

thymic factor - pig

N:Alternate names: FTS (facteur thymique serieque)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 03-Jul-2004

C:Accession: A01523; A60983

R:Pleau, J.M.; Dardenne, M.; Blouguit, Y.; Bach, J.F.

J. Biol. Chem. 252, 8045-8047, 1977

A:Title: Structural study of circulating thymic factor: a peptide isolated from pig seru

A:Reference number: A01523; PMID:78026571; PMID:914862

A:Accession: A01523

A:Molecule type: protein

A:Residues: 1-9

A:Cross-references: UNIPROT:P01255

R:Bach, J.F.; Dardenne, M.; Pleau, J.M.; Rosa, J.

Nature 266, 55-57, 1977

A:Title: Biochemical characterisation of a serum thymic factor.

A:Reference number: A60983; PMID:77123829; PMID:300146

A:Accession: A60983

A:Molecule type: protein

A:Residues: 'Z', '2-4', 'Z', '6-9 <BAC>

C:Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral

in a variety of immunosassays.

C:Comment: See PIR:A60957 (sheep) for discussion of another possible N-terminal modifica

C:Superfamily: thymic factor

C:Keyword: pyroglutamic acid

F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match

25.6%; Score 22; DB 1; Length 9;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 ARSMG 8

I:| | |

DB 2 AKSOG 7

RESULT 15

A60957

thymocyte growth peptide - sheep

N:Contains: FTS (facteur thymique serieque)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 03-Jul-2004

C:Accession: A60957

R:Ernstroem, U.; Gafvelin, G.; Rudja, J.M.

Biosci. Rep. 10, 403-412, 1990

A:Title: Purification of thymocyte growth peptide (TGP) from sheep thymus. Relationship

A:Reference number: A60957; PMID:91064427; PMID:2249004

A:Accession: A60957

A:Molecule type: protein

A:Residues: 1-9

A:Cross-references: UNIPROT:Q7M3C5

C:Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral

in a variety of immunosassays.

C:Comment: This peptide was isolated in two forms. One form contained the pyrrolidone ca

r form (thymocyte growth peptide) contains a large, non-peptide blocking group with a hi

C:Superfamily: thymic factor

C:Keywords: blocked amino end, pyroglutamic acid

F:/Modified site: pyrrolidone carboxylic acid (Gln) (in FTS) #status experimental

F:/Modified site: pyrrolidone carboxylic acid (Gln) (in thymocyte growth peptide) #status experim

F:/Modified site: blocked amino end (Gln) (in thymocyte growth peptide) #status experim

Query Match 25.6%; Score 22; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 ARSMG 8

I:| | |

DB 2 AKSOG 7

Search completed: November 1, 2005, 13:32:32

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:57:41 ; Search time 167 Seconds

(without alignments)
52.128 Million cell updates/sec

Title: US-10-612-162a-1

Sequence: 1 VVARSMGKEDLIWELL 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 8390

Minimum DB seq length: 0
Maximum DB seq length: 17

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	33.7	17	2	Q6LDL9
2	29	33.7	17	2	Q6LEA8
3	28	32.6	15	2	Q6SLP7
4	27	31.4	13	2	Q9UDE0
5	25	29.1	10	2	Q76ML6
6	24	27.9	12	1	UR2B_CYPCA
7	24	27.9	13	1	CRBL_VESXA
8	24	27.9	13	2	Q7M1I1
9	24	27.9	15	1	RL11_STRAU
10	24	27.9	15	2	Q6QCR7
11	23	26.7	12	2	Q9H1Z6
12	23	26.7	13	2	Q9UPES
13	23	26.7	14	1	UP07_ORYSA
14	23	26.7	16	2	Q8UUE1
15	23	26.7	16	2	Q8UUE2
16	23	26.7	16	2	Q8UUE3
17	23	26.7	16	2	Q8UUE4
18	23	26.7	16	2	Q8UUE5
19	23	26.7	16	2	Q8UUE6
20	23	26.7	16	2	Q8UUE7
21	23	26.7	16	2	Q8UUE8
22	23	26.7	16	2	Q8UUE9
23	23	26.7	16	2	Q8UUF0
24	23	26.7	16	2	Q8UUF2
25	23	26.7	16	2	Q8UUF3
26	23	26.7	16	2	Q8UUF4
27	23	26.7	16	2	Q8UUF5
28	23	26.7	16	2	Q8UUF6
29	23	26.7	16	2	Q8UUF7
30	23	26.7	16	2	Q8UUF8
31	23	26.7	17	2	Q7M432

32	23	26.7	17	2	Q9R4A5	Q9R4A5 oerakovia x
33	22	25.6	8	2	Q7R6C3	Q7R6C3 largemouth
34	22	25.6	9	1	MEF_HV1Z8	P12481 human immun
35	22	25.6	9	1	THYF_PIG	P01255 sus scrofa
36	22	25.6	9	2	Q7M3C5	Q7M3C5 ovis aries
37	22	25.6	11	2	Q9UEL0	Q9UEL0 homo sapien
38	22	25.6	12	2	Q8L1C3	Q8L1C3 trifolium r
39	22	25.6	12	2	Q41611	Q41611 human immun
40	22	25.6	12	2	Q75729	Q75729 human immun
41	22	25.6	13	1	CRBL_VESAN	P17233 vespa anali
42	22	25.6	13	2	Q9AMK2	Q9AMK2 xanthomonas
43	22	25.6	15	2	Q8R5G1	Q8R5G1 spermophilu
44	22	25.6	15	2	Q8UM88	Q8UM88 human immun
45	22	25.6	15	2	Q8USK4	Q8USK4 human immun

ALIGNMENTS

```

RESULT 1
Q6LDL9 PRELIMINARY; PRT; 17 AA.
ID Q6LDL9
AC Q6LDL9;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN Name=NCAM-C;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=90287121; PubMed=1694009;
RA Chen A., Reyes A., Akesson R.A.;
RT "Transcription initiation sites and structural organization of the
RL Mol. Cell. Biol. 10:3314-3324 (1990).
DR EMBL; M32612; AAA41680.1; -.
FT NON TER 1
SQ SEQUENCE 17 AA; 2026 MW; AEALBBSF252E84F5 CRC64;

Query Match 33.7%; Score 29; DB 2; Length 17;
Best Local Similarity 71.4%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 EDLIWEL 16
Db 5 KDLIWL 11

RESULT 2
Q6LEA8 PRELIMINARY; PRT; 17 AA.
ID Q6LEA8
AC Q6LEA8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN Name=NCAM;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnson A.D., Ovesnek N., Tonissen K.F., Kriegl P.A.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; L26396; AAA49911.1; -.
FT NON TER 17

```

SQL SEQUENCE 17 AA; 2005 MW; AEBD9B5855262107 CRC64;

Query Match 33.7%; Score 29; DB 2; Length 17;
Best Local Similarity 71.4%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 10 EDLWEL 16
DB 5 KDLIWL 11

RESULT 3

Q6SLF7 PRELIMINARY; PRT; 15 AA.
ID Q6SLF7;
AC Q6SLF7;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Ghrelin (Fragment).
OS Rangifer tarandus (Reindeer) (Caribou).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Odocoileinae; Rangifer.
NCBI_TaxId=9870;

RA SEQUENCE FROM N.A.
RA Dickin J.C., Thue T.D., Buchanan F.C.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY455989; AAS67354.1; -.

FT NON_TER 1
SQ SEQUENCE 15 AA; 1763 MW; CBSEFF57F7D20AF8 CRC64;

Query Match 32.6%; Score 28; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 10 EDLWEL 15
DB 1 QDLWEL 6

RESULT 4

Q9UDE0 PRELIMINARY; PRT; 13 AA.
AC Q9UDE0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
OS Aggreccan core protein (Fragment).
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxId=9606;

RA SEQUENCE FROM N.A.
RA MEDLINE=92235266; PubMed=1569188;
RA Sandy J.D., Flannery C.R., Neame P.J., Lohmeyer L.S.;
RL J. Clin. Invest. 89:1512-1516(1992).
DR GO; GO:0030021; Extracellular matrix structural constituent. . .; ISS.
DR GO; GO:0005540; Extracellular matrix organization and bioge. . .; ISS.
DR GO; GO:0030196; Extracellular matrix organization and bioge. . .; ISS.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1407 MW; 3A1B032DD2751B18 CRC64;

Query Match 31.4%; Score 27; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 1.8e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 6 MGKEDL 12
DB 4 VGGEDI 10

RESULT 5

Q76ML6 PRELIMINARY; PRT; 10 AA.
ID Q76ML6;
AC Q76ML6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE NADH dehydrogenase subunit 4 (Fragment).
OS Eurypharynx pelicanoides (pelican eel).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
OC Eurypharyngidae; Eurypharynx.
NCBI_TaxId=55117;

RA SEQUENCE FROM N.A.
RA MEDLINE=22967687; PubMed=12949142; DOI=10.1093/molbev/msg206;
RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
RT "Evolution of the deep-sea gulper eel mitochondrial genomes: large-scale gene rearrangements originated within the eels";
RL Mol. Biol. Evol. 20:1917-1924(2003).

RA SEQUENCE FROM N.A.
RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB046482; BAB87149.1; -.
DR EMBL; AB046486; BAB87157.1; -.
DR EMBL; AB046490; BAB87165.1; -.
DR EMBL; AB046478; BAB87141.1; -.
DR GO; GO:0005739; Mitochondrion; IEA.

FT NON_TER 1
SQ SEQUENCE 10 AA; 1263 MW; 62D604786370572B CRC64;

Query Match 29.1%; Score 25; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 9 KEDLIW 14
DB 1 KPELIW 6

RESULT 6

UR2B_CYPCA STANDARD; PRT; 12 AA.
ID UR2B_CYPCA;
AC P04561;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Urotensin II-beta (U-II-beta).
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
NCBI_TaxId=7962;

RA SEQUENCE.
RA Munekata E., Ohtaki T., Ichikawa T., McMaster D., Lederis K.;
RL (in) Rich D.H., Gross E. (eds.);
RL Proceedings of the 7th American peptide symposium, pp.69-72, Pierce Chemical Co., Rockford IL. (1981)
CC -!- FUNCTION: Urotensin is found in the teleost caudal neurosecretory system. It has a suggested role in osmoregulation and as a corticotrophin-releasing factor.

CC -!- SUBCELLULAR LOCATION: Secreted.
CC InterPro: IPR001483; Urotensin II.
DR Pfam; PF02083; Urotensin II; 1.
DR PROSITE; PS00984; UROTENSIN_II; 1.

KM Direct protein sequencing; Hormone.
 FT DISUFID 6 11
 FT VARIANT 2 2 G->S
 SQ SEQUENCE 12 AA; 1407 MW; 73960A9FB879CEBB CRC64;
 Query Match 27.9%; Score 24; DB 1; Length 12;
 Best Local Similarity 33.3%; Pred. No. 5.5e+03;
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 GCKEDLWE 15
 DB 1 GGNTCECFWK 9

RESULT 7
 ID CRBL_VESXA STANDARD; PRT; 13 AA.
 AC P17234;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Vespid chemotactic peptide X (VSCP-X).
 OS Vespa xanthoptera (Japanese hornet).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vespidae; Vespinae; Vespa.
 NC NCB1_TaxID=7448;
 RN [1]
 RC SEQUENCE.
 RP TISSUE=Venom;
 RA Yasuhara T., Iokawa H., Suzuki N., Nakamura H., Nakajima T.;
 RL (in) Izumiya N. (eds.);
 RL Peptide chemistry 1984, pp.177-182, Protein Research Foundation, Osaka
 CC (1985).
 CC -1- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
 of neutrophils.
 CC Amidation; Chemotaxis; Direct protein sequencing;
 CC Mast cell degranulation.
 KW MOD.RES 13
 FT MOD.RES 13
 SQ SEQUENCE 13 AA; 1368 MW; C85040365DF9233D CRC64;
 Query Match 27.9%; Score 24; DB 1; Length 13;
 Best Local Similarity 37.5%; Pred. No. 5.9e+03;
 Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSMCG 8
 DB 4 IIAKLGG 11

RESULT 8
 ID Q7M1U1 PRELIMINARY; PRT; 13 AA.
 AC Q7M1U1;
 DT 01-MAR-2004 (T-EMBLrel. 26, Created)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Unidentified 6.3/40K protein (Fragment).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriarthoidae; Oryzaceae; Oryza.
 NC NCB1_TaxID=4530;
 RN [1]
 RP SEQUENCE.
 RA Komatsu S., Kajiwara H., Hirano H.;
 RT "A rice proteol library: a data-file of rice proteins separated by
 RT two-dimensional electrophoresis";
 RL Theor. Appl. Genet. 86:935-942(1993).
 DR PIR; P00700; P00700.
 DR Grameine; Q7M1U1; -.
 FT NON_TER 1 1
 FT NON_TER 13 13

SQ SEQUENCE 13 AA; 1218 MW; 27EA7291E7DD878 CRC64;
 Query Match 27.9%; Score 24; DB 2; Length 13;
 Best Local Similarity 41.7%; Pred. No. 5.9e+03;
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 VVARSMCGDLI 13
 DB 1 VAGAYGADIL 12

RESULT 9
 ID RL11_STRAU STANDARD; PRT; 15 AA.
 AC Q9X520;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE 50S ribosomal protein L11 (Fragment).
 GN Name=rpL1;
 OS Streptomyces aureofaciens.
 OC Bacteria; Actinobacteria; Actinomycetales;
 OC Streptomycetales; Streptomycetaceae; Streptomyces.
 NC NCB1_TaxID=1894;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 10762 / CCM 3239;
 RA Kormanec J., Novakova R., Klucar L., Homerova D., Sevcikova B.,
 RA Sprusansky O.;
 RT "Cloning of the rplA gene encoding ribosomal protein L1 from
 RT Streptomyces aureofaciens, and its transcriptional analysis in the
 RT course of differentiation";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: This protein binds directly to 23S ribosomal RNA (by
 CC similarity).
 CC -1- PTM: One or more lysine residues are methylated (by similarity).
 CC -1- SIMILARITY: Belongs to the ribosomal protein L11P family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF120458; AAD24568.1; -.
 DR HAMAP; MF_00736; -; 1.
 DR InterPro; IPR006911; Ribosomal_L11.
 DR Pfam; PF00288; Ribosomal_L11; 1.
 DR PROSITE; PS00359; RIBOSOMAL_L11; PARTIAL.
 KW Methylation; Ribosomal protein; rRNA-binding.
 FT NON_TER 1 1
 SQ SEQUENCE 15 AA; 1476 MW; 80B147826B0701A8 CRC64;
 Query Match 27.9%; Score 24; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.8e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ARSMG 7
 DB 6 ARSMG 10

RESULT 10
 ID Q6QOR7 PRELIMINARY; PRT; 15 AA.
 AC Q6QOR7;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Hypothetical protein (Fragment).
 NC ORFNames=HP1080;
 GN

```

OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=92-28;
RA Terry C., Madigan K., McGinnis L., Cao P., Cover T., Liechti G.,
RA Peek R., Jr., Forsyth M.; to the EMBL/GenBank/DBJ databases.
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF529680; AAS20947.1; -.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 15 AA; 1780 MW; 4F3C63D9DD7D6BED CRC64;

Query Match
Best Local Similarity 27.9%; Score 24; DB 2; Length 15;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 RSMGKED 11
DB 6 RFLGSKNE 13

RESULT 11
O9H1Z6 PRELIMINARY; PRT; 12 AA.
ID O9H1Z6
AC O9H1Z6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Estrogen receptor 1 (Fragment).
GN Name=ESR1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN
RP SEQUENCE FROM N.A.
RA Gonzalez-Gomez F., Vergara F., Pedrosa C., Ramirez J.P.,
RA Castrilla J.A., Yoldi A., Ruiz A., Real L.M.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF326912; AAG42501.1; -.
GO GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER
FT NON_TER
SQ SEQUENCE 12 AA; 1385 MW; 09168BCB76C41404 CRC64;

Query Match
Best Local Similarity 26.7%; Score 23; DB 2; Length 12;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RSMGKKE 10
DB 6 RROGGRRE 12

RESULT 12
O9UPB5 PRELIMINARY; PRT; 13 AA.
ID O9UPB5
AC O9UPB5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Inosine monophosphatase 2 (Fragment).
GN Name=IMP2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN
RP SEQUENCE FROM N.A.

```

```

RX MEDLINE=97463449; PubMed=9322233;
RA Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,
RA Decker-Wadleigh S.D.;
RL "A novel human myo-inositol monophosphatase gene, IMP18p, maps to a
RL susceptibility region for bipolar disorder.";
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=20284187;
RA Yoshikawa T., Padigaru M., Karkera J.D., Sharma M., Berrettini W.H.,
RA Esterling L.E., Decker-Wadleigh S.D.;
RL "Genomic structure and novel variants of myo-inositol monophosphatase
RL 2.";
RN
RX MEDLINE=5165-171(2000).
DR EMBL; AF025886; AAD22138.1; -.
DR EMBL; AF025885; AAD22138.1; JOINED.
FT NON_TER
FT NON_TER
SQ SEQUENCE 13 AA; 1331 MW; 89C724C8E3457865 CRC64;

Query Match
Best Local Similarity 26.7%; Score 23; DB 2; Length 13;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLI 13
DB 1 IVIDTSGGPLDLM 13

RESULT 13
ID U07_ORYSA STANDARD; PRT; 14 AA.
AC P83648;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of leaf (OsL8) (Fragments).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriocarideae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN
RP SEQUENCE.
RA STRAIN=cv. Indica / IR64; TISSUE=leaf;
RA Hosseini Salekdeh S.G., Bennett J.;
RL "Proteome analysis of rice leaf.";
RL Submitted (JUL-2003) to Swiss-Prot.
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.2, its MW is: 28 kDa.
CC -1- CAUTION: The order of the peptides is uncertain.
KW Chloroplast; Direct protein sequencing.
FT NON_TER
FT UNSTRE
FT UNSTRE
FT NON_CONS
FT UNSTRE
FT NON_TER
SQ SEQUENCE 14 AA; 1403 MW; CC78FBF817B5C8FB2 CRC64;

Query Match
Best Local Similarity 26.7%; Score 23; DB 1; Length 14;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 VVARSMGKEDLI 12
DB 1 VVANIGVTTEL 11

RESULT 14
O8UUE1 PRELIMINARY; PRT; 16 AA.
ID O8UUE1
AC O8UUE1;
DT 01-MAR-2002 (TREMBLrel. 20, Created)

```

```

DT 01-MAR-2002 (T-EMBLrel. 20, last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, last annotation update)
DE Rhodospirillum rubrum (Fragment).
GN Name=RDPI;
OS Megapodius tentativus (Tentative scrubfowl).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Megapodidae; Megapodius.
OX NCBI_TaxID=17170;
RN [1]
RP SEQUENCE FROM N.A.
RA Birks S.M., Edwards S.V.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF394659; AAL36887.1; -.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1683 MW; CDC571884A940BF0 CRC64;

Query Match
Best Local Similarity 40.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 8 GKEDLIWBL 17
Db 2 GGEIALMSLV 11

```

RESULT 15

```

ID Q8UUE2 PRELIMINARY; PRT; 16 AA.
AC Q8UUE2;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, last annotation update)
DE Rhodospirillum rubrum (Fragment).
GN Name=RDPI;
OS Megapodius tentativus (Tentative scrubfowl).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Megapodidae; Megapodius.
OX NCBI_TaxID=17170;
RN [1]
RP SEQUENCE FROM N.A.
RA Birks S.M., Edwards S.V.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF394658; AAL36886.1; -.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1683 MW; CDC571884A940BF0 CRC64;

```

```

Query Match
Best Local Similarity 40.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy 8 GKEDLIWBL 17
Db 2 GGEIALMSLV 11

```

Search completed: November 1, 2005, 13:31:48
Job time : 169 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:28:13; Search time 131.574 Seconds

(without alignments)
67.608 Million cell updates/sec

Title: US-10-612-162a-2

Sequence: 1 TTEDSIAXKIMNGEADMSLDGCF 23

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

A_Geneseq_16Dec04:*
1: geneseq1980a:*
2: geneseq1990a:*
3: geneseq2000a:*
4: geneseq2001a:*
5: geneseq2002a:*
6: geneseq2003a:*
7: geneseq2003b:*
8: geneseq2004a:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	100.0	23	ADG46076	Adg46076 Human CDT
2	110	95.7	328	AA884371	Aa884371 Angiotens
3	110	95.7	539	AAU02980	Aau02980 Human met
4	110	95.7	575	ABR82321	AbR82321 Human dia
5	110	95.7	609	ABM63782	Abm63782 Human dia
6	110	95.7	627	ABM83781	Abm83781 Human dia
7	110	95.7	628	ABM83779	Abm83779 Human dia
8	110	95.7	643	ABM83778	Abm83778 Human dia
9	110	95.7	645	ABM83783	Abm83783 Human dia
10	110	95.7	646	AAU02938	Aau02938 Angiotens
11	110	95.7	646	ABM83780	Abm83780 Human dia
12	110	95.7	665	AAU02937	Aau02937 Angiotens
13	110	95.7	679	ABP72820	Abp72820 Human tra
14	110	95.7	679	ADH89360	Adh89360 Human tra
15	110	95.7	679	ADK15869	Adk15869 Mature hu
16	110	95.7	679	ADL70732	Adl70732 Human tra
17	110	95.7	679	ADL24413	Adl24413 Human tra
18	110	95.7	698	AAK12499	AaK12499 Human tra
19	110	95.7	698	AAK66492	AaK66492 Human tra
20	110	95.7	698	AAK66492	AaK66492 Human tra
21	110	95.7	698	AAK66492	AaK66492 Human tra
22	110	95.7	698	ABP72819	Abp72819 Human tra
23	110	95.7	698	ADK15869	Adk15869 Mature hu
24	110	95.7	698	ADL70732	Adl70732 Human tra
25	110	95.7	698	ADL24413	Adl24413 Human tra

ALIGNMENTS

RESULT 1	ADG46076	standard; peptide; 23 AA.
ADG46076	ADG46076	
AC	ADG46076	
XX		
DT	25-MAR-2004	(first entry)
XX		
DE	Human CDT peptide fragment #2.	
XX		
KM	antibody; carbohydrate-deficient transferrin; CDT;	
KW	non-glycosylated transferrin; alcoholism; alcoholic; diagnosis; human.	
XX		
OS	Homo sapiens.	
XX		
PN	EP1378521-A1.	
XX		
PD	07-JAN-2004.	
XX		
PF	19-MAY-2003; 2003EP-00011334.	
XX		
PR	05-JUL-2002; 2002DE-01030550.	
XX		
PA	(DADE-) DADE BEHRING MARBURG GMBH.	
XX		
PI	Althaus H;	
XX		
DR	WPI; 2004-073743/08.	
XX		
PT	New antibody specific for carbohydrate-deficient transferrin, useful for	
PT	diagnosis of alcoholism, can bind its target in solution, eliminating	
PT	need for immobilization.	
XX		
PS	Claim 4; SEQ ID NO 2; 21pp; German.	
XX		
CC	This invention describes a novel antibody that, in aqueous solution,	
CC	binds selectively to carbohydrate-deficient transferrin (CDT) without	
CC	having to bind CDT to a solid phase. The invention also describes an	
CC	antibody that binds selectively to CDT at regions containing the	
CC	sequences VVARSMGSGEDLWEL, TTEDSIAXKIMNGEADMSLDGCF, SKLSGSLNUEPN and	
CC	YEKYLGEERYKAV (ADG46075-ADG46078) and an immunoassay for detecting CDT	
CC	using the antibodies of the invention. The antibodies of the invention	
CC	are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The	
CC	antibodies are obtained by immunisation with non-glycosylated	
CC	transferrin, or a fragment, then generation of hybridomas by standard	
CC	fusion of spleen and myeloma cells. Hybridomas are then selected for	
CC	production of antibodies that specifically bind CDT from the aqueous	
CC	phase. The antibodies are useful for diagnosis of alcoholism, CDT, which	

26	110	95.7	698	8	ADH34559	Adh34559 Human tra
27	110	95.7	698	8	ADH89359	Adh89359 Human tra
28	110	95.7	698	8	ADK15868	Adk15868 Human tra
29	110	95.7	698	8	ADL70731	Adl70731 Human tra
30	110	95.7	698	8	ADL24412	Adl24412 Human tra
31	110	95.7	698	8	ADP21259	Adp21259 Human tra
32	110	95.7	1074	2	AAW07621	Aaw07621 LDR/TF C
33	110	95.7	1410	2	AAW07622	Aaw07622 LDR/TF C
34	110	95.7	1410	6	ABU04139	Abu04139 Human exp
35	110	95.7	1418	4	AAU32831	Aau32831 Novel hum
36	110	95.7	1418	6	ABU04138	Abu04138 Human exp
37	101	87.8	676	8	ADL70764	Adl70764 Rabbit tr
38	101	87.8	676	8	ADL24458	Adl24458 Rabbit tr
39	96	83.5	688	8	ADL70767	Adl70767 Horse tra
40	96	83.5	688	8	ADL24461	Adl24461 Horse tra
41	93.5	81.3	696	1	AAU70384	Aau70384 Sequence
42	92	80.0	677	8	ADL70766	Adl70766 Mouse tra
43	92	80.0	677	8	ADL24460	Adl24460 Murine tr
44	92	80.0	685	2	AAK11664	AaK11664 Partial p
45	92	80.0	685	2	AAK11663	AaK11663 Partial p

CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
CC alcohols. The antibodies allow direct detection of CPT in solution,
CC eliminating the need for immobilising it on a solid phase (as required
CC when using known antibodies). ADG46075-ADG4694 represent CPT peptide
CC fragments used in the method of the invention.

XX Sequence 23 AA;

Query Match 100.0%; Score 115; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 4e-11; Mismatches 0; Gaps 0;
Matches 23; Conservative 0; Indels 0;

Qy 1 TTEDSIKIMNGEADAMSLDGGF 23
Db 1 TTEDSIKIMNGEADAMSLDGGF 23

RESULT 2
AAB84371
ID AAB84371 standard; protein; 328 AA.

XX AAB84371;

XX 22-AUG-2001 (first entry)

XX Amino acid sequence of a human transferrin.

XX Humen; transferrin; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; cerebral ischemia;
KW angiogenesis; nervous system disorder; Alzheimer's disease; infection;
KW ocular disorder; corneal infection; wound healing;
KW epithelial cell proliferation; aging; organ transplant.

XX Homo sapiens.

XX WO200146254-A1.

XX 28-JUN-2001.

XX 21-DEC-2000; 2000WO-US034769.

XX 23-DEC-1999; 99US-0171595P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Shi Y, Choi GH;

XX WPI, 2001-381910/40.

XX N-PSDB; AAH25190.

XX Isolated nucleic acid molecule encoding a human transferrin protein is
XX used in preventing, treating or ameliorating a medical condition.

XX Claim 11; Page 286-287; 290pp; English.

XX The present sequence represents human transferrin polypeptide.

XX Transferrin polypeptides and polynucleotides are used to prevent, treat
CC or ameliorate a medical condition in e.g. humans, mice, rabbits, goats,
CC horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or
CC treated include autoimmune diseases e.g. Rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and
CC ocular disorders e.g. corneal infection. The polypeptides can also be
CC used to aid wound healing and epithelial cell proliferation, to prevent
CC skin aging due to sunburn, to maintain organs before transplantation, for
CC supporting cell culture of primary tissues, to regenerate tissues and in
CC chemotaxis. The polypeptides can also be used as a food additive or
CC preservative to increase or decrease storage capabilities

XX Sequence 328 AA;

Query Match 95.7%; Score 110; DB 4; Length 328;
Best Local Similarity 95.7%; Pred. No. 5.6e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTEDSIKIMNGEADAMSLDGGF 23
Db 56 TTEDSIKIMNGEADAMSLDGGF 78

RESULT 3
AAU02980
ID AAU02980 standard; protein; 539 AA.

XX AAU02980;

XX 12-SEP-2001 (first entry)

XX Angiotensin converting enzyme (ACEV) splice variant protein #80.

XX Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW platelet-derived endothelial cell growth factor; cardiovascular disease;
KW cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
KW vasodilative intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW myocardial infarction; coronary arterial thrombosis; renal disease;
KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW nonarctoidic pulmonary granulomatous disease; endothelial abnormality;
KW vascular disorder; asbestosis.

XX Homo sapiens.

XX WO200136632-A2.

XX 25-MAY-2001.

XX 17-NOV-2000; 2000WO-IL000766.

XX 17-NOV-1999; 99IL-00132978.

XX 10-DEC-1999; 99IL-00133455.

XX (COMP-) COMPUGEN LTD.

XX Levine Z, David A, Azar I, Khosravi R, Bernstein J;

XX WPI, 2001-336004/35.

XX N-PSDB; AAS06080.

XX Novel alternative splicing variants e.g. variant of angiotensin
XX converting enzyme (ACEV), useful in identifying candidate compounds
XX capable of binding to the variant and to detect anti-variant antibodies.

XX Claim 4; Fig 80; 519pp; English.

XX The sequence represents an angiotensin converting enzyme splice variant
CC (ACEV) polypeptide. The polypeptides of the invention include variants of
CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
CC inhibitor 1C, cellular tumour antigen P53, and vasodilative intestinal
CC polypeptide receptor 2. The polypeptides and their associated nucleic
CC acids are useful for identification of variant sequences and detection of
CC candidate compounds capable of binding the molecules. The sequences of
CC the invention can be used in the treatment and diagnosis of various
CC disorders including cardiovascular diseases such as arteriosclerosis,
CC myocardial infarction and coronary arterial thrombosis, renal diseases
CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
CC immune disorders such as immune complex nephritis, multiple sclerosis,
CC cancer, sarcoidosis, nonarctoidic pulmonary granulomatous diseases such
CC as asbestosis and vascular pathologies involving an endothelial
CC abnormality such as deep vein thrombosis

XX Sequence 539 AA;

	Query Match	95.7%	Score 110,	DB 4;	Length 539;
	Best Local Similarity	95.7%;	Pred. No. 1e-08;		
	Matches 22;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 6
Oy	1 TTEDSIAKINMGADAMSLDGGF 23 				
Dd	265 TTEDCIAKINMGADAMSLDGCF 267				
RESULT 4					
ID	ABR82321 standard; protein; 575 AA.				
XX	ABR82321:				
AC					
XX					
DT	06-NOV-2003 (first entry)				
DE	Human metalloprotein (MEPR) polypeptide (id=750932BODL).				
KM	MEPR; metalloproteins; anti-HIV; antiallergic; antiinflammatory; human;				
KW	antianemic; antidyskinesia; neurotropic; anticoagulant; cytotoxic;				
KX	antiarteriosclerotic; antiaslomatic; immunosuppressive; antithyroid;				
KY	hepatotropic; dermatological; antidiabetic; nephrotropic; antigout;				
LK	thyromimetic; neuroprotective; osteoparatic; arthritis; utrophathic;				
KM	antiparasitic; anthelmintic; antispasmodic; ophthalmological; virucide;				
KH	antineuragic; haemostatic; antibacterial; protozoacide; fungicide;				
KS	gene therapy; transgenic.				
OS	Homo sapiens.				
XX					
PN	WO2003060089-A2.				
PD					
XX	24-JUL-2003.				
PF					
XX	14-JAN-2003; 2003WO-US001485.				
PR	14-JAN-2002; 2002US-034876P.				
PR	18-JAN-2002; 2002US-035070IP.				
PR	19-MAR-2002; 2002US-036059P.				
PR	10-MAY-2002; 2002US-0379907P.				
PA	(INCY-) INCYTE GENOMICS INC.				
XI					
PI	Kable AE, Griffin JA, Gervad AE, Becha SD, Richardson TW;				
EI	Emerling BM, Chien D, Jin F, Chawla NK, Yue H, Khare R, Marguis JP				
PT	Tang YT;				
DR	N-PSDb; ACPFS5812.				
XX					
XX	WPJ; 2003-598523/56.				
PS					
XX	Claim 1; Page 146-148; 153pp; English.				
CC	The invention relates to novel human metalloproteins (MEPR) and encoding				
CC	polynucleotides. The human MEPR polypeptides, polynucleotides and				
CC	molecules are useful for diagnosing, treating or preventing disorders				
CC	associated with aberrant expression of MEPR, particularly cell				
CC	proliferative disorders (e.g. arterio sclerosis, atherosclerosis,				
CC	cirrhosis, hepatitis, paroxysmal nocturnal hemoglobinuria, polycythemia				
CC	vera, psoriasis), primary thrombocytopenia or cancer); developmental				
CC	disorders (e.g. renal tubular acidosis, anemia or mental retardation),				
CC	neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or				
CC	epilepsy), autoimmune/inflammatory disorders (e.g. AIDS, allergies,				
CC	asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease,				
CC	diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout,				
CC	Graves' disease, Hashimoto's thyroiditis, irritable bowel syndrome,				
CC	multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's				
CC	sndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,				

bacteria, fungal, parasitic, protozoan or helminthic infections. The polynucleotides encoding MEPR are useful for creating transgenic animals to model human disease. Sequences ABR82316-323 represent the human MEPR polypeptides of the invention

Sequence 575 AA:

Query Match 95.7%; Score 110; DB 6; Length 575;
Best Local Similarity 95.7%; Pred. NO. 1.1e-06;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 269 TTEDCIKINMGADAMSLDGGF 291
1 TTEDSIKINMGADAMSLDGGF 23
|||||||
|||||||

RESULT 5
ABM83782
ID ABM83782 standard; protein; 609 AA.
XX AC
XX AEM83782;
XX 18-NOV-2004 (first entry)
DT Human diagnostic and therapeutic pprotein SEQ ID NO.4031.
DE gene therapy; human diagnostic and therapeutic polynucleotide; dtbp.
XX
XX Homo sapiens.
OS
PN WO2004023973-A2.
PD
PD 25-MAR-2004.
PE
PE 12-SEP-2003; 2003MO-US028227.
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic NM, Shen F;
PI Hachbornre TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstlin EH;
PI Peralla CH, Anderson SB, Rious P, Shen EJ, Wu MC, Stuve LJ;
PI Lagace RE, Spico PA, Stewart EA, Wingrove J, Vitt UA, Kitron ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patrucy S, Shi X, Suarez CJ;
XX
XX WPI; 2004-329368/30.
DR N-PSDB; ACN42434.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
XX Claim 27; Page; 190pp; English.

The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dtbp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorder, gastrointestinal disorders, infectious diseases caused by virus, bacteria, fungi or parasite. The dtbp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dtbp protein of the

CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX SQ Sequence 609 AA;

Query Match 95.7%; Score 110; DB 8; Length 609;
Best Local Similarity 95.7%; Pred. No. 1.2e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIATKIMGADAMSJDGF 23
|||
DB 321 TTEDCIATKIMGADAMSJDGF 343

RESULT 6

ABM83781
ID ABM83781 standard; protein; 627 AA.

XX AC ABM83781;

XX DT 18-NOV-2004 (first entry)

XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:4030.

XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dthp.

XX OS Homo sapiens.

XX PN WO2004023973-A2.

XX PD 25-MAR-2004.

XX PF 12-SEP-2003; 2003WO-US028227.

XX PR 12-SEP-2002; 2002US-0410259P.

XX PR 12-SEP-2002; 2002US-0410260P.

XX PA (INCY-) INCYTE CORP.

XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Hartschorn TR, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve IL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;

XX WIPI; 2004-329368/30.

XX DR N-PSDB; ACN42433.

XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

XX PS Claim 27; Page: 190pp; English.

XX CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dthp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly

CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX SQ Sequence 627 AA;

Query Match 95.7%; Score 110; DB 8; Length 627;
Best Local Similarity 95.7%; Pred. No. 1.2e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIATKIMGADAMSJDGF 23
|||
DB 321 TTEDCIATKIMGADAMSJDGF 343

RESULT 7

ABM83779
ID ABM83779 standard; protein; 628 AA.

XX AC ABM83779;

XX DT 18-NOV-2004 (first entry)

XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:4028.

XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dthp.

XX OS Homo sapiens.

XX PN WO2004023973-A2.

XX PD 25-MAR-2004.

XX PF 12-SEP-2003; 2003WO-US028227.

XX PR 12-SEP-2002; 2002US-0410259P.

XX PR 12-SEP-2002; 2002US-0410260P.

XX PA (INCY-) INCYTE CORP.

XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Hartschorn TR, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve IL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;

XX WIPI; 2004-329368/30.

XX DR N-PSDB; ACN42431.

XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

XX PS Claim 27; Page: 190pp; English.

XX CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dthp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly

CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 628 AA;
Query Match 95.7%; Score 110; DB 8; Length 628;
Best Local Similarity 95.7%; Pred. No. 1.2e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTEDSIATKIMNGEADAMSIDGGF 23
DB 340 TTEDCIATKIMNGEADAMSIDGGF 362
RESULT 8
ABM83778 ID ABM83778 standard; protein; 643 AA.
XX
XX ABM83778;
AC
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic protein SEQ ID NO:4027.
XX
KM gene therapy; human diagnostic and therapeutic polynucleotide; dittp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PP 12-SEP-2003; 2003MO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
XX
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Hartschorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kitton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
XX WPI; 2004-329368/30.
XX
XX N-PsDB; ACN42430.
XX
DR
XX
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
XX
PS Claim 27; Page; 190pp; English.
XX
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dittp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders, endocrine
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dittp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dittp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX
SQ Sequence 643 AA;
Query Match 95.7%; Score 110; DB 8; Length 643;
Best Local Similarity 95.7%; Pred. No. 1.2e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTEDSIATKIMNGEADAMSIDGGF 23
DB 355 TTEDCIATKIMNGEADAMSIDGGF 377
RESULT 9
ABM83783 ID ABM83783 standard; protein; 645 AA.
XX
XX ABM83783;
AC
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4032.
XX
KM gene therapy; human diagnostic and therapeutic polynucleotide; dittp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PP 12-SEP-2003; 2003MO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
XX
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Hartschorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kitton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
XX WPI; 2004-329368/30.
XX
XX N-PsDB; ACN42435.
XX
DR
XX
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
XX
PS Claim 27; Page; 190pp; English.
XX
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dittp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders, endocrine
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dittp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dittp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

SQ Sequence 645 AA;
 Query Match 95.7%; Score 110; DB 8; Length 645;
 Best Local Similarity 95.7%; Pred. No. 1.2e-08;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTEDSIKIMNGEADAMSJDGGF 23
 |||
 DB 339 TTEDCIKIMNGEADAMSJDGGF 361
 RESULT 10
 AAU02938
 ID AAU02938 standard; protein; 646 AA.
 XX
 AC AAU02938;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Angiotensin converting enzyme (ACEV) splice variant protein #38.
 XX
 KM Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
 KM granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
 KM platelet-derived endothelial cell growth factor; cardiovascular disease;
 KM cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
 KM vasodilator intestinal polypeptide receptor 2; arteriosclerosis; cancer;
 KM myocardial infarction; coronary arterial thrombosis; renal disease;
 KM diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
 KM multiple sclerosis; immune complex nephritis; deep vein thrombosis;
 KM noncardiotoxic pulmonary granulomatous disease; endothelial abnormality;
 KM vascular disorder; asbestosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200136632-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 17-NOV-2000; 2000MO-IL000766.
 XX
 PR 17-NOV-1999; 99IL-00132978.
 XX
 PR 10-DEC-1999; 99IL-00133455.
 XX
 PA (COMP-) COMPUGEN LTD.
 XX
 PI Levine Z, David A, Azar I, Khosravi R, Bernstein J;
 XX
 DR WPI, 2001-336004/35.
 DR N-PSDB; AAS06038.
 XX
 PT Novel alternative splicing variants e.g. variant of angiotensin
 PT converting enzyme (ACEV), useful in identifying candidate compounds
 PT capable of binding to the variant and to detect anti-variant antibodies.
 XX
 PS Claim 4; Fig 38; 519pp; English.
 XX
 CC The sequence represents an angiotensin converting enzyme splice variant
 CC (ACEV) polypeptide. The polypeptides of the invention include variants of
 CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
 CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
 CC inhibitor 1C, cellular tumour antigen P53, and vasodilator intestinal
 CC polypeptide receptor 2. The polypeptides and their associated nucleic
 CC acids are useful for identification of variant sequences and detection of
 CC candidate compounds capable of binding to the molecules. The sequences of
 CC the invention can be used in the treatment and diagnosis of various
 CC disorders including cardiovascular diseases such as arteriosclerosis,
 CC myocardial infarction and coronary arterial thrombosis, renal diseases
 CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
 CC immune disorders such as immune complex nephritis, multiple sclerosis,
 CC cancer, sarcoidosis, noncardiotoxic pulmonary granulomatous diseases such
 CC as asbestosis and vascular pathologies involving an endothelial
 CC abnormality such as deep vein thrombosis
 XX

SQ Sequence 646 AA;
 Query Match 95.7%; Score 110; DB 4; Length 646;
 Best Local Similarity 95.7%; Pred. No. 1.2e-08;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTEDSIKIMNGEADAMSJDGGF 23
 |||
 DB 392 TTEDCIKIMNGEADAMSJDGGF 414
 RESULT 11
 ABM83780
 ID ABM83780 standard; protein; 646 AA.
 XX
 AC ABM83780;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human diagnostic and therapeutic protein SEQ ID NO:4029.
 XX
 KM gene therapy; human diagnostic and therapeutic polynucleotide; ditnp.
 XX
 OS Homo sapiens.
 XX
 PN WO2004023973-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 12-SEP-2003; 2003MO-US028227.
 XX
 PR 12-SEP-2002; 2002US-0410259P.
 XX
 PR 12-SEP-2002; 2002US-0410260P.
 XX
 PA (INCY-) INCYTE CORP.
 XX
 PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
 PI Hartschorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV;
 PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
 PI Peralta CH, Anderson SB, Rioux P, Shen E, Wu MC, Stuve LI;
 PI Lagace RE, Spilo PA, Stewart EA, Wingrove J, Vile UA, Kirton BS;
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patury S, Shi X, Suarez CJ;
 XX
 DR WPI, 2004-329368/30.
 DR N-PSDB; ACN42432.
 XX
 PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 XX
 PS Claim 27; Page; 190pp; English.
 XX
 CC The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (ditnp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The ditnp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germ-line
 CC gene therapy. The present sequence represents a ditnp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX
 SQ Sequence 646 AA;
 XX

Query Match 95.7%; Score 110; DB 8; Length 646;
Best Local Similarity 95.7%; Pred. No. 1.2e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTEDSIKIMNGEADAMSJDGF 23
Db 340 TTEDCIKIMNGEADAMSJDGF 362

RESULT 12

AAU02937
ID AAU02937 standard; protein; 665 AA.

XX AAU02937;

DT 12-SEP-2001 (first entry)

DE Angiotensin converting enzyme (ACEV) splice variant protein #37.

XX Angiotensin converting enzyme splice variant; ACEV, interleukin 6;
KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW platelet-derived endothelial cell growth factor; cardiovascular disease;
KW cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW myocardial infarction; coronary arterial thrombosis; renal disease;
KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW nonarctoidic pulmonary granulomatous disease; endothelial abnormality;
KW vascular disorder; atherosclerosis.

XX Homo sapiens.

XX WO200136632-A2.

XX 25-MAY-2001.

XX 17-NOV-2000; 2000MO-IL000766.

XX 17-NOV-1999; 99IL-00132978.

XX 10-DEC-1999; 99IL-00133455.

XX (COMP-) COMPUGEN LTD.

XX PA Levine Z, David A, Azar I, Khosravi R, Bernstejn J;

XX PI WPI; 2001-336004/35.

XX DR N-PSDB; AAS06037.

XX Novel alternative splicing variants e.g. variant of angiotensin
PT converting enzyme (ACEV), useful in identifying candidate compounds
PT capable of binding to the variant and to detect anti-variant antibodies.

XX Claim 4; Fig 37; 519pp; English.

XX The sequence represents an angiotensin converting enzyme splice variant
CC (ACEV) polypeptide. The polypeptides of the invention include variants of
CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
CC inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal
CC polypeptide receptor 2. The polypeptides and their associated nucleic
CC acids are useful for identification of variant sequences and detection of
CC candidate compounds capable of binding the molecules. The sequences of
CC the invention can be used in the treatment and diagnosis of various
CC disorders including cardiovascular diseases such as arteriosclerosis,
CC myocardial infarction and coronary arterial thrombosis, renal diseases
CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
CC immune disorders such as immune complex nephritis, multiple sclerosis,
CC cancer, sarcoidosis, nonarctoidic pulmonary granulomatous diseases such
CC as atherosclerosis and vascular pathologies involving an endothelial
CC abnormality such as deep vein thrombosis

XX Sequence 665 AA;

Query Match 95.7%; Score 110; DB 4; Length 665;
Best Local Similarity 95.7%; Pred. No. 1.3e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTEDSIKIMNGEADAMSJDGF 23
Db 392 TTEDCIKIMNGEADAMSJDGF 414

RESULT 13

ABP72820
ID ABP72820 standard; protein; 679 AA.

XX ABP72820;

DT 11-AUG-2003 (first entry)

DE Human transferrin (mature polypeptide).

XX Human; transferrin; neuroprotective; cerebroprotective; vasotropic;
KW antiparkinsonian; nootropic; anti-HIV; antiallergic; antiasthmatic;
KW cytotactic; immunosuppressive; antiatherosclerotic; cardiac;
KW gynaecological; immunostimulant; antinaemic; haemostatic;
KW antiinflammatory; dermatological; antibacterial; virucide; antiparasitic;
KW fungicide; hepatotropic; antineumatic; antiarthritic; antigout;
KW tranquilizer; vulnary; antidiabetic; nephrotropic; antipyretic;
KW gastrointestinal; gene therapy; transgenic animal.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FH Binding-site 63 /note= "Iron binding site"

XX FT Region 94..96 /note= "Hinge region"

XX FT Binding-site 95 /note= "Hinge region"

XX FT Binding-site 120 /note= "Iron binding site"

XX FT Binding-site 124 /note= "Carbonate ion binding site"

XX FT Binding-site 126 /note= "Carbonate ion binding site"

XX FT Binding-site 127 /note= "Carbonate ion binding site"

XX FT Binding-site 188 /note= "Carbonate ion binding site"

XX FT Binding-site 188 /note= "Iron binding site"

XX FT Region 245..247 /note= "Hinge region"

XX FT Binding-site 249 /note= "Hinge region"

XX FT Binding-site 316..318 /note= "Iron binding site"

XX FT Region 316..318 /note= "Hinge region"

XX FT Binding-site 392 /note= "Iron binding site"

XX FT Modified-site 413 /note= "N-glycosylated"

XX FT Region 425..427 /note= "Hinge region"

XX FT Binding-site 426 /note= "Hinge region"

XX FT Binding-site 452 /note= "Iron binding site"

XX FT Binding-site 452 /note= "Carbonate ion binding site"

XX FT Binding-site 456 /note= "Carbonate ion binding site"

XX FT Binding-site 458 /note= "Carbonate ion binding site"

XX FT Binding-site 459 /note= "Carbonate ion binding site"

XX FT Binding-site 514 /note= "Carbonate ion binding site"

XX FT Binding-site 517 /note= "Iron binding site"

KM fusion protein; transferrin; Tf; beta-interferon; beta-IFN;
 KM glucagon-like peptide; GLP-1; erythropoietin mimetic peptide; EMP1;
 KM T-20; soluble toxin receptor; epitope tagging; human.

OS Homo sapiens.

PN US2003221201-A1.

PD 27-NOV-2003.

PF 04-MAR-2003; 2003US-00378094.

PR 30-AUG-2001; 2001US-0315745P.

PR 30-NOV-2001; 2001US-0334059P.

PR 30-AUG-2002; 2002US-00231494.

PR 30-AUG-2002; 2002US-0406977P.

PA (BIOR-) BIOREXIS PHARM CORP.

PI Prior CP, Lai C, Sadeghi H, Turner A;

DR WPI; 2004-010899/01.

PT New fusion protein comprising a modified transferrin (Tf) protein fused
 to a therapeutic protein or peptide, useful for epitope tagging.

PS Example 5; SEQ ID NO 3; 70pp; English.

CC The invention comprises a fusion protein that contains a modified
 CC transferrin (Tf) protein fused to a therapeutic protein/peptide (e.g.
 CC beta-interferon - IFN, glucagon-like peptide - GLP-1, erythropoietin
 CC mimetic peptide - EMP1, T-20 and soluble toxin receptor). The fusion
 CC protein of the invention is useful for epitope tagging. The present amino
 CC acid sequence represents the mature human Tf protein.

XX Sequence 679 AA;

XX Query Match 95.7%; Score 110; DB 8; Length 679;

XX Best Local Similarity 95.7%; Pred. No. 1,3e-08;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTEDSIKINNGEADAMSLDGGF 23

DB 373 TTEDCIKINNGEADAMSLDGGF 395

Search completed: November 1, 2005, 12:48:52
 Job time : 132.574 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: November 1, 2005, 12:37:09 ; Search time 33.8235 Seconds
(without alignments)
50.761 Million cell updates/sec

Title: US-10-612-162A-2

Perfect score: 115
Sequence: 1 TTEDSLAKIMNGEADMSUDGR 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfilea1.pep:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	110	95.7	698	2	US-08-175-158A-2
2	110	95.7	698	4	US-09-439-740-2
3	110	95.7	1074	2	US-08-470-058-2
4	110	95.7	1074	3	US-09-037-188-2
5	110	95.7	1074	3	US-09-285-310-2
6	110	95.7	1410	2	US-08-470-058-4
7	110	95.7	1410	3	US-09-037-188-4
8	110	95.7	1410	3	US-09-285-310-4
9	93.5	81.3	696	6	5262177-4
10	93.5	81.3	696	6	5262177-4
11	92	80.0	697	3	US-09-724-864-54
12	92	80.0	703	1	US-08-145-681-6
13	92	80.0	703	1	US-08-453-703-6
14	92	80.0	703	2	US-08-456-106-6
15	92	80.0	703	3	US-08-456-108-6
16	92	80.0	703	3	US-09-265-577-6
17	92	80.0	703	3	US-09-633-739-6
18	92	80.0	703	4	US-08-724-586-2
19	90	78.3	694	4	US-09-421-632-2
20	90	78.3	694	4	US-09-332-190-2
21	90	78.3	705	2	US-08-655-640-2
22	90	78.3	705	2	US-08-655-640-2
23	90	78.3	709	1	US-08-154-019-2
24	90	78.3	709	1	US-08-461-333-2
25	90	78.3	709	3	US-08-464-167-2
26	90	78.3	709	3	US-09-158-313-2
27	90	78.3	709	3	US-08-476-798-2

28	90	78.3	711	1	US-08-145-681-2	Sequence 2, App11
29	90	78.3	711	1	US-08-250-308-2	Sequence 2, App11
30	90	78.3	711	1	US-08-154-019-4	Sequence 4, App11
31	90	78.3	711	1	US-08-461-333-4	Sequence 4, App11
32	90	78.3	711	2	US-08-453-703-2	Sequence 2, App11
33	90	78.3	711	2	US-08-456-106-2	Sequence 2, App11
34	90	78.3	711	3	US-08-464-167-4	Sequence 4, App11
35	90	78.3	711	3	US-09-158-313-4	Sequence 4, App11
36	90	78.3	711	3	US-08-456-108-2	Sequence 2, App11
37	90	78.3	711	3	US-08-476-798-2	Sequence 2, App11
38	90	78.3	711	3	US-09-265-577-2	Sequence 2, App11
39	90	78.3	711	4	US-09-633-739-2	Sequence 2, App11
40	90	78.3	711	5	PCT-US93-03614-2	Sequence 2, App11
41	77	67.0	708	1	US-08-145-681-4	Sequence 4, App11
42	77	67.0	708	1	US-08-453-703-4	Sequence 4, App11
43	77	67.0	708	2	US-08-456-106-4	Sequence 4, App11
44	77	67.0	708	3	US-08-456-108-4	Sequence 4, App11
45	77	67.0	708	3	US-09-265-577-4	Sequence 4, App11

ALIGNMENTS

RESULT 1
US-08-175-158A-2

; Sequence 2, Application US/08175158A

; Patent No. 5986067

; GENERAL INFORMATION:

; APPLICANT: FUNK, Walter D.

; APPLICANT: MACGILLIVRAY, Ross T.A.

; APPLICANT: MASON, Anne B.

; APPLICANT: WOODMORTH, Robert C.

; TITLE OF INVENTION: RECOMBINANT TRANSFERRINS, TRANSFERRIN HALF-

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/175,158A

; FILING DATE: 28-DEC-1993

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/832,029

; FILING DATE: 06-FEB-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: DeConti, Giulio A.

; REGISTRATION NUMBER: 31,503

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 698 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-175-158A-2

Query Match 95.7%; Score 110; DB 2; Length 698;
Best Local Similarity 95.7%; Prod. No. 1e-09; 1; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKINGEADAMSJDGF 23
|||||
Db 392 TTEDCIKINGEADAMSJDGF 414

RESULT 2

US-09-439-740-2
Sequence 2, Application US/09439740
Patent No. 6825037
GENERAL INFORMATION:
APPLICANT: FUNK, Walter D.
APPLICANT: MACGILLIVRAY, Rose T.A.
APPLICANT: MASON, Anne B.
APPLICANT: WOODMORTH, Robert C.
TITLE OF INVENTION: RECOMBINANT TRANSFERRINS, TRANSFERRIN HALF-TITLE OF INVENTION: MOLECULES AND MUTANTS THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSES:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/439,740
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/175,158
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: UVI-005CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 698 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-439-740-2

Query Match 95.7%; Score 110; DB 4; Length 698;
Best Local Similarity 95.7%; Pred. No. 1e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKINGEADAMSJDGF 23
|||||
Db 392 TTEDCIKINGEADAMSJDGF 414

RESULT 3
US-08-470-058-2
Sequence 2, Application US/08470058
Patent No. 5817789
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
TITLE OF INVENTION: Chimeric Proteins For Use in Transport
TITLE OF INVENTION: of a Selected Substance Into Cells
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Millicia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TKT93-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-058-2

Query Match 95.7%; Score 110; DB 2; Length 1074;
Best Local Similarity 95.7%; Pred. No. 1.7e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKINGEADAMSJDGF 23
|||||
Db 768 TTEDCIKINGEADAMSJDGF 790

RESULT 4
US-09-037-188-2
Sequence 2, Application US/09037188
Patent No. 6027921
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,188
FILING DATE: 02-MAR-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-037-188-2

Query Match 95.7%; Score 110; DB 3; Length 1074;
Best Local Similarity 95.7%; Pred. No. 1.7e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEADAMSIDGCF 23
DB 768 TTEDCIKIMNGEADAMSIDGCF 790

RESULT 5
US-09-285-310-2
Sequence 2, Application US/09285310
Patent No. 6262026
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,310
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/037,188
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Frazer, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-285-310-2

Query Match 95.7%; Score 110; DB 3; Length 1074;
Best Local Similarity 95.7%; Pred. No. 1.7e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEADAMSIDGCF 23
DB 768 TTEDCIKIMNGEADAMSIDGCF 790

RESULT 6
US-08-470-058-4
Sequence 4, Application US/08470058
Patent No. 5817789
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
TITLE OF INVENTION: Chimeric Proteins For Use in Transport
OF A Selected Substance Into Cells
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TKT93-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-058-4

Query Match 95.7%; Score 110; DB 2; Length 1410;
Best Local Similarity 95.7%; Pred. No. 2.4e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEADAMSIDGCF 23
DB 1104 TTEDCIKIMNGEADAMSIDGCF 1126

RESULT 7
US-09-037-188-4
Sequence 4, Application US/09037188
Patent No. 6027921
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

```

; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/037,188
; FILING DATE: 02-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Ph.D., J.D., Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 07236/009002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1410 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
;
US-09-037-188-4

Query Match          95.7%; Score 110; DB 3; Length 1410;
Best Local Similarity 95.7%; Pred. No. 2,4e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEADAMSLDGGF 23
DB 1104 TTEDCIKIMNGEADAMSLDGGF 1126

RESULT 8
US-09-285-310-4
; Sequence 4, Application US/09285310
; Patent No. 6262026
; GENERAL INFORMATION:
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Lemont, Jeffrey F.
; APPLICANT: Concino, Michael F.
; TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
; TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,310
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/037,188
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Ph.D., J.D., Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 07236/009002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1410 amino acids
```

```

; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
;
US-09-285-310-4

Query Match          95.7%; Score 110; DB 3; Length 1410;
Best Local Similarity 95.7%; Pred. No. 2,4e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEADAMSLDGGF 23
DB 1104 TTEDCIKIMNGEADAMSLDGGF 1126

RESULT 9
5262177-4
; Patent No. 5262177
; APPLICANT: BROWN, J. JOSEPH P.; ESTIN, CHARLES D.; FLOWMAN, GREGORY
; D.; HELLSROM, KARL E.; ROSE, TIMOTHY M.; HELLSROM, INGEGERD;
; PURCHIO, ANTHONY F.; HU, SHU-LOK; PENNATHUR, SRIDHAR
; TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HHUMAN
; MELANOMA-ASSOCIATED ANTIGEN
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/7230
; FILING DATE: 27-JAN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 827,313
; FILING DATE: 07-FEB-1986
; SEQ ID NO: 4:
; LENGTH: 696
;
5262177-4

Query Match          81.3%; Score 93.5; DB 6; Length 696;
Best Local Similarity 91.3%; Pred. No. 5,4e-07;
Matches 21; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 TTEDSIKIMNGEADAMSLDGGF 23
DB 392 TTEDCIKIMN-EDAMSLDGGF 413

RESULT 10
5262177-4
; Patent No. 5262177
; APPLICANT: BROWN, J. JOSEPH P.; ESTIN, CHARLES D.; FLOWMAN, GREGORY
; D.; HELLSROM, KARL E.; ROSE, TIMOTHY M.; HELLSROM, INGEGERD;
; PURCHIO, ANTHONY F.; HU, SHU-LOK; PENNATHUR, SRIDHAR
; TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HHUMAN
; MELANOMA-ASSOCIATED ANTIGEN
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/7230
; FILING DATE: 27-JAN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 827,313
; FILING DATE: 07-FEB-1986
; SEQ ID NO: 4:
; LENGTH: 696
;
5262177-4

Query Match          81.3%; Score 93.5; DB 6; Length 696;
Best Local Similarity 91.3%; Pred. No. 5,4e-07;
Matches 21; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 TTEDSIKIMNGEADAMSLDGGF 23
DB 392 TTEDCIKIMN-EDAMSLDGGF 413

RESULT 11
US-09-724-864-54
; Sequence 54, Application US/09724864
```

```
/ Patent No. 6380362
/ GENERAL INFORMATION:
/ APPLICANT: Watson, James D
/ APPLICANT: Watson, James G.
/ TITLE OF INVENTION: Polynucleotides, polypeptides expressed
/ TITLE OF INVENTION: by the polynucleotides and methods for their use.
/ FILE REFERENCE: 11000.105001
/ CURRENT APPLICATION NUMBER: US/09/724,864
/ CURRENT FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 54
/ LENGTH: 697
/ TYPE: PRT
/ ORGANISM: Mouse
/ US-09-724-864-54

Query Match      80.0%; Score 92; DB 3; Length 697;
Best Local Similarity 81.8%; Pred. No. 9.7e-07;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEADAMSIDG 22
DB 391 TTEDCIKIVLKGADAMSIDG 412

RESULT 12
US-08-145-681-6
/ Sequence 6, Application US/08145681
/ Patent No. 5571691
/ GENERAL INFORMATION:
/ APPLICANT: Conneely, Orla M.
/ APPLICANT: Headon, Denis R.
/ APPLICANT: O'Malley, Bert W.
/ APPLICANT: May, Gregory S.
/ TITLE OF INVENTION: Production of Recombinant Lactoferrin
/ TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Baker & Botts, L.L.P.
/ STREET: 910 Louisiana St
/ CITY: Houston
/ STATE: Texas
/ COUNTRY: USA
/ ZIP: 77002
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/145,681
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McGregor, Martin L.
/ REGISTRATION NUMBER: 29,329
/ REFERENCE/DOCKET NUMBER: 19928-0125
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 713/229/1874
/ TELEFAX: 713/229/1522
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 703 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHEICAL: YES
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Sus scrofa
```

```
/ ORGANISM: Sus scrofa
/ US-08-145-681-6

Query Match      80.0%; Score 92; DB 1; Length 703;
Best Local Similarity 73.9%; Pred. No. 9.7e-07;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEADAMSIDG 23
DB 390 TTEDCIKIVLKGADAMSIDG 412

RESULT 13
US-08-453-703-6
/ Sequence 6, Application US/08453703
/ Patent No. 5766939
/ GENERAL INFORMATION:
/ APPLICANT: Conneely, Orla M.
/ APPLICANT: Headon, Denis R.
/ APPLICANT: O'Malley, Bert W.
/ APPLICANT: May, Gregory S.
/ TITLE OF INVENTION: Production of Recombinant Lactoferrin
/ TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/453,703
/ FILING DATE: Concurrently herewith
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/145,681
/ FILING DATE: October 28, 1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Albert P. Halluin
/ REGISTRATION NUMBER: 25,227
/ REFERENCE/DOCKET NUMBER: 8206-024
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-854-3660
/ TELEFAX: 415-854-3694
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 703 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHEICAL: YES
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Sus scrofa
/ US-08-453-703-6

Query Match      80.0%; Score 92; DB 1; Length 703;
Best Local Similarity 73.9%; Pred. No. 9.7e-07;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEADAMSIDG 23
DB 390 TTEDCIKIVLKGADAMSIDG 412

RESULT 14
```

US-08-456-106-6
; Sequence 6, Application US/08456106
; Patent No. 5849881
; GENERAL INFORMATION:
; APPLICANT: Conneely, Orla M.
; APPLICANT: Headon, Denis R.
; APPLICANT: O'Malley, Bert W.
; APPLICANT: May, Gregory S.
; TITLE OF INVENTION: Production of Recombinant Lactoferrin
; TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,106
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/145,681
; FILING DATE: October 28, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8206-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 703 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Sus scrofa
; US-08-456-106-6

Query Match 80.0%; Score 92; DB 2; Length 703;
Best Local Similarity 73.9%; Pred. No. 9.7e-07;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTEDSIKIMNGEADAMSLDGGF 23
||| |:::|||||||
Db 390 TTEDCIVVLKGEADAMSLDGGF 412

RESULT 15
US-08-456-108-6
; Sequence 6, Application US/08456108
; Patent No. 6100054
; GENERAL INFORMATION:
; APPLICANT: Conneely, Orla M.
; APPLICANT: Headon, Denis R.
; APPLICANT: O'Malley, Bert W.
; APPLICANT: May, Gregory S.
; TITLE OF INVENTION: Production of Recombinant Lactoferrin
; TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,108
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/145,681
FILING DATE: October 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8206-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 703 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Sus scrofa
US-08-456-108-6

Query Match 80.0%; Score 92; DB 3; Length 703;
Best Local Similarity 73.9%; Pred. No. 9.7e-07;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTEDSIKIMNGEADAMSLDGGF 23
||| |:::|||||||
Db 390 TTEDCIVVLKGEADAMSLDGGF 412

Search completed: November 1, 2005, 12:57:30
Job time : 34.8235 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:54:52 ; Search time 116.353 Seconds
(without alignments)
82.636 Million cell updates/sec

Title: US-10-612-162a-2

Perfect score: 115
Sequence: 1 TTEDSIKIMNGEADAMSJDGSR 23Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 1865214

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

```
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pap:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pap:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pap:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pap:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pap:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pap:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pap:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pap:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pap:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pap:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pap:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pap:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pap:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pap:*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pap:*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pap:*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pap:*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pap:*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pap:*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pap:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	100.0	23	15	US-10-612-162-2
2	110	95.7	328	9	US-09-891-126-5
3	110	95.7	328	14	US-10-266-745-5
4	110	95.7	679	15	US-10-378-094-3
5	110	95.7	679	15	US-10-384-060-3
6	110	95.7	679	15	US-10-331-494-3
7	110	95.7	679	16	US-10-429-482-4
8	110	95.7	679	16	US-10-429-482-4
9	110	95.7	679	16	US-10-429-515-4
10	110	95.7	679	16	US-10-429-598-4
11	110	95.7	679	16	US-10-429-635-4

12	110	95.7	679	16	US-10-429-653-4	Sequence 4, Appli
13	110	95.7	679	16	US-10-429-659-4	Sequence 4, Appli
14	110	95.7	679	16	US-10-429-661-4	Sequence 4, Appli
15	110	95.7	679	16	US-10-429-660-4	Sequence 4, Appli
16	110	95.7	679	16	US-10-429-665-4	Sequence 4, Appli
17	110	95.7	679	16	US-10-429-655-4	Sequence 4, Appli
18	110	95.7	679	16	US-10-429-654-4	Sequence 4, Appli
19	110	95.7	698	10	US-09-935-642-6	Sequence 6, Appli
20	110	95.7	698	15	US-10-378-094-2	Sequence 2, Appli
21	110	95.7	698	15	US-10-384-060-2	Sequence 2, Appli
22	110	95.7	698	15	US-10-231-494-2	Sequence 2, Appli
23	110	95.7	698	15	US-10-383-201-10	Sequence 10, Appli
24	110	95.7	698	15	US-10-383-201-14	Sequence 14, Appli
25	110	95.7	698	17	US-10-887-711-2	Sequence 2, Appli
26	110	95.7	698	18	US-10-513-523-3	Sequence 3, Appli
27	110	95.7	1074	9	US-09-753-385-2	Sequence 2, Appli
28	110	95.7	1410	9	US-09-753-385-4	Sequence 4, Appli
29	110	95.7	1410	16	US-10-473-127-805	Sequence 805, App
30	110	95.7	1418	16	US-10-473-127-804	Sequence 804, App
31	92	80.0	703	17	US-10-620-256-6	Sequence 6, Appli
32	92	80.0	704	18	US-10-513-523-4	Sequence 4, Appli
33	90	78.3	359	14	US-10-169-297-49	Sequence 49, Appli
34	90	78.3	690	14	US-10-076-816-4	Sequence 4, Appli
35	90	78.3	690	14	US-10-077-381-4	Sequence 4, Appli
36	90	78.3	690	16	US-10-639-835-4	Sequence 4, Appli
37	90	78.3	694	13	US-10-023-095-2	Sequence 2, Appli
38	90	78.3	695	14	US-10-316-253-273	Sequence 273, App
39	90	78.3	698	14	US-10-316-253-275	Sequence 275, App
40	90	78.3	698	15	US-10-205-331-55	Sequence 55, Appli
41	90	78.3	709	14	US-10-170-221-2	Sequence 2, Appli
42	90	78.3	709	18	US-10-987-587-9	Sequence 9, Appli
43	90	78.3	711	14	US-10-169-297-9	Sequence 4, Appli
44	90	78.3	711	14	US-10-170-221-4	Sequence 202, App
45	90	78.3	711	15	US-10-341-434-202	

ALIGNMENTS

```
RESULT 1
US-10-612-162-2
; Sequence 2, Appli Application US/10612162
; Publication No. US20040014145A1
; GENERAL INFORMATION:
; APPLICANT: Dade Behring Marburg GmbH
; TITLE OF INVENTION: Carbohydrate deficient transferrin (CDT)-specific
; FILE REFERENCE: 2002/B001
; CURRENT APPLICATION NUMBER: US/10/612,162
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 10230550.1
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 03011334.4
; PRIOR FILING DATE: 2003-05-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-162-2
```

Query Match 100.0%; Score 115; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.5e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTEDSIKIMNGEADAMSJDGSR 23
Db 1 TTEDSIKIMNGEADAMSJDGSR 23

RESULT 2
US-09-891-126-5

```
/ Sequence 5, Application US/09891126
/ Patent No. US20020072596A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruden et al.
/ TITLE OF INVENTION: Transferrin Polynucleotides, Polypeptides, and Antibodies
/ FILE REFERENCE: PT035P1
/ CURRENT APPLICATION NUMBER: US/09/891,126
/ PRIOR FILING DATE: 2001-06-26
/ PRIOR APPLICATION NUMBER: PCT/US00/34769
/ PRIOR FILING DATE: 2000-12-21
/ PRIOR APPLICATION NUMBER: 60/171,595
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 328
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-891-126-5
```

```
Query Match          95.7%; Score 110; DB 9; Length 328;
Best Local Similarity 95.7%; Pred. No. 7, 6e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 TTEDSIKIMNGEADAMSLDGGF 23
    |||||
Db 56 TTEDCIKIMNGEADAMSLDGGF 78
```

```
RESULT 3
US-10-266-745-5
/ Sequence 5, Application US/10266745
/ Publication No. US20030149256A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruden et al.
/ TITLE OF INVENTION: Transferrin Polynucleotides, Polypeptides, and Antibodies
/ FILE REFERENCE: PT035P1
/ CURRENT APPLICATION NUMBER: US/10/266,745
/ PRIOR FILING DATE: 2002-10-09
/ PRIOR APPLICATION NUMBER: US/09/891,126
/ PRIOR FILING DATE: 2001-06-26
/ PRIOR APPLICATION NUMBER: PCT/US00/34769
/ PRIOR FILING DATE: 2000-12-21
/ PRIOR APPLICATION NUMBER: 60/171,595
/ PRIOR FILING DATE: 1999-12-23
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 328
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-266-745-5
```

```
Query Match          95.7%; Score 110; DB 14; Length 328;
Best Local Similarity 95.7%; Pred. No. 7, 6e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 TTEDSIKIMNGEADAMSLDGGF 23
    |||||
Db 56 TTEDCIKIMNGEADAMSLDGGF 78
```

```
RESULT 4
US-10-378-094-3
/ Sequence 3, Application US/10378094
/ Publication No. US20030221201A1
/ GENERAL INFORMATION:
/ APPLICANT: PRIOR, Christopher P.
/ APPLICANT: LAI, Char-Huei
/ APPLICANT: SADEGHI, Homayoun
/ APPLICANT: TURNER, Andrew
/ TITLE OF INVENTION: MODIFIED TRANSFERRIN FUSION PROTEINS
/ FILE REFERENCE: 54710-5001-01-US
```

```
/ CURRENT APPLICATION NUMBER: US/10/378,094
/ CURRENT FILING DATE: 2003-03-04
/ PRIOR APPLICATION NUMBER: US 10/231,494
/ PRIOR FILING DATE: 2002-08-30
/ PRIOR APPLICATION NUMBER: US 60/334,059
/ PRIOR FILING DATE: 2001-11-30
/ PRIOR APPLICATION NUMBER: US 60/315,745
/ PRIOR FILING DATE: 2001-08-30
/ NUMBER OF SEQ ID NOS: 66
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 3
/ LENGTH: 679
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: MISC_FEATURE
/ OTHER INFORMATION: Mature Transferrin Protein
US-10-378-094-3
```

```
Query Match          95.7%; Score 110; DB 15; Length 679;
Best Local Similarity 95.7%; Pred. No. 1, 8e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 TTEDSIKIMNGEADAMSLDGGF 23
    |||||
Db 373 TTEDCIKIMNGEADAMSLDGGF 395
```

```
RESULT 5
US-10-384-060-3
/ Sequence 3, Application US/10384060
/ Publication No. US20030226155A1
/ GENERAL INFORMATION:
/ APPLICANT: SADEGHI, Homayoun
/ APPLICANT: PRIOR, Christopher P.
/ TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
/ FILE REFERENCE: 54710-5004-US
/ CURRENT APPLICATION NUMBER: US/10/384,060
/ PRIOR FILING DATE: 2003-03-10
/ PRIOR APPLICATION NUMBER: US 10/231,494
/ PRIOR FILING DATE: 2002-08-30
/ PRIOR APPLICATION NUMBER: US 60/334,059
/ PRIOR FILING DATE: 2001-11-30
/ PRIOR APPLICATION NUMBER: US 60/315,745
/ PRIOR FILING DATE: 2001-08-30
/ PRIOR APPLICATION NUMBER: US 60/406,977
/ PRIOR FILING DATE: 2002-08-30
/ NUMBER OF SEQ ID NOS: 80
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 3
/ LENGTH: 679
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: MISC_FEATURE
/ OTHER INFORMATION: Mature Transferrin Protein
US-10-384-060-3
```

```
Query Match          95.7%; Score 110; DB 15; Length 679;
Best Local Similarity 95.7%; Pred. No. 1, 8e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 TTEDSIKIMNGEADAMSLDGGF 23
    |||||
Db 373 TTEDCIKIMNGEADAMSLDGGF 395
```

```
RESULT 6
US-10-231-494-3
/ Sequence 3, Application US/10231494
/ Publication No. US20040023334A1
/ GENERAL INFORMATION:
```

```

; APPLICANT: Prior, Christopher P.
; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
; FILE REFERENCE: 54710-5001-US
; CURRENT APPLICATION NUMBER: US/10/231,494
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Mature transferrin protein
US-10-231-494-3
```

```

Query Match          95.7%; Score 110; DB 16; Length 679;
Best Local Similarity 95.7%; Pred. No. 1.8e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 1 TTEDSIKIMNGEADAMSIDGCF 23
Db 373 TTEDCIKIMNGEADAMSIDGCF 395
```

```

RESULT 7
US-10-429-482-4
; Sequence 4, Application US/10429482
; Publication No. US20040219097A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For The Diagnosis, Imaging and Treatment Of Tu
; FILE REFERENCE: 2537,000001
; CURRENT APPLICATION NUMBER: US/10/429,482
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-482-4
```

```

Query Match          95.7%; Score 110; DB 16; Length 679;
Best Local Similarity 95.7%; Pred. No. 1.8e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 1 TTEDSIKIMNGEADAMSIDGCF 23
Db 373 TTEDCIKIMNGEADAMSIDGCF 395
```

```

RESULT 8
US-10-429-497-4
; Sequence 4, Application US/10429497
; Publication No. US20040219098A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For The Treatment Of Tumors
; FILE REFERENCE: 2537,000006
; CURRENT APPLICATION NUMBER: US/10/429,497
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-497-4
```

```

Query Match          95.7%; Score 110; DB 16; Length 679;
Best Local Similarity 95.7%; Pred. No. 1.8e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 1 TTEDSIKIMNGEADAMSIDGCF 23
Db 373 TTEDCIKIMNGEADAMSIDGCF 395
```

```

RESULT 9
US-10-429-515-4
; Sequence 4, Application US/10429515
; Publication No. US20040219099A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For The Treatment Of Tumors
; FILE REFERENCE: 2537,000005
; CURRENT APPLICATION NUMBER: US/10/429,515
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-515-4
```

```

Query Match          95.7%; Score 110; DB 16; Length 679;
Best Local Similarity 95.7%; Pred. No. 1.8e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 1 TTEDSIKIMNGEADAMSIDGCF 23
Db 373 TTEDCIKIMNGEADAMSIDGCF 395
```

```

RESULT 10
US-10-429-598-4
; Sequence 4, Application US/10429598
; Publication No. US20040219100A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For The Treatment Of Tumors
; FILE REFERENCE: 2537,000003
; CURRENT APPLICATION NUMBER: US/10/429,598
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-598-4
```

```

Query Match          95.7%; Score 110; DB 16; Length 679;
Best Local Similarity 95.7%; Pred. No. 1.8e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 1 TTEDSIKIMNGEADAMSIDGCF 23
Db 373 TTEDCIKIMNGEADAMSIDGCF 395
```

```

RESULT 11
US-10-429-635-4
; Sequence 4, Application US/10429635
; Publication No. US20040219101A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For Treatment Of Tumors
; FILE REFERENCE: 2537,000007
; CURRENT APPLICATION NUMBER: US/10/429,635
; CURRENT FILING DATE: 2003-05-02
```

```
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-653-4
```

```
Query Match          95.7%; Score 110; DB 16; Length 679;
Best Local Similarity 95.7%; Pred. No. 1.8e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 TTEDSIKIMNGEADAMSIDGGF 23
Db 373 TTEDCIKIMNGEADAMSIDGGF 395
```

```
RESULT 12
US-10-429-653-4
; Sequence 4, Application US/10429653
; Publication No. US20040219102A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Compositions For Drug Delivery
; FILE REFERENCE: 2537.000009
; CURRENT APPLICATION NUMBER: US/10/429,653
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-653-4
```

```
Query Match          95.7%; Score 110; DB 16; Length 679;
Best Local Similarity 95.7%; Pred. No. 1.8e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 TTEDSIKIMNGEADAMSIDGGF 23
Db 373 TTEDCIKIMNGEADAMSIDGGF 395
```

```
RESULT 13
US-10-429-659-4
; Sequence 4, Application US/10429659
; Publication No. US20040219103A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods Useful For The Diagnosis, Imaging and Treatment Of Tumors
; FILE REFERENCE: 2537.000004
; CURRENT APPLICATION NUMBER: US/10/429,659
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-659-4
```

```
Query Match          95.7%; Score 110; DB 16; Length 679;
Best Local Similarity 95.7%; Pred. No. 1.8e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 TTEDSIKIMNGEADAMSIDGGF 23
Db 373 TTEDCIKIMNGEADAMSIDGGF 395
```

```
RESULT 14
US-10-429-661-4
```

```
; Sequence 4, Application US/10429661
; Publication No. US20040219104A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For Treatment Of Tumors
; FILE REFERENCE: 2537.000008
; CURRENT APPLICATION NUMBER: US/10/429,661
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-661-4
```

```
Query Match          95.7%; Score 110; DB 16; Length 679;
Best Local Similarity 95.7%; Pred. No. 1.8e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 TTEDSIKIMNGEADAMSIDGGF 23
Db 373 TTEDCIKIMNGEADAMSIDGGF 395
```

```
RESULT 15
US-10-429-660-4
; Sequence 4, Application US/10429660
; Publication No. US20040220084A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For Nucleic Acid Delivery
; FILE REFERENCE: 2537.000012
; CURRENT APPLICATION NUMBER: US/10/429,660
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-660-4
```

```
Query Match          95.7%; Score 110; DB 16; Length 679;
Best Local Similarity 95.7%; Pred. No. 1.8e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 TTEDSIKIMNGEADAMSIDGGF 23
Db 373 TTEDCIKIMNGEADAMSIDGGF 395
```

```
Search completed: November 1, 2005, 13:26:06
Job time : 116.353 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: November 1, 2005, 12:35:39 / Search time 23.3382 Seconds
(Without alignments)
94.822 Million cell updates/sec

Title: US-10-612-162A-2

Perfect score: 115
Sequence: 1 TTEDSLAKIMNGEADAMSLDGR 23

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	110	95.7	698	1 TFHUP	transferrin precur
2	101	87.8	694	1 TFRBP	transferrin precur
3	96	83.5	706	2 S33761	transferrin precur
4	92	80.0	311	2 A28446	transferrin - mous
5	92	80.0	696	1 S01384	transferrin - pig
6	92	80.0	703	2 A45543	transferrin precur
7	90	78.3	695	2 S49163	transferrin precur
8	90	78.3	711	1 TFRUL	transferrin precur
9	88	76.5	707	1 A28438	transferrin precur
10	86	74.8	704	2 I47228	carbonic anhydrase
11	84	73.0	708	2 JC2323	lactoferrin - goat
12	77	67.0	705	1 TFCHE	ovotransferrin pre
13	77	67.0	708	1 TFRBL	lactotransferrin p
14	71	61.7	717	2 S12100	transferrin precur
15	66	57.4	690	2 T11749	transferrin - Acla
16	50	43.5	280	1 G70126	phosphate ABC tran
17	48	41.7	609	2 E86780	hypothetical prote
18	47	40.9	466	2 D72733	probable membrane-
19	46	40.0	47	2 S13486	transferrin - bovl
20	46	40.0	737	2 AE0819	probable membrane
21	46	40.0	1238	1 A40185	virulence protein
22	46	40.0	1238	1 S17944	virulence sensor p
23	46	40.0	1238	1 S17946	virulence sensor p
24	45.5	39.6	483	2 D87752	protein C18B3.6 [i
25	45.5	39.6	483	2 T15180	hypothetical prote
26	45	39.1	110	2 E83571	conserved hypotet
27	45	39.1	288	2 F69973	transcription regu
28	45	39.1	491	2 A86824	sensor protein kin
29	45	39.1	505	1 P5XR44	outer capsid prote

30	45	39.1	852	2 D72230	conserved hypotet
31	44	38.3	339	2 G69253	hypothetical prote
32	44	38.3	371	2 A69379	conserved hypotet
33	44	38.3	461	2 D84971	phosphotransferase
34	44	38.3	747	2 E91049	probable cytochrom
35	44	38.3	747	2 A85894	probable cytochrom
36	44	38.3	747	2 P65026	hypothetical prote
37	44	38.3	1012	2 T13503	probable N-methyl-
38	43.5	37.8	187	2 D82794	limbilitin AF0339
39	43.5	37.8	738	1 TFRUM	melanotransferrin
40	43	37.4	246	2 A64326	hypothetical prote
41	43	37.4	298	2 B71317	hypothetical prote
42	43	37.4	320	2 JC7929	ATP-dependent gluc
43	43	37.4	352	2 AC0299	probable membrane
44	43	37.4	358	2 A82206	protein-glucanase
45	43	37.4	376	2 F72514	probable glucokina

ALIGNMENTS

RESULT 1
TFHUP
transferrin precursor [validated] - human
N/Alternate names: siderophilin
C/Species: Homo sapiens (man)
C/Date: 15-Oct-1982 #sequence, revision 30-Sep-1993 #ext. change 09-Jul-2004
C/Accession: A20981; A92417; A94044; A23090; A23739; I51959; I63133; I54011; I68160; A0
R/Yang, F.; Lum, J.B.; McGill, J.R.; Moore, C.M.; Naylor, S.L.; van Bragt, P.H.; Baldwi
Proc. Natl. Acad. Sci. U.S.A. 81, 2752-2756, 1984
A/Title: Human transferrin: cDNA characterization and chromosomal localization.
A/Reference number: A20981; PMID:84194084; PMID:6585826
A/Contents: variant C
A/Accession: A20981
A/Molecule type: mRNA
A/Residues: 1-698 <YAN>
A/Cross-references: UNIPROT:P02787; EMBL:M12530; NID:G339452; PDB:AAA61140.1; PID:G339
A/Note: the authors translated the codon CAA for residue 203 as Glu
R/MacGillivray, R.T.A.; Mendes, E.; Shewale, J.G.; Sinha, S.K.; Lineback-Zins, J.; Brew
J. Biol. Chem. 258, 3543-3553, 1983
A/Title: The primary structure of human serum transferrin. The structures of seven cyan
A/Reference number: A92417; PMID:83160878; PMID:6833213
A/Accession: A92417
A/Molecule type: protein
A/Residues: 20-263, 'E', 265-328, 'N', 330-379, 'SD', 382-435, 'D', 437-557, 'T', 559-560, 'P', 562
A/Note: the sequence shown is the predominant electrophoretic genetic variant (C or TFC
R/Park, I.; Schaeffer, E.; Stoll, A.; Baralle, F.E.; Cohen, G.N.; Zakin, M.M.
Proc. Natl. Acad. Sci. U.S.A. 82, 3149-3153, 1985
A/Title: Organization of the human transferrin gene: direct evidence that it originated
A/Reference number: A94044; PMID:85216459; PMID:3858812
A/Accession: A94044
A/Molecule type: DNA
A/Residues: 73-263, 'E', 265-328, 'N', 330-562 <PAR>
A/Cross-references: EMBL:M1361
R/Adrian, G.S.; Korinek, B.W.; Bowman, B.H.; Yang, F.
Gene 49, 167-175, 1986
A/Title: The human transferrin gene: 5' region contains conserved sequences which match
A/Reference number: A29090; PMID:87192006; PMID:3106157
A/Accession: A29090
A/Molecule type: DNA
A/Residues: 1-72; 291-300 <ADR>
A/Cross-references: EMBL:M5673
R/Uzan, G.; Frain, M.; Park, I.; Besmond, C.; Maessen, G.; Trepac, J.S.; Zakin, M.M.; K
Biochem. Biophys. Res. Commun. 119, 273-281, 1984
A/Title: Molecular cloning and sequence analysis of cDNA for human transferrin.
A/Reference number: A37339; PMID:84153910; PMID:6322780
A/Accession: A37339
A/Molecule type: mRNA
A/Residues: 422-690, 'G', 692-698 <UZA>
A/Cross-references: EMBL:M2525; NID:G339468; PDB:AAA61142.1; PID:G339469
R/MacGillivray, R.T.A.; Mendes, E.; Sinha, S.K.; Sutton, M.R.; Lineback-Zins, J.; Brew,
Proc. Natl. Acad. Sci. U.S.A. 79, 2504-2508, 1982

A>Title: The complete amino acid sequence of human serum transferrin.
A:Reference number: A93913; MUID:82222166; PMID:6553407
A:Comments: annotation; disulfide bonds
R:Herberberger, C.L.; Larson, J.L.; Arnold, B.; Roelcke, P.R.
Ann. N. Y. Acad. Sci. 646, 140-154, 1991
A>Title: A cloned gene for human transferrin.
A:Reference number: I51959; MUID:92231399; PMID:1809186
A:Accession: I51959
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-638 <RES>
A:Cross-references: GB:SP5936; NID:G248647; PIDN:AA622049.1; PID:G248648
R:Duguid, J.R.; Bohmter, C.W.; Liu, N.G.; Tourtellotte, W.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 7260-7264, 1989
A>Title: Changes in brain gene expression shared by scrapie and Alzheimer disease.
A:Reference number: I48174; MUID:89386721; PMID:2780570
A:Accession: I63133
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 636-696 <RE2>
A:Cross-references: GB:M26641; NID:G339988; PIDN:AA61233.1; PID:G339989
R:Scheffer, E.; Lucero, M.A.; Jeltch, J.M.; Py, M.C.; Levin, M.J.; Chabon, P.; Cohen, Gene 56, 109-116, 1987
A>Title: Complete structure of the human transferrin gene. Comparison with analogous chi
A:Reference number: I54011; MUID:88056305; PMID:3678832
A:Accession: I54011
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-72 <RE3>
A:Cross-references: GB:M17611; NID:G339480; PIDN:AA61147.1; PID:G339485
A:Accession: I68160
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 564-698 <RE4>
A:Cross-references: GB:M17614; NID:G339483; PIDN:AA61148.1; PID:G339486
C:Comment: Each of the two repetitive domains binds a ferric ion and a bicarbonate anion
C:Genetics:
A:Gene: GDB:TF
A:Cross-references: GDB:120432; OMIM:190000
A:Map position: 3q21-3q21
A:Intron: 15/1, 72/3, 119/1, 166/1, 212/2, 231/1, 290/3, 350/1, 401/3, 433/1, 444/1, 49
C:Function:
A:Description: binds iron for delivery into cells
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; glycoprotein; iron transport; metal binding; plasma
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-698/Product: transferrin #status experimental <MAT>
F:20-350/Domain: transferrin repeat homology <TRH2>
F:356-686/Domain: transferrin repeat homology <TRH2>
F:28-67,38-58,137-213,156-350,177-193,180-196,190-198,246-260,358-615,364-396,374-387,42
F:432,630/Binding site: carbohydrate (Aan) (covalent) #status experimental
Query Match 95.7%; Score 110; DB 1; Length 698;
Best Local Similarity 95.7%; Pred. No. 2,5e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEADAMSJDGF 23
DB 392 TTEDCIKIMNGEADAMSJDGF 414

RESULT 2
TFRBP
transferrin precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 22-Jun-1999
C:Accession: S16246; A61239; G61573; S00335; S02654; A26504; S14853
R:Banfield, D.K.; Chow, B.K.C.; Funk, W.D.; Robertson, K.A.; Umels, T.M.; Woodworth, R.
Biochim. Biophys. Acta 1089, 262-265, 1991
A>Title: The nucleotide sequence of rabbit liver transferrin cDNA.
A:Reference number: S16246; MUID:91274362; PMID:2054387
A:Accession: S16246
A:Molecule type: mRNA

A:Residues: 1-694 <BAN>
A:Cross-references: EMBL:X58533; NID:G1750; PIDN:CAA41424.1; PID:G1751
R:Pierpaoli, W.; Dall'Ara, A.; Yi, C.; Neri, P.; Santucci, A.; Choay, J.
Cell. Immunol. 134, 225-234, 1991
A>Title: Iron carrier proteins facilitate engraftment of allogeneic bone marrow and enb
A:Reference number: A61239; MUID:91191584; PMID:2013104
A:Accession: A61239
A:Molecule type: protein
A:Residues: 19-36 <PIE>
R:Chung, M.C.M.; Chan, S.L.; Shimizu, S.
In. J. Biochem. 23, 609-616, 1991
A>Title: Purification of transferrins and lactoferrin using DEAE Affi-Gel Blue.
A:Reference number: A61573; MUID:91293379; PMID:2065820
A:Accession: G61573
A:Molecule type: protein
A:Residues: 19-26, 'X', 28-36, 'X', 38-53 <CHU>
R:Godovac-Zimmermann, J.
Biol. Chem. Hoppe-Seyler 369, 93-96, 1988
A>Title: Isolation, characterization and N-terminal amino-acid sequence of rabbit transf
A:Reference number: S00335; MUID:88209278; PMID:3365331
A:Accession: S00335
A:Molecule type: protein
A:Residues: 19-45, 'S', 47-48, 'Y', 50 <GOD>
R:Evans, R.W.; Aitken, A.; Patel, K.J.
FEBS Lett. 238, 39-42, 1988
A>Title: Evidence for a single glycan moiety in rabbit serum transferrin and location of
A:Reference number: S02694; MUID:89005676; PMID:3169252
A:Accession: S02694
A:Molecule type: protein
A:Residues: 482-515, 'V', 517-544 <EVA>
A:Note: 516-11e was also found
R:Heaphy, S.; Williams, J.
Biochem. J. 205, 611-617, 1982
A>Title: The preparation and partial characterization of N-terminal and C-terminal iron-
A:Reference number: A26504; MUID:83074540; PMID:6816218
A:Accession: A26504
A:Molecule type: protein
A:Residues: 19-24, 'N', 26, 'X', 28-29, 'S' <HEA>
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; glycoprotein; iron transport; metal binding; plasma
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-694/Product: transferrin #status experimental <MAT>
F:19-349/Domain: transferrin repeat homology <TRH2>
F:355-682/Domain: transferrin repeat homology <TRH2>
F:27-66,37-57,136-212,155-349,176-192,179-195,189-197,245-259,357-611,363-395,373-386,42
F:508/Binding site: carbohydrate (Aan) (covalent) #status experimental
Query Match 87.8%; Score 101; DB 1; Length 694;
Best Local Similarity 87.0%; Pred. No. 6,8e-08;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEADAMSJDGF 23
DB 391 TTEDCIKIMNGEADAMSJDGF 413

RESULT 3
S33761
transferrin precursor - horse
N:Alternate names: growth-promoting factor
C:Species: Equus caballus (domestic horse)
C:Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 09-Jul-2004
C:Accession: S33761; S02145
R:Carpenier, M.A.; Broad, T.E.
Biochim. Biophys. Acta 1173, 230-232, 1993
A>Title: The cDNA sequence of horse transferrin.
A:Reference number: S33761; MUID:93277958; PMID:8504171
A:Accession: S33761
A:Molecule type: mRNA
A:Residues: 1-706 <CAR>
A:Cross-references: UNIPROT:P27425; EMBL:M69020; NID:G1644242; PIDN:AAA30958.1; PID:G1642
R:Yoshinari, K.; Yotaka, F.; Mimura, A.

Biochim. Biophys. Acta 1010, 28-34, 1989
 A>Title: A growth-promoting factor for human myeloid leukemia cells from horse serum ide
 A/Reference number: S02145; MUID:80076897; PMID:2909248
 A/Accession: S02145
 A/Molecule type: protein
 A/Residues: 20-35,'X',37,'X',39-40,'X',43-44 <YOS>
 A/Complex: monomer
 C/Superfamily: transferrin; transferrin repeat homology
 C/Keywords: duplication; glycoprotein; iron transport; metal binding; plasma
 F/1-19/Domain: signal sequence #status predicted <SIG>
 F/20-76/Product: transferrin #status experimental <MAT>
 F/358-694/Domain: transferrin repeat homology <TRH2>
 F/26-64,36-55,134-215,174-190,177-198,187-200,248-262,360-623,366-398,376-389,423-701,44

Query Match 83.5%; Score 96; DB 2; Length 706;
 Best Local Similarity 82.6%; Pred. No. 4,4e-07;
 Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTEDSIKINMGADAMSLDGGF 23
 :|||||:|||||:
 Db 394 STEDCIKIVKGEADAMSLDGGF 416

RESULT 4
 A28446
 C/Species: Mus musculus (house mouse)
 C/Date: 30-Jun-1989 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C/Accession: A28446; A34482; B28438
 R/Chen, L.H.; Biesecl, M.J.
 J. Biol. Chem. 262, 17247-17250, 1987
 A>Title: Transferrin mRNA level in the mouse mammary gland is regulated by pregnancy and
 A/Reference number: A28446; MUID:8008692; PMID:3653348
 A/Accession: A28446
 A/Molecule type: mRNA
 A/Residues: 15-80/81-141,217-251,252-301 <CHE>
 A/Cross-references: UNIPROT:Q92111
 A/Note: the authors translated the codon ACC for residue 61 as Tyr, TCC for residue 62 &
 R/Idzerda, R.L.; Behringer, R.R.; Theisen, M.; Hugeniyk, J.I.; McKnight, G.S.; Brinster
 Mol. Cell. Biol. 9, 5154-5162, 1989
 A>Title: Expression from the transferrin gene promoter in transgenic mice.
 A/Reference number: A34482; MUID:90097932; PMID:2601714
 A/Accession: A34482
 A/Molecule type: DNA
 A/Residues: 114,302-311 <IDZ>
 A/Cross-references: GB:M30819; GB:M30820
 R/Pentecost, B.T.; Teng, C.T.
 J. Biol. Chem. 262, 10134-10139, 1987
 A>Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secret
 A/Reference number: A92596; MUID:8728003; PMID:3611056
 A/Accession: B28438
 A/Molecule type: mRNA
 A/Residues: 86-216 <PEN>
 A/Cross-references: GB:J02377; GB:J02377; PIDN:AAA39438.1; PID:G198848
 C/Superfamily: transferrin; transferrin repeat homology
 C/Keywords: duplication

Query Match 80.0%; Score 92; DB 2; Length 311;
 Best Local Similarity 81.8%; Pred. No. 7,4e-07;
 Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTEDSIKINMGADAMSLDGG 22
 :|||||:|||||:
 Db 195 TTEDCIKIVKGEADAMSLDGG 216

RESULT 5
 S01384
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C/Accession: S01384; A60520; A61573
 R/Baldwin, G.S.; Weinstock, J.

Nucleic Acids Res. 16, 8720, 1988
 A>Title: Nucleotide sequence of porcine liver transferrin.
 A/Reference number: S01384; MUID:88335629; PMID:3419534
 A/Accession: S01384
 A/Status: translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-696 <BAL>
 A/Cross-references: UNIPROT:P09571; EMBL:X12386; NID:92126; PIDN:CAA30943.1; PID:G83380
 A/Note: 308-Arg was also found
 R/Baldwin, G.S.; Bacie, T.; Chandler, R.; Grego, B.; Pedersen, J.; Simpson, R.J.; Toh,
 Comp. Biochem. Physiol. B 95, 261-268, 1990
 A>Title: Isolation of transferrin from porcine gastric mucosa: comparison with porcine
 A/Reference number: A60520; MUID:90227903; PMID:2338566
 A/Accession: A60520
 A/Molecule type: protein
 A/Residues: 1-8,'X',10-11,'X',13-15 <BA2>
 A/Experimental source: gastric mucosa
 A/Note: the authors suggest transferrin from gastric mucosa may act in dietary iron upt
 R/Chung, M.C.M.; Chan, S.L.; Shimizu, S.
 Int. J. Biochem. 23, 609-616, 1991
 A>Title: Purification of transferrin and lactoferrin using DEAE Affi-gel Blue.
 A/Reference number: A61573; MUID:9129379; PMID:2065820
 A/Accession: A61573
 A/Molecule type: protein
 A/Residues: 1-8,'X',10-18,'X' <CHU>
 C/Superfamily: transferrin; transferrin repeat homology
 C/Keywords: duplication; glycoprotein; iron transport; plasma
 F/1-696/Product: transferrin #status predicted <MAT>
 F/1-335/Domain: transferrin repeat homology <TRH1>

Query Match 80.0%; Score 92; DB 1; Length 696;
 Best Local Similarity 81.8%; Pred. No. 1,9e-06;
 Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 TEDSIKINMGADAMSLDGGF 23
 :|||||:|||||:
 Db 378 TEDCIKIVKGEADAMSLDGGY 399

RESULT 6
 A45543
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
 C/Accession: A45543; S24173
 R/Alexander, L.J.; Levine, W.B.; Teng, C.T.; Beattie, C.W.
 Anim. Genet. 23, 251-256, 1992
 A>Title: Cloning and sequencing of the porcine lactoferrin cDNA.
 A/Reference number: A45543; MUID:92367939; PMID:1503259
 A/Accession: A45543
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-703 <ALE>
 A/Cross-references: UNIPROT:P14632
 A/Note: experimental source: mammary gland
 A/Note: sequence extracted from NCBI backbone (NCBIN:111151, NCBIP:111153)
 R/Lydon, J.P.; O'Malley, B.R.; Sancedo, O.; Lee, T.; Heaton, D.R.; Connely, O.M.
 Biochim. Biophys. Acta 1133, 97-99, 1992
 A>Title: Nucleotide and primary amino acid sequence of porcine lactoferrin.
 A/Reference number: S24173; MUID:92379101; PMID:1511016
 A/Accession: S24173
 A/Molecule type: mRNA
 A/Residues: 111,'W',13-50,'I',52-84,'G',86-120,'U',121-130,'I',132-282,'S',284-571,'Q'
 A/Cross-references: EMBL:M20689; NID:G164613; PIDN:AAA31102.1; PID:G164614
 A/Experimental source: mammary gland
 C/Superfamily: transferrin; transferrin repeat homology
 C/Keywords: duplication; glycoprotein; iron; iron binding; metalloprotein; milk
 F/1-19/Domain: signal sequence #status predicted <SIG>
 F/20-703/Product: lactoferrin #status predicted <TRH1>
 F/20-350/Domain: transferrin repeat homology <TRH2>
 F/35-48/Region: antimicrobial
 F/354-691/Domain: transferrin repeat homology <TRH2>
 F/28-66,38-53,129-212,171-187,184-195,245-259,362-394,372-385,419-698,439-661,471-546,4

F:77,107,206,267/Binding site: iron (Asp, Tyr, Tyr, His) #status predicted
 F:135/Binding site: carbonate (Arg) #status predicted
 F:409,447,540,609/Binding site: iron (Asp, Tyr, Tyr, His) #status predicted
 F:477/Binding site: carbonate (Arg) #status predicted
 F:490/Binding site: carbonyldiure (Asn) (covalent) #status predicted

Query Match 80.0%; Score 92; DB 2; Length 703;
 Best Local Similarity 73.9%; Pred. No. 1,9e-06;
 Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTEDSIATKMGADAMSJDGCF 23
 Db 390 TTEDCIVQVLKGEADAMSJDGCF 412

RESULT 7

transferrin precursor - rat
 N:Alternate names: lung-derived growth factor; siderophilin
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 16-Feb-1995 #sequence revision 12-May-1995 #ext change 09-Jul-2004
 C:Accession: S49163; S54980; A30014; A14679; A53289; A30512; I52203

R:Resciva, H.; Pierce, A.; Coddeville, B.; Gonzalez, F.; Benalosa, M.; Leger, D.; Wienus
 submitted to the EMBL Data Library, January 1994
 A:Description: Rat mammary gland transferrin: glycan structure, nucleotide sequence and
 A:Reference number: S49163

A:Accession: S49163

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-695 <ES>

A:Cross-references: UNIPROT:P12346; UNIPROT:Q63602; EMBL:X77158; NID:G510195; PIDN:CAA54
 R:Resciva, H.; Pierce, A.; Coddeville, B.; Gonzalez, F.; Benalosa, M.; Leger, D.; Wienus
 Blochem. J. 307, 47-55, 1995

A:Title: Rat mammary-gland transferrin: nucleotide sequence, phylogenetic analysis and
 A:Reference number: S54980; NID:95234054; PMID:7717992

A:Accession: S54980

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-695 <ES>

A:Cross-references: EMBL:X77158; NID:G510195; PIDN:CAA54403.1; PID:G510196

R:Hugueny, J.; Idzerda, R.L.; Haywood, L.; Lee, D.C.; McKnight, G.S.; Griswold, M.D.
 Endocrinology 120, 332-340, 1987

A:Title: Transferrin messenger ribonucleic acid: molecular cloning and hormonal regulati
 A:Reference number: A30014; NID:87053639; PMID:3023031

A:Accession: A30014

A:Molecule type: mRNA

A:Residues: 518-687, 'D', 688-692, 'TA', 695 <HUG>

A:Cross-references: GB:M27966; NID:G207439; PIDN:AAA42267.1; PID:G207440

R:Schreiber, G.; Dryburgh, H.; Millership, A.; Matsuda, Y.; Inglier, A.; Phillips, J.; Ed
 J. Biol. Chem. 254, 12013-12019, 1979

A:Title: The synthesis and secretion of rat transferrin.
 A:Reference number: A14679; NID:80049855; PMID:500669

A:Accession: A14679

A:Molecule type: protein

A:Residues: 20-47 <SCH>

R:Cavanaugh, P.G.; Nicolson, G.L.
 J. Cell. Biochem. 47, 261-271, 1991

A:Title: Lung-derived growth factor that stimulates the growth of lung-metastasizing tum
 A:Reference number: A53289; NID:92165927; PMID:1791188

A:Accession: A53289

A:Status: preliminary

A:Molecule type: protein

A:Residues: 89, 'Y', 91, 'A', 93-99, 'V', 101-102, 'N', 213, 'AN', 236-243, 401-406, 'N', 408 <CAV>

A:Experimental source: lung

A:Note: sequence modified after extraction from NCBI backbone

R:Payre, L.R.; Payre, M.; Linon, N.; Brandt, W.; Johnson, G.; Jacobs, P.
 Biochem. Biophys. Acta 966, 318-327, 1998

A:Title: Properties of the transferrin associated with rat intestinal mucosa.
 A:Reference number: A30512; NID:88327006; PMID:3046665

A:Accession: A30512

A:Molecule type: protein

A:Residues: 20-30, 639-643, 'KD', 646, 'LKACD' <PDR>

R:Aldred, A.R.; Howlett, G.J.; Schreiber, G.

Biochem. Biophys. Res. Commun. 122, 960-965, 1984

A:Title: Synthesis of rat transferrin in *Escherichia coli* containing a recombinant bact

A:Reference number: I52203; NID:84307580; PMID:6236811

A:Accession: I52203

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 7-25, 'X', 27-56, 'A', 58-64, 267-295 <RES>

A:Cross-references: GB:M26113; NID:G207437; PIDN:AAA42266.1; PID:G207438

C:Genetics: TF

C:Superfamily: transferrin; transferrin repeat homology

C:Keywords: duplication

F:20-348/Domain: transferrin repeat homology <TRH1>

Query Match 78.3%; Score 90; DB 2; Length 695;
 Best Local Similarity 81.8%; Pred. No. 3.9e-06;
 Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTEDSIATKMGADAMSJDGCF 22
 Db 388 STEDCIDTIVNGEADAMSJDGCF 409

transferrin precursor [validated] - human
 N:Alternate names: lactoferrin
 C:Species: Homo sapiens (man)
 C:Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #ext change 08-Dec-2000
 C:Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74

R:Cho, Y.
 submitted to the EMBL Data Library, March 1994
 A:Reference number: G06820

A:Accession: G01394

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-711 <CHO>

A:Cross-references: EMBL:U07643; NID:G467236; PIDN:AAB60324.1; PID:G467237

R:Rev, M.W.; Moloshuk, S.L.; deBoer, H.A.; Pleper, F.R.
 Nucleic Acids Res. 18, 5288, 1990

A:Title: Complete nucleotide sequence of human mammary gland lactoferrin.
 A:Reference number: S11228; NID:90384839; PMID:2402455

A:Accession: S11228

A:Molecule type: mRNA

A:Residues: 1-148, 'T', 150-422, 'C', 424-711 <REV>

A:Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R:Rieg, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.
 Mol. Endocrinol. 6, 1969-1981, 1992

A:Title: Differential molecular mechanism of the estrogen action that regulates lactofer
 A:Reference number: A45401; NID:93125571; PMID:1480183

A:Accession: A45401

A:Molecule type: DNA

A:Residues: 1-15 <TEN>

A:Cross-references: GB:S52659; NID:G263311; PIDN:AAB24877.1; PID:G263312

A:Experimental source: placenta

A:Note: sequence extracted from NCBI backbone (NCBI:P.122202)

R:Powell, M.J.; Ogden, J.B.
 Nucleic Acids Res. 18, 4013, 1990

A:Title: Nucleotide sequence of human lactoferrin cDNA.
 A:Reference number: S10324; NID:90326549; PMID:2374734

A:Accession: S10324

A:Molecule type: mRNA

A:Residues: 3-711 <POW>

A:Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412

R:Stowell, K.M.; Redo, T.A.; Funk, W.D.; Tweedie, J.W.
 Biochem. J. 276, 349-355, 1991

A:Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.
 A:Reference number: S15853; NID:91264786; PMID:2049066

A:Accession: S15853

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 20-31 <STI>


```

A:Accession: S20841
A:Molecule type: protein
A:Residues: 20-28,'X',30-31 <ST2>
R:Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-993, 1987
A:Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of m
A:Reference number: S07160; MUID:8001031; PMID:3477300
A:Accession: S07160
A:Molecule type: mRNA
A:Residues: 436-487,'A',489-711 <RAD>
A:Cross-references: EMBL:M8642; NID:9186815; PIDN:AAA86665.1; PID:9386855
R:Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
A:Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocy
A:Accession: A61169; MUID:91235214; PMID:1674448
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 3-701,'SMKPVN' <PAN>
A:Experimental source: normal breast tissue
R:Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
Eur. J. Biochem. 145, 659-666, 1994
A:Title: Human lactotransferrin: amino acid sequence and structural comparisons with oth
A:Reference number: A31000; MUID:85076667; PMID:6510420
A:Accession: A31000
A:Molecule type: protein
A:Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4
A:Note: this is the final paper in a series
R:Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norokov, L.
Eur. J. Biochem. 241, 303-308, 1996
A:Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affini
A:Reference number: S74119; MUID:97054624; PMID:8898921
A:Accession: S74119
A:Molecule type: protein
A:Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
A:Experimental source: neutrophil granulocytes
C:Genetics:
A:Gene: GDB:LTF
A:Cross-references: GDB:119368; OMIM:150210
A:Map position: 3q21-3q23
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; glycoprotein; iron binding; milk
F:1-19/Domain: signal sequence #status predicted <Sig>
F:20-71/Product: lactotransferrin #status experimental <MAT>
F:21-356/Domain: transferrin repeat homology <TRH1>
F:360-699/Domain: transferrin repeat homology <TRH2>
F:729-65,39-56,135-218,177-193,190-201,251-265,503-697,595-609/Disulfide bonds: #status e
F:157,498/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
Query Match 78.3%; Score 90; DB 1; Length 711;
Best Local Similarity 73.9%; Pred. No. 4e-06;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 TTEDSIATKTMNGEADMSLDGCF 23
DB 396 TTEDCIATVAKGADAMSIDGCF 418

```

```

A:Cross-references: EMBL:J03298
R:Li, Y.; Teng, C.T.
U. Biol. Chem. 266, 21880-21885, 1991
A:Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
A:Reference number: A41205; MUID:92042099; PMID:1939212
A:Accession: A41205
A:Molecule type: DNA
A:Residues: 115 <LIU>
A:Cross-references: GB:M74778
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; glycoprotein
F:1-19/Domain: signal sequence #status predicted <Sig>
F:20-707/Product: lactotransferrin #status predicted <MAT>
F:358-695/Domain: transferrin repeat homology <TRH2>
F:494/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 76.5%; Score 88; DB 1; Length 707;
Best Local Similarity 73.9%; Pred. No. 8.3e-06;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 TTEDSIATKTMNGEADMSLDGCF 23
DB 394 TTEDCIATVAKGADAMSIDGCF 416

```

RESULT 10

14728
carbonic anhydrase II inhibitor (transferrin homolog) precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: I47228
R:Houen, E.D.; Fierke, C.A.
Biochemistry 31, 12536-12542, 1992
A:Title: Purification and characterization of a carbonic anhydrase II inhibitor from po
A:Reference number: I47228; MUID:93099129; PMID:1463741
A:Accession: I47228
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-704 <ROU>
A:Cross-references: UNIPROT:Q29545; EMBL:U36916; NID:G1016329; PIDN:AAB58956.1; PID:G10
C:Genetics:
A:Gene: PICA
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication
F:20-350/Domain: transferrin repeat homology <TRH1>

Query Match 74.8%; Score 86; DB 2; Length 704;
Best Local Similarity 78.3%; Pred. No. 1.7e-05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TTEDSIATKTMNGEADMSLDGCF 23
DB 388 TTEDCIATVAKGADAMSIDGCF 410

RESULT 11

UC2323
lactoferrin - goat
C:Species: Capra aegagrus hircus (domestic goat)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C:Accession: JC2323
R:Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
A:Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locu
A:Reference number: JC2323; MUID:94380047; PMID:8093048
A:Accession: JC2323
A:Molecule type: mRNA
A:Residues: 1-708 <LEP>
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; glycoprotein
F:359-696/Domain: transferrin repeat homology <TRH2>
F:252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 73.0% Score 84; DB 2; Length 708;
Best Local Similarity 65.2%; Pred. No. 3 6e-05;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTEDSIKIMGEADAMSJDGGF 23
DB 395 TTDDCIATLVKGEADALSDJGCV 417

RESULT 12

TFEBE
Ovotransferrin precursor - chicken
N:Alternate names: conalbumin; transferrin
C:Species: Gallus gallus (chicken)
C>Date: 24-Apr-1984 #sequence revision 30-Sep-1993 #text change 09-Jul-2004
C:Accession: A26845; A91115; A92229; A91116; A40674; B61573; A90282; S02476; A03262
R:Jeltsch, J.M.; Hen, R.; Marcoteaux, L.; Garner, J.M.; Chambon, P.
Nucleic Acids Res. 15, 7643-7645, 1987
A>Title: Sequence of the chicken ovotransferrin gene.
A:Reference number: A26845; PMID:88015626; PMID:3658709
A:Accession: A26845

A:Molecule type: DNA
A:Residues: 1-705 <JE1>
A:Cross-references: UNIPROT:P02789; GB:X0407; NID:963131; PIDN:CAA68468.1; PID:9295721
R:Jeltsch, J.M.; Chambon, P.
Eur. J. Biochem. 122, 291-295, 1982
A>Title: The complete nucleotide sequence of the chicken ovotransferrin mRNA.
A:Reference number: A91115; PMID:82138851; PMID:7060577

A:Accession: A91115

A:Molecule type: mRNA
A:Residues: 1-82; 'V', 84-99; 'I', 101-153; 'W', 155-238; 'LN', 241-685; 'N', 687-705 <JE2>
A:Cross-references: EMBL:X02009
A>Note: The codons given for residues 132 (AAC) and 317 (UUC) are inconsistent with the R:Rihbodeau, S.N.; Lee, D.C.; Palmiter, R.D.
J. Biol. Chem. 253, 3771-3774, 1978
A>Title: Identical precursors for serum transferrin and egg white conalbumin.
A:Reference number: A92229; PMID:78171533; PMID:649604

A:Accession: A92229

A:Molecule type: protein
A:Residues: 1-23 <TH1>
R:Williams, J.; Ellemann, T.C.; Kingston, I.B.; Wilkins, A.G.; Kuhn, K.A.
Eur. J. Biochem. 122, 297-303, 1982
A>Title: The primary structure of hen ovotransferrin.
A:Reference number: A91116; PMID:82138852; PMID:6895872

A:Accession: A91116

A:Molecule type: protein
A:Residues: 1-50; 54-82; 'V', 84-92; 102-146; 162-168; 170-228; 241-283; 289-333; 338-344; 350-351
R:Gentili, C.; Bianco, P.; Neri, M.; Campanile, G.; Castagnola, P.; Cancedo
J. Cell Biol. 122, 703-712, 1993
A>Title: Cell proliferation, extracellular matrix mineralization, and ovotransferrin tra

A:Reference number: A40674; PMID:93328771; PMID:8393014

A:Accession: A40674

A:Molecule type: protein
A:Residues: 20-28; 'X', 30-38; 'X', 40-44 <GEN>
R:Chung, M.C.M.; Chan, S.L.; Shimizu, S.
Int. J. Biochem. 23, 609-616, 1991
A>Title: Purification of transferrins and lactoferrin using DEAE Affi-Gel Blue.
A:Reference number: A61573; PMID:91293379; PMID:2065820

A:Accession: B61573

A:Molecule type: protein
A:Residues: 20-28; 'X', 30-38; 'X', 40-43; 'S' <CHU>
R:Kingston, I.B.; Williams, J.
Biochem. J. 147, 463-472, 1975
A>Title: The amino acid sequence of a carbohydrate-containing fragment of hen ovotransf

A:Reference number: A90282; PMID:76039467; PMID:1172663

A:Accession: A90282

A:Molecule type: protein
A:Residues: 480-582 <KIN>
R:Ellemann, T.C.; Williams, J.
Biochem. J. 116, 515-532, 1970
A>Title: The amino acid sequences of cytochrome acid-containing peptides from performic aci

A:Reference number: A90246; PMID:70141846; PMID:4907959

A:Contents: annotation; disulfide bonds
R:Williams, J.; Moreton, K.
Biochem. J. 251, 849-855, 1988
A>Title: The dimerization of half-molecule fragments of transferrin.
A:Reference number: S02476; PMID:88326225; PMID:3415649

A:Accession: S02476

A:Molecule type: protein
A:Residues: 20-23; 295-302; 336-366; 674-679; 'T', 681; 'F', 683-685; 'N', 687-705 <W12>
C:Comment: Ovotransferrin (conalbumin) and transferrin have identical protein components
xrin is synthesized in the liver.
C:Comment: Ovotransferrin has a bacteriostatic function. Its concentration in avian egg
C:Comment: Plasma apotransferrin promotes the oxidation of ferrous ions, which would oth
C:Comment: In electrophoretic and genetic studies, transferrin shows strong polymorphism
C:Genetics:
A:Introns: 15/1; 69/3; 106/1; 170/1; 215/2; 234/1; 290/3; 353/1; 404/3; 436/1; 448/1; 50
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; egg white; glycoprotein; iron binding; plasma
F:1-19/Domain: signal sequence #status experimental <SIG>
F:20-705/Product: transferrin #status experimental <MAT>
F:21-355/Domain: transferrin repeat homology <TRH1>
F:359-692/Domain: transferrin repeat homology <TRH2>
F:29-64; 134-216; 179-193; 190-201; 247-261; 367-399; 424-699; 440-662; 473-549; 497-690/Disulfid
F:339-55; 377-390; 585-603/Disulfide bonds: #status predicted
F:492/Binding site: carbohydrate (asn) (covalent) (partial) #status experimental
F:507-521; 518-532/Disulfide bonds: (or 507-518; 521-532) #status predicted

Query Match 67.0% Score 77; DB 1; Length 705;
Best Local Similarity 71.4%; Pred. No. 0.00047;
Matches 15; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TTEDSIKIMGEADAMSJDGG 22
DB 396 TTDDCIKIMKGEADALVDGG 416

RESULT 13

TFEBL
Lactotransferrin precursor - bovine
N:Alternate names: lactoferrin
C:Species: Bos primigenius taurus (cattle)
C>Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 09-Jul-2004
C:Accession: I45919; S14674; S14110; S18517; J05095; S13097; S18518; S13681; PLO148; S21
R:Tsang, T.C.; Burns, D.K.; Wang, F.; Pan, Y.
FASEB J. 6, 233, 1991
A>Title: Cloning of a 80-kD advanced glycosylation end product (AGE) binding protein fro
A:Reference number: I45919

A:Accession: I45919

A:Stacus: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-708 <TSA>
A:Cross-references: UNIPROT:P24627; GB:L08604; NID:9163269; PIDN:AAA30609.1; PID:9163270
R:Pierce, A.
Submitted to the EMBL Data Library, November 1990

A:Reference number: S14674

A:Accession: S14674

A:Molecule type: mRNA
A:Residues: 1-144; 'V', 146-163; 'P', 166-339; 'A', 341-438; 'Y', 440-513; 'R', 515-708 <PI1>
A:Cross-references: EMBL:X57084; NID:9505; PIDN:CAA40366.1; PID:9506
R:Pierce, A.; Colavizza, D.; Benalosa, M.; Mees, P.; Tartar, A.; Montreuil, J.; Spik, G
Eur. J. Biochem. 196, 177-184, 1991
A>Title: Molecular cloning and sequence analysis of bovine lactotransferrin.
A:Reference number: S14110; PMID:91160550; PMID:2001696

A:Accession: S14110

A:Molecule type: mRNA
A:Residues: 3-14; 'V', 146-339; 'A', 341-438; 'Y', 440-513; 'R', 515-708 <PI2>
A:Cross-references: EMBL:X57084

A:Accession: S18517

A:Molecule type: protein
A:Residues: 20-35; 82-114; 148-163; 'P', 166-178; 'V', 'P', 183-190; 205-212; 230-239; 304-339; 59
R:Goodman, R.B.; Schanbacher, F.L.
Biochem. Biophys. Res. Commun. 180, 75-84, 1991
A>Title: Bovine lactoferrin mRNA: sequence, analysis, and expression in the mammary glan
A:Reference number: J05095; PMID:92028986; PMID:1718281

A:Accession: J70595
A:Molecule type: mRNA
A:Residues: 1-65, 'PC', 68-296, 'S', 298-339, 'A', 341-708 <GO>
A:Cross-references: GB:M63502
A:Notes: the authors translated the codon CCG for residue 66 as Arg and TCT for residue 2
R:Mead, P.E.; Tweedie, J.W.
Nucleic Acids Res. 18, 7167, 1990
A:Title: cDNA and protein sequence of bovine lactoferrin.
A:Reference number: S13097; MUID:91088328; PMID:2263492
A:Accession: S13097
A:Molecule type: mRNA
A:Residues: 28-33, 'DS', 36-38, 'P', 40-708 <MEA>
A:Cross-references: EMBL:X54801
A:Accession: S18518
A:Molecule type: protein
A:Residues: 20-47;59-66;132-139;256-277;278,305-332;343-351;361-363;586,587-589;598-619
R:Mead, P.E.
Submitted to the EMBL Data Library, October 1990
A:Reference number: S13881
A:Accession: S13881
A:Molecule type: mRNA
A:Residues: 28-38, 'P', 40-86, 'C', 88-708 <ME3>
A:Cross-references: EMBL:X54801
R:Rejman, J.J.; Hegarty, H.M.; Hurley, W.L.
Comp. Biochem. Physiol. B 93, 929-934, 1989
A:Title: Purification and characterization of bovine lactoferrin from secretions of the
A:Reference number: P10148; MUID:90031466; PMID:2805645
A:Accession: P10148
A:Molecule type: protein
A:Residues: 20-27,'X',29-37,'X',39-54,'X',56-59 <RE3>
R:Ballamy, W.; Takeae, M.; Yamuchi, K.; Wakabayashi, H.; Kawase, K.; Tomita, M.
Biochim. Biophys. Acta 1121, 130-136, 1992
A:Title: Identification of the bactericidal domain of lactoferrin.
A:Reference number: S21756; MUID:92287941; PMID:1599934
A:Accession: S21756
A:Molecule type: protein
A:Residues: 36-60 <RBL>
R:Shimazaki, K.; Tanaka, T.; Kon, H.; Oota, K.; Kawaguchi, A.; Maki, Y.; Sato, T.
J. Dairy Sci. 76, 946-955, 1993
A:Title: Separation and characterization of the C-terminal half molecule of bovine lactoferrin.
A:Reference number: A56659; MUID:93253156; PMID:8486845
A:Accession: A56659
A:Molecule type: protein
A:Residues: 20-25;302-308;359-366,'X',368-376,'X',378 <SHI>
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; glycoprotein; iron; iron binding; metalloprotein; milk
F:1-19/Dominant: signal sequence #status predicted <SIG>
F:20-708/Product: lactotransferrin #status experimental <MAT>
F:20-355/Dominant: transferrin repeat homology <TRH1>
F:359-60/Region: antimicrobial
F:359-696/Dominant: transferrin repeat homology <TRH2>
F:28-64,134-217,176-192,179-200,189-202,250-264,367-399,377-390,424-703,444-666,476-551,
F:38-55/Duplicate bonds: #status predicted
F:79,111,211,277/Binding site: iron (Asp, Tyr, Tyr, His) #status experimental
F:146/Binding site: carbonate (Arg) #status experimental
F:252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:414,457,545,614/Binding site: iron (Asp, Tyr, Tyr, His) #status experimental
F:482/Binding site: carbonate (Arg) #status experimental

RESULT 14
S12100
transferrin precursor - African clawed frog
C1Species: *Xenopus laevis* (African clawed frog)
C1Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C:Accession: S12100
R:Mokaitis, J.E.; Pastori, R.L.; Schoenberg, D.R.
Nucleic Acids Res. 18, 6135, 1990
A:Title: The nucleotide sequence of *Xenopus laevis* transferrin mRNA.
A:Reference number: S12100; MUID:91045087; PMID:2235503
A:Accession: S12100
A:Molecule type: mRNA
A:Residues: 1-717 <MOS>
A:Cross-references: UNIPROT:P20233; EMBL:X54530; NID:G65158; PIDN:CNA38396.1; PID:G6515
C:Superfamily: transferrin; transferrin repeat homology
F:346-669/Domain: transferrin repeat homology <TRH2>

	Query Match	61.7%	Score 71;	DB 2;	Length 717;
	Best Local Similarity	52.2%;	Pred. No.	0.0043;	
Matches	12;	Conservative	7;	Mismatches	4;
				Indels	0;
				Gaps	0;
Oy	1 TTEDSIKIMNGEADAMSLOGCF	23			
	: :				
	: :				
Db	385 TAEECTVQILKEGDADVATLDDGGY	407			

RESULT 15
T11749
transferrin - Atlantic salmon
C:Species: Salmo salar (Atlantic salmon)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T11749
R:Kvangedal, A.M.; Rorvik, K.A.; Alestrom, P.
Mol. Marine Biol. Biotechnol. 2, 233-238, 1993
A:Title: Cloning and characterization of Atlantic salmon (Salmo salar) serum transferrin
A:Reference number: Z17332; MUID:94122797; PMID:8293074
A:Accession: T11749
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-690 <KVI>
A:Cross-references: UNIPROT:P80426; EMBL:L20313; NID:g431609; PION:AA18638.1; PID:g4311
A:Experimental source: liver
A:Superfamily: transferrin; transferrin repeat homology
C:Keywords: iron binding

	Query Match	57.4%	Score 66	DB 2	Length 690
	Best Local Similarity	59.1%	Pred. No.	0.026	
	Matches 13	Conservative 4	Mismatches 5	Indels 0	Gaps 0
Oy	1 TTEDSIKXINNGEADAMSLDGG	22			
	: : : : : : : : : : : : : : : :				
Nb	375 TVECCIKIRKEADALAVDDG	396			

Search completed: November 1, 2005, 12:55:47
Job time : 25.3382 secs

```

Oy      1  TTEDSIKINNGEADAMSLODG  22
      |  |  |  |  |  |  |  |  |  |  |
Db      375  IVEECIKIKIRKEADAIAYVDG  396

Search completed: November 1, 2005, 12:55:47
Job time : 25.382 secs

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:34:09 / Search time 112.632 Seconds
(without alignments)
104.569 Million cell updates/sec

Title: US-10-612-162A-2

Perfect score: 115

Sequence: 1 TTEDSIKIMNGEADMSLDGCF 23

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	110	95.7	698	1	TRFE_HUMAN	P02787 homo sapien
2	103	89.6	694	2	OTRFX6	OTRFX6 marmota mon
3	101	87.8	695	1	TRFE_RABIT	P19134 oryctolegus
4	96	83.5	706	1	TRFE_HORSE	P27425 equus caball
5	92	80.0	696	1	TRFE_PIG	P09571 sus scrofa
6	92	80.0	697	1	TRFE_MOUSE	Q92141 mus musculu
7	92	80.0	704	1	TRFE_BOVIN	Q29443 bos taurus
8	92	80.0	704	1	TRFL_PIG	P14632 sus scrofa
9	92	80.0	704	2	Q8WMA8	Q8WMA8 sus scrofa
10	92	80.0	704	2	Q6Y739	Q6Y739 sus scrofa
11	92	80.0	704	2	Q7YS20	Q7YS20 sus scrofa
12	90	78.3	698	1	TRFE_RAT	P12346 rattus norv
13	90	78.3	698	1	Q7TNX0	Q7TNX0 rattus norv
14	90	78.3	711	1	TRFL_HUMAN	P02788 homo sapien
15	90	78.3	979	2	Q7TMC7	Q7TMC7 rattus norv
16	90	78.3	980	2	Q7TP24	Q7TP24 rattus norv
17	88	76.5	705	2	Q6A169	Q6A169 chryseomys s
18	88	76.5	707	1	TRFL_MOUSE	P08071 mus musculu
19	88	76.5	707	2	Q8CBA0	Q8CBA0 mus musculu
20	87	75.7	700	2	Q8VC96	Q8VC96 mus musculu
21	87	75.7	700	2	Q9DBD0	Q9DBD0 mus musculu
22	87	75.7	708	1	TRFL_CAMDR	Q9TUN0 camelus dro
23	86	73.0	704	1	ICA_PIG	Q29545 sus scrofa
24	84	73.0	421	2	Q7TP83	Q7TP83 rattus norv
25	84	73.0	708	1	TRFL_BUBBU	Q77688 bubalus bub
26	84	73.0	708	1	TRFL_CAPHI	Q29477 capra hircu
27	83	72.2	695	1	TRFL_HORSE	Q77811 equus caball
28	83	72.2	711	2	Q9XT72	Q9XT72 trichosurus
29	82	71.3	701	2	Q6A168	Q6A168 struthio ca
30	80	69.6	462	2	Q6Q147	Q6Q147 rattus norv
31	77	67.0	355	2	Q8MI10	Q8MI10 bos taurus

ALIGNMENTS

RESULT 1	TRFE_HUMAN	STANDARD;	PRT;	698 AA.
ID	P02787; O43890; Q9NQB8; Q9UHV0;			
AC	21-JUL-1986 (Rel. 01, Created)			
DT	01-OCT-1989 (Rel. 12, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal binding globulin) (PRO1400).			
GN	Name=TF;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND VARIANTS TF*B2; TF*CHI AND TF*DL.			
RX	MDL:LINE=64194084; PubMed=6585826;			
RA	Yang F., Lum J.B., McGill J.R., Moore C.M., Naylor S.L.,			
RA	van Bragt P.H., Baldwin W.D., Bowman B.H.,			
RT	"Human transferrin: cDNA characterization and chromosomal localization."			
RL	Proc. Natl. Acad. Sci. U.S.A. 81:2752-2756(1984).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MDL:LINE=88056305; PubMed=3678832; DOI=10.1016/0378-1119(87)90163-6;			
RA	Schaeffer E., Lucero M.A., Jelech J.-M., Py M.-C., Levin M.J.,			
RA	Chambon P., Cohen G.N., Zakim M.W.,			
RT	"Complete structure of the human transferrin gene. Comparison with analogous chicken gene and human pseudogene."			
RL	Gene 56:109-116(1987).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MDL:LINE=92221399; PubMed=1809186;			
RA	Hershenberger C.L., Larson J.L., Arnold B., Roestek P.R. Jr.,			
RA	Williams P., Dehoff B., Dunn P., O'Neal K.L., Rlemen M.W., Tice P.A.;			
RT	"A cloned gene for human transferrin."			
RL	Am. N. Y. Acad. Sci. 646:140-154(1991).			
RN	[4]			
RP	SEQUENCE FROM N.A., AND VARIANT ATRANSFERRINEMIA PRO-477.			
RX	MDL:LINE=20563920; PubMed=11110675;			
RA	Beutler E., Gelbart T., Lee P.L., Trevino R., Fernandez M.A.,			
RA	Faipbanks V.F.;			
RT	"Molecular characterization of a case of atransferrinemia."			
RL	Blood 96:4071-4074(2000).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,			
RA	Ahearn M.O., Koldanek S.A., Rajkumar N., Toth E.J., Yi Q.,			
RA	Nickerson D.A.;			
RT	"SeattleSNP: NHGRI HU66682 program for genomic applications, UW-			
RT	PHRC, Seattle, WA (URL: http://pga.gs.washington.edu)."			
RL	Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.			
RN	[6]			

32	77	67.0	681	2	Q6LAN7	Q6LAN7 bos taurus
33	77	67.0	705	1	TRFE_CHICK	P02789 gallus gall
34	77	67.0	708	1	TRFL_BOVIN	P24627 bos taurus
35	77	67.0	708	2	Q6LEC7	P61ec7 bos taurus
36	76	66.1	686	1	TRFE_ANAPL	P56410 anas platyr
37	71	61.7	532	2	Q7SYA2	Q7SYA2 xenopus lae
38	71	61.7	701	1	TRFE_XENLA	P20233 xenopus lae
39	71	61.7	701	2	Q6PGT3	Q6PGT3 xenopus lae
40	71	61.7	720	2	Q7ZTQ7	Q7ZTQ7 xenopus lae
41	70	60.9	615	2	Q6TXX2	Q6TXX2 xenopharyn
42	70	60.9	685	1	TRFE_PAROL	Q93429 paralicthy
43	70	60.9	686	2	Q9IA82	Q9IA82 paralicthy
44	70	60.9	686	2	Q9IA83	Q9IA83 paralicthy
45	70	60.9	691	2	Q6UPC0	Q6UPC0 acanthopagr

RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22286257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Urdin T.B., Toehlyuk S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalys D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP SEQUENCE OF 99-698 FROM N.A.
RC TISSUE=Fetal liver;
RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M.,
RA He P.;
RT "Functional prediction of the coding sequences of 33 new genes deduced
RL by analysis of cDNA clones from human fetal liver.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE OF 422-698 FROM N.A.
RX MEDLINE=84153910; PubMed=6322780;
RA Uzan G., Frain M., Park I., Besmond C., Maessen G., Trepac J.S.,
RA Zakin M.M., Kahn A.;
RT "Molecular cloning and sequence analysis of cDNA for human
RL transferrin.";
RL Biochem. Biophys. Res. Commun. 119:273-281(1984).
RN [9]
RP SEQUENCE OF 20-698.
RX MEDLINE=83160878; PubMed=6833213;
RA McGillivray R.T.A., Mendez E., Shewale J.G., Sinha S.K.,
RA Linbeck-Zins J., Brew K.;
RT "The primary structure of human serum transferrin. The structures of
RL seven cyanogen bromide fragments and the assembly of the complete
RT structure.";
RL J. Biol. Chem. 258:3543-3553(1983).
RN [10]
RP SEQUENCE OF 73-698 FROM N.A.
RX MEDLINE=85216459; PubMed=3858812;
RA Park I., Schaeffer E., Sidoti A., Baralle F.E., Cohen G.N.,
RA Zakin M.M.;
RT "Organization of the human transferrin gene: direct evidence that it
RL originated by gene duplication.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:3149-3153(1985).
RN [11]
RP SEQUENCE OF 1-14 FROM N.A.
RX MEDLINE=87066744; PubMed=3786138;
RA Lucero M.A., Schaeffer E., Cohen G.N., Zakin M.M.;
RT "The 5' region of the human transferrin gene: structure and potential
RL regulatory sites.";
RL Nucleic Acids Res. 14:8692-8692(1986).
RN [12]
RP SEQUENCE OF 1-72 AND 291-300 FROM N.A.
RX MEDLINE=87192006; PubMed=3106157; DOI=10.1016/0378-1119(86)90277-5;
RA Adrian G.S., Korinek B.W., Bowman B.H., Yang F.;
RT "The human transferrin gene: 5' region contains conserved sequences
RL which match the control elements regulated by heavy metals,
RL glucocorticoids and acute phase reaction.";
RL Gene 49:167-175(1986).
RN [13]
RP SEQUENCE OF 45-72 FROM N.A.

RX MEDLINE=20392111; PubMed=10931525;
RX DOI=10.1002/1097-4547(20000815)61:4<388::AID-JMR5>3.0.CO;2-O;
RA de Arriba Zepa G.A., Saleh M.C., Fernandez P.M., Guillou F.,
RA Espinosa de los Monteros A., de Vellis J., Zakin M.M., Baron B.;
RT "Alternative splicing prevents transferrin secretion during
RL differentiation of a human oligodendrocyte cell line.";
RL J. Neurosci. Res. 61:388-395(2000).
RN [14]
RP SEQUENCE OF 564-624 FROM N.A., AND VARIANT TP+C2.
RC TISSUE=Brain;
RX MEDLINE=97418135; PubMed=9272172;
RA Namakata K., Oyama F., Imagawa M., Ihara Y.;
RT "Human transferrin (Tf): a single mutation at codon 570 determines Tf
RL C1 or Tf C2 variant.";
RL Hum. Genet. 100:457-458(1997).
RN [15]
RP SEQUENCE OF 564-624 FROM N.A.
RA Tsuchida S., Ikemoto S., Kajii E.;
RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
RN [16]
RP SEQUENCE OF 636-696 FROM N.A.
RX MEDLINE=89386721; PubMed=2780570;
RA Duguid J.R., Bohmont C.W., Liu N.G., Tourtellotte W.W.;
RT "Changes in brain gene expression shared by scrapie and Alzheimer
RL disease.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:7260-7264(1989).
RN [17]
RP SEQUENCE OF 263-266; 454-458; 531-538 AND 589-595.
RC TISSUE=Heart;
RX MEDLINE=96007936; PubMed=7498159;
RA Kovalyov L.I., Shishkin S.S., Efimochkin A.S., Kovalyova M.A.,
RA Ershova E.S., Egorov T.A., Musalyanov A.K.;
RT "The major protein expression profile and two-dimensional protein
RL database of human heart.";
RL Electrophoresis 16:1160-1169(1995).
RN [18]
RP DISULFIDE BONDS.
RX MEDLINE=8222166; PubMed=6953407;
RA McGillivray R.T.A., Mendez E., Sinha S.K., Sutton M.R.,
RA Linbeck-Zins J., Brew K.;
RT "The complete amino acid sequence of human serum transferrin.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2504-2508(1982).
RN [19]
RP MUTAGENESIS.
RX MEDLINE=92031536; PubMed=1932003;
RA Woodworth R.C., Mason A.B., Funk W.D., McGillivray R.T.A.;
RT "Expression and initial characterization of five site-directed mutants
RL of the N-terminal half-molecule of human transferrin.";
RL Biochemistry 30:10824-10829(1991).
RN [20]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 22-350.
RX MEDLINE=98272665; PubMed=9609685; DOI=10.1021/bi980355f;
RA McGillivray R.T.A., Moore S.A., Chen J., Anderson B.F., Baker H.,
RA Luo Y., Bewley M.C., Smith C.A., Murphy M.E.P., Wang Y., Mason A.B.,
RA Woodworth R.C., Brayer G.D., Baker E.N.;
RT "Two high-resolution crystal structures of the recombinant N-lobe of
RL human transferrin reveal a structural change implicated in iron
RL release.";
RL Biochemistry 37:7919-7928(1998).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-350.
RX MEDLINE=98434369; PubMed=9760232; DOI=10.1021/bi9812064;
RA Jeffrey P.D., Bewley M.C., McGillivray R.T.A., Mason A.B.,
RA Woodworth R.C., Baker E.N.;
RT "Ligand-induced conformational change in transferrins: crystal
RL structure of the open form of the N-terminal half-molecule of human
RL transferrin.";
RL Biochemistry 37:13978-13986(1998).
RN [22]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 23-352.
RX MEDLINE=99155227; PubMed=10029548; DOI=10.1021/bi9924543;
RA Bewley M.C., Tam B.M., Grewal J., He S., Shewry S., Murphy M.E.P.,
RA Mason A.B., Woodworth R.C., Baker E.N., McGillivray R.T.A.;

```

RT "X-ray crystallography and mass spectroscopy reveal that the N-lobe of
human transferrin expressed in Pichia pastoris is folded correctly but

Query Match 95.74; Score 110; DB 1; Length 698;
Best Local Similarity 95.74; Pred. No. 3.3e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTEDSTAKINGGADAMSLDGGF 23
Db 392 STEDCIKIMNGGADAMSLDGGF 414

RESULT 2
O7TSX8 PRELIMINARY; PRT; 694 AA.
AC O7TSX8;
DT 01-OCT-2003 (TEMBLrel. 25, Created)
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Transferrin.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Rinaldo J.A.S., Gerlin J.L.;
RA Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transferrin are iron binding transport proteins which
CC bind ferric iron in association with the binding of an anion,
CC usually bicarbonate (by similarity).
CC -1- DOMAIN: Composed of two homologous domains (by similarity).
CC -1- SIMILARITY: Belongs to the transferrin family.
DR EMBL; AY288100; AAP37129.1; -.
DR HSSP; P19134; IJNF.
DR GO; GO:0005576; Cytoplasm; IEA.
DR GO; GO:0008199; Ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin; 2.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
DR Iron transport; Metal-binding; Transport.
DR Iron transport; Metal-binding; Transport.
SO SEQUENCE 694 AA; 76466 MW; 40053F7DC1CFCAB7 CRC64;

Query Match 89.64; Score 103; DB 2; Length 694;
Best Local Similarity 87.04; Pred. No. 4e-07;
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTEDSTAKINGGADAMSLDGGF 23
Db 392 STEDCIKIMNGGADAMSLDGGF 414

RESULT 3
TRFE_RABIT STANDARD; PRT; 695 AA.
AC P19154; O46514;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal
DE binding globulin).
GN Name=Trf;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA BMDLINE=91274362; PubMed=2054387; DOI=10.1016/0167-4781(91)90021-D;
RA Banfield D.K., Chow B.K.-C., Funk W.D., Robertson K.A., Umelas T.M.,
RA Woodworth R.C., McGillivray R.T.A.;
RA "The nucleotide sequence of rabbit liver transferrin cDNA.";
RA Biochim. Biophys. Acta 1089:262-265(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white;
RA Chareeb B.A.A., Thepot D., Puisant C., Cajero-Juarez M.,
RA Houdebine L.M.;
RA "Cloning and structural organisation of the rabbit transferrin encoding
RA gene.";
RA Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 20-51.
RX MEDLINE=88209278; PubMed=3365331;
RX Godoyac-Zimmermann J.;
RX "Isolation, characterization and N-terminal amino-acid sequence of
RX rabbit transferrin.";
RX Biol. Chem. Hoppe-Seyler 369:93-96(1988).
RN [4]
RP SEQUENCE OF 483-545.
RX MEDLINE=89005676; PubMed=3169252; DOI=10.1016/0014-5793(88)80221-7;
RX Evans R.W., Altken A., Patel K.J.;
RX "Evidence for a single glycan moiety in rabbit serum transferrin and
RX location of the glycan within the polypeptide chain.";
RX FEBS Lett. 238:39-42(1988).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).
RC TISSUE=Plasma;
RX MEDLINE=89026775; PubMed=3179277;
RX Bailey S., Evans R.W., Garratt R.C., Gorinsky B., Hasnain S.,
RX Horsburgh C., Jhoti H., Lindley P.F., Mydin A., Sarrat R., Watson J.L.;
RX "Molecular structure of serum transferrin at 3.3-A resolution.";
RX Biochemistry 27:5804-5812(1988).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RA Sarrat R., Garratt R.C., Gorinsky B., Jhoti H., Lindley P.F.;
RA "High-resolution X-ray studies on rabbit serum transferrin:
RA preliminary structure analysis of the N-terminal half-molecule at 2.3-
RA A resolution.";
RA Acta Crystallogr. B 46:763-771(1990).
RN [7]
RP -1- FUNCTION: Transferrins are iron binding transport proteins which
RP can bind two atoms of ferric iron in association with the binding
RP of an anion, usually bicarbonate. It is responsible for the
RP transport of iron from sites of absorption and heme degradation to
RP those of storage and utilization. Serum transferrin may also have
RP a further role in stimulating cell proliferation.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC -1- DOMAIN: Composed of two homologous domains.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X58533; CAA41424.1; -.
DR EMBL; AF031625; AAB94136.1; -.
DR EMBL; AF031611; AAB94136.1; JOINED.
DR EMBL; AF031612; AAB94136.1; JOINED.
DR EMBL; AF031613; AAB94136.1; JOINED.
DR EMBL; AF031614; AAB94136.1; JOINED.
DR EMBL; AF031615; AAB94136.1; JOINED.

```

```

DR EMBL; AF031616; AAB94136.1; JOINED.
DR EMBL; AF031617; AAB94136.1; JOINED.
DR EMBL; AF031618; AAB94136.1; JOINED.
DR EMBL; AF031619; AAB94136.1; JOINED.
DR EMBL; AF031620; AAB94136.1; JOINED.
DR EMBL; AF031621; AAB94136.1; JOINED.
DR EMBL; AF031622; AAB94136.1; JOINED.
DR EMBL; AF031623; AAB94136.1; JOINED.
DR EMBL; AF031624; AAB94136.1; JOINED.
DR PDB; 1JNP; X-ray; A=20-695.
DR PDB; 1TFD; X-ray; @=20-323.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin; 2.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW 3D-structure; Direct protein sequencing; Glycoprotein; Iron transport;
KW Metal-binding; Repeat; Signal; Transport.
FT CHAIN 1 695
FT REPEAT 20 355 Serotransferrin.
FT REPEAT 356 695 1.
FT DISULFID 28 67 2.
FT DISULFID 38 58
FT DISULFID 137 213
FT DISULFID 156 350
FT DISULFID 177 193
FT DISULFID 180 196
FT DISULFID 190 198
FT DISULFID 246 260
FT DISULFID 358 612
FT DISULFID 364 396
FT DISULFID 374 387
FT DISULFID 421 690
FT DISULFID 436 653
FT DISULFID 468 539
FT DISULFID 492 681
FT DISULFID 502 516
FT DISULFID 513 522
FT DISULFID 579 593
FT DISULFID 631 636
FT CARBOHYD 509
FT METAL 82 82 N-linked (GLCNAC. . .).
FT METAL 114 114 Iron 1.
FT METAL 207 207 Iron 1.
FT METAL 268 268 Iron 1.
FT METAL 411 411 Iron 2.
FT METAL 444 444 Iron 2.
FT METAL 533 533 Iron 2.
FT METAL 601 601 Iron 2.
FT BINDING 139 139 Carbonate 1.
FT BINDING 143 143 Carbonate 1.
FT BINDING 145 145 Carbonate 1 (via amide nitrogen).
FT BINDING 146 146 Carbonate 1 (via amide nitrogen).
FT BINDING 470 470 Carbonate 2.
FT BINDING 474 474 Carbonate 2.
FT BINDING 476 476 Carbonate 2 (via amide nitrogen).
FT BINDING 477 477 Carbonate 2 (via amide nitrogen).
FT VARIANT 517 517 V -> I.
FT CONFLICT 7 7 Missing (in Ref. 1).
FT CONFLICT 47 47 K -> S (in Ref. 3).
FT CONFLICT 50 50 P -> Y (in Ref. 3).
FT STRAND 24 30
FT HELIX 31 48
FT TURN 51 52
FT STRAND 55 61
FT HELIX 64 72
FT TURN 73 74
FT STRAND 78 81
FT HELIX 83 90
FT TURN 92 94

```

```

FT STRAND 96 104
FT STRAND 111 111
FT STRAND 113 121
FT STRAND 122 123
FT TURN 128 130
FT HELIX 132 133
FT TURN 136 138
FT STRAND 141 142
FT TURN 144 147
FT HELIX 148 154
FT HELIX 155 157
FT HELIX 165 172
FT STRAND 176 177
FT TURN 179 180
FT TURN 183 185
FT TURN 187 190
FT HELIX 191 192
FT TURN 194 195
FT TURN 200 201
FT TURN 203 204
FT HELIX 206 215
FT TURN 216 217
FT STRAND 221 225
FT TURN 226 227
FT HELIX 228 232
FT HELIX 236 239
FT TURN 240 241
FT STRAND 242 245
FT TURN 247 248
FT STRAND 251 253
FT HELIX 254 256
FT TURN 257 258
FT STRAND 263 266
FT STRAND 269 273
FT HELIX 279 293
FT TURN 303 304
FT TURN 307 308
FT TURN 316 317
FT STRAND 320 323
FT TURN 326 327
FT HELIX 330 334
FT HELIX 336 346
FT TURN 347 348

Query Match      87.8%; Score 101; DB 1; Length 695;
Best Local Similarity 87.0%; Pred. No. 8.2e-07;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 TTEDSIKIMNGEADMSLDGGE 23
Db      392 TPEDCIKIMNGEADMSLDGGE 414

RESULT 4
ID TRPE HORSE STANDARD; PRT; 706 AA.
AC P27425;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal
DE binding globulin).
DE Name:TF;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OK NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93277958; PubMed=8504171; DOI=10.1016/0167-4781(93)90186-H;
RA "The cDNA sequence of horse transferrin.";
RT Biochim. Biophys. Acta 1173:230-232(1993).
RL

```



```

RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE: Extracellular tissue;
RA McDowell K.J., Adams M.H., Baker C.B.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transferrin are iron binding transport proteins which
CC can bind two atoms of ferric iron in association with the binding
CC of an anion, usually bicarbonate. It is responsible for the
CC transport of iron from sites of absorption and heme degradation to
CC those of storage and utilization. Serum transferrin may also have
CC a further role in stimulating cell proliferation.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -1- DOMAIN: Composed of two homologous domains.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M69020; AAA30958.1; -.
DR EMBL: U21127; AAA63684.1; -.
DR PIR: S33761; S33761.
DR HSSP: P02787; 1A8E.
DR InterPro: IPR001156; Peptidase_S60.
DR Pfam: PF00405; Transferrin_2.
DR PRINTS: PRO0422; TRANSFERRIN.
DR SMART: SM00094; TR_FER; 2.
DR PROSITE: PS00205; TRANSFERRIN_1; 2.
DR PROSITE: PS00206; TRANSFERRIN_2; 2.
DR PROSITE: PS00207; TRANSFERRIN_3; 2.
DR GlycoProtein: Iron transport; Metal-binding; Repeat; Signal;
KW Transport.
FT SIGNAL 1 19 By similarity.
FT CHAIN 20 706 Serotransferrin.
FT REPEAT 20 357 1.
FT REPEAT 358 706 2.
FT DISULFID 26 64 By similarity.
FT DISULFID 36 55 By similarity.
FT DISULFID 134 215 By similarity.
FT DISULFID 174 190 By similarity.
FT DISULFID 177 198 By similarity.
FT DISULFID 187 200 By similarity.
FT DISULFID 248 262 By similarity.
FT DISULFID 360 623 By similarity.
FT DISULFID 366 398 By similarity.
FT DISULFID 376 389 By similarity.
FT DISULFID 423 701 By similarity.
FT DISULFID 441 664 By similarity.
FT DISULFID 474 550 By similarity.
FT DISULFID 498 692 By similarity.
FT DISULFID 508 522 By similarity.
FT DISULFID 519 533 By similarity.
FT DISULFID 590 604 By similarity.
FT DISULFID 642 647 By similarity.
FT METAL 79 79 Iron 1 (By similarity).
FT METAL 111 111 Iron 1 (By similarity).
FT METAL 209 209 Iron 1 (By similarity).
FT METAL 270 270 Iron 1 (By similarity).
FT METAL 413 413 Iron 2 (By similarity).
FT METAL 449 449 Iron 2 (By similarity).
FT METAL 544 544 Iron 2 (By similarity).
FT METAL 612 612 Iron 2 (By similarity).
FT BINDING 136 136 Carbonate 1 (By similarity).
FT BINDING 140 140 Carbonate 1 (By similarity).
FT BINDING 142 142 Carbonate 1 (via amide nitrogen) (By
FT BINDING 143 143 similarity).
FT BINDING 143 143 Carbonate 1 (via amide nitrogen) (By

```

```

FT BINDING 476 476 similarity).
FT BINDING 480 480 Carbonate 2 (By similarity).
FT BINDING 482 482 Carbonate 2 (via amide nitrogen) (By
FT BINDING 483 483 similarity).
FT BINDING 483 483 Carbonate 2 (via amide nitrogen) (By
FT CARBOHYD 515 515 similarity).
SQ SEQUENCE 706 AA; 78094 MW; 1A0F5A6C0409DBA CRC64;
Query Match 83.5%; Score 96; DB 1; Length 706;
Best Local Similarity 82.6%; Pred. No. 5e-06;
Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 TTEDSIATKIMGADAMSIDGCF 23
DB 394 STEDCIATKIVGGEADAMSIDGCF 416
:|||||:|||||:
RESULT 5
ID TREE_PIG STANDARD; PRT; 696 AA.
AC P09571;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Serotransferrin (Transferrin) (Siderophilin) (Beta-1-metal binding
DE globulin).
GN Name=TF;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sui.
OX NCBI_TaxId=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=8835629; Pubmed=3419934;
RA Baldwin G.S., Weinstein J.;
RL "Nucleotide sequence of porcine liver transferrin.";
Nucleic Acids Res. 16:8720-8720(1988).
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC can bind two atoms of ferric iron in association with the binding
CC of an anion, usually bicarbonate. It is responsible for the
CC transport of iron from sites of absorption and heme degradation to
CC those of storage and utilization. Serum transferrin may also have
CC a further role in stimulating cell proliferation.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -1- DOMAIN: Composed of two homologous domains.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X12386; CAA30943.1; -.
DR PIR: S01384; S01384.
DR PDB: 1H76; X-ray; A=1-696.
DR InterPro: IPR001156; Peptidase_S60.
DR Pfam: PF00405; Transferrin_2.
DR PRINTS: PRO0422; TRANSFERRIN.
DR SMART: SM00094; TR_FER; 2.
DR PROSITE: PS00205; TRANSFERRIN_1; 2.
DR PROSITE: PS00206; TRANSFERRIN_2.
DR PROSITE: PS00207; TRANSFERRIN_3; 2.
KW 3D-structure; Glycoprotein; Iron transport; Metal-binding; Repeat;
KW Transport.
FT REPEAT 1 340 1.

```

FT	REPEAT	341	696	2.
FT	DISULFID	9	47	By similarity.
FT	DISULFID	19	38	By similarity.
FT	DISULFID	117	198	By similarity.
FT	DISULFID	157	173	By similarity.
FT	DISULFID	160	181	By similarity.
FT	DISULFID	170	183	By similarity.
FT	DISULFID	231	245	By similarity.
FT	DISULFID	343	605	By similarity.
FT	DISULFID	349	381	By similarity.
FT	DISULFID	359	372	By similarity.
FT	DISULFID	406	682	By similarity.
FT	DISULFID	423	646	By similarity.
FT	DISULFID	456	532	By similarity.
FT	DISULFID	480	673	By similarity.
FT	DISULFID	490	504	By similarity.
FT	DISULFID	501	515	By similarity.
FT	DISULFID	572	586	By similarity.
FT	DISULFID	624	629	By similarity.
FT	METAL	62	62	Iron 1 (By similarity).
FT	METAL	94	94	Iron 1 (By similarity).
FT	METAL	192	192	Iron 1 (By similarity).
FT	METAL	253	253	Iron 1 (By similarity).
FT	METAL	396	336	Iron 2 (By similarity).
FT	METAL	431	431	Iron 2 (By similarity).
FT	METAL	526	526	Iron 2 (By similarity).
FT	METAL	594	594	Iron 2 (By similarity).
FT	BINDING	119	119	Carbonate 1 (By similarity).
FT	BINDING	123	123	Carbonate 1 (By similarity).
FT	BINDING	125	125	Carbonate 1 (via amide nitrogen) (By similarity).
FT	BINDING	126	126	Carbonate 1 (via amide nitrogen) (By similarity).
FT	BINDING	458	458	Carbonate 2 (By similarity).
FT	BINDING	462	462	Carbonate 2 (By similarity).
FT	BINDING	464	464	Carbonate 2 (via amide nitrogen) (By similarity).
FT	BINDING	465	465	Carbonate 2 (via amide nitrogen) (By similarity).
FT	CARBOHYD	25	25	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	497	497	N-linked (GlcNAc. . .) (Potential).
FT	VARIANT	308	308	K -> R.
FT	STRAND	5	10	
FT	HELIX	13	29	
FT	STRAND	35	40	
FT	HELIX	44	52	
FT	TURN	53	54	
FT	STRAND	58	61	
FT	HELIX	63	69	
FT	TURN	70	70	
FT	TURN	72	74	
FT	STRAND	76	84	
FT	TURN	87	88	
FT	STRAND	91	91	
FT	STRAND	93	101	
FT	TURN	102	103	
FT	HELIX	108	110	
FT	TURN	112	113	
FT	STRAND	115	118	
FT	TURN	121	122	
FT	TURN	124	127	
FT	HELIX	128	134	
FT	HELIX	135	137	
FT	HELIX	145	152	
FT	STRAND	155	157	
FT	TURN	159	160	
FT	TURN	163	165	
FT	HELIX	167	170	
FT	TURN	171	172	
FT	HELIX	177	179	
FT	TURN	180	181	
FT	TURN	185	186	
FT	TURN	188	189	
FT	HELIX	191	200	
FT	TURN	201	202	
FT	STRAND	206	210	
FT	TURN	211	212	
FT	HELIX	213	217	
FT	HELIX	224	226	
FT	STRAND	227	230	
FT	TURN	232	233	
FT	STRAND	236	238	
FT	HELIX	239	244	
FT	STRAND	248	251	
FT	STRAND	254	258	
FT	HELIX	264	278	
FT	TURN	280	281	
FT	TURN	288	289	
FT	TURN	292	293	
FT	TURN	301	302	
FT	STRAND	305	308	
FT	TURN	311	312	
FT	HELIX	315	319	
FT	HELIX	321	331	
FT	STRAND	346	351	
FT	HELIX	352	365	
FT	TURN	366	368	
FT	STRAND	370	375	
FT	HELIX	378	387	
FT	TURN	388	388	
FT	STRAND	392	395	
FT	HELIX	397	405	
FT	TURN	406	407	
FT	STRAND	409	415	
FT	TURN	421	422	
FT	HELIX	423	425	
FT	STRAND	431	438	
FT	TURN	439	440	
FT	TURN	443	444	
FT	HELIX	447	449	
FT	TURN	451	452	
FT	STRAND	455	457	
FT	TURN	460	461	
FT	TURN	463	466	
FT	HELIX	467	477	
FT	STRAND	482	485	
FT	TURN	490	490	
FT	TURN	492	493	
FT	TURN	496	497	
FT	HELIX	499	501	
FT	TURN	502	503	
FT	TURN	511	512	
FT	TURN	514	515	
FT	TURN	519	520	
FT	TURN	522	523	
FT	HELIX	525	535	
FT	TURN	536	536	
FT	STRAND	539	543	
FT	TURN	544	545	
FT	HELIX	546	549	
FT	TURN	550	550	
FT	TURN	552	553	
FT	TURN	558	562	
FT	HELIX	565	567	
FT	STRAND	568	571	
FT	TURN	573	574	
FT	STRAND	577	579	
FT	HELIX	580	585	
FT	STRAND	589	591	
FT	STRAND	595	598	
FT	HELIX	600	602	
FT	HELIX	603	617	
FT	TURN	619	620	
FT	STRAND	624	624	
FT	TURN	625	626	
FT	STRAND	627	627	

RA Altschuld S.F., Jordan B., Bietow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Zeeberg H., Moore T., Max S.I., Wang J., Heieh P.,
RA Datchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapellato M., Soares M.B., Bonaldi M.F., Casavant T.L., Schaefer T.E.,
RA Brompton M.J., Usdin T.B., Tochiyuki S., Carninci P., Pirange C.,
RA Sosa S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bohak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gundarene P.H.,
RA Richards S., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smalov D.B.,
RA Schmeich A., Schein J.E., Jones S.U.M., Marra W.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
RP SEQUENCE OF 1-11 FROM N.A.
RC STRAIN=BALE/c;
RX MEDLINE=98284323; PubMed=9621303;
RX DOI=10.1002/(SICI)1098-2795(199807)50:3<273::AID-MRD3>3.3.CO;2-C;
RA Chaudhary J., Skinner M.K.;
RT "Comparative sequence analysis of the mouse and human transferrin
RT promoter: hormonal regulation of the transferrin promoter in Sertoli
RT cells.",
RL Mol. Reprod. Dev. 50:273-283(1998).
[5]
RN SEQUENCE OF 277-337; 462-496 AND 526-575 FROM N.A.
RX MEDLINE=88086992; PubMed=3693348;
RX Chen L.-H., Bissell M.J.;
RT "transferrin mRNA level in the mouse mammary gland is regulated by
RT pregnancy and extracellular matrix.",
RL J. Biol. Chem. 262:17247-17250(1987).
[6]
RP SEQUENCE OF 268-307 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94068311; PubMed=8248032;
RA Kasik J.W., Rice E.J.;
RT "transferrin gene expression in maternal liver, fetal liver and
RT placenta during pregnancy in the mouse.",
RL Placenta 14:365-371(1993).
[7]
RP SEQUENCE OF 282-412 FROM N.A.
RX MEDLINE=87280033; PubMed=3611056;
RA Pentecost B.T., Teng C.T.;
RT "Lactoferrin is the major estrogen inducible protein of mouse
RT uterine secretions.",
RL J. Biol. Chem. 262:10134-10139(1987).
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC can bind two atoms of ferric iron in association with the binding
CC of an anion, usually bicarbonate. It is responsible for the
CC transport of iron from sites of absorption and heme degradation to
CC those of storage and utilization. Serum transferrin may also have
CC a further role in stimulating cell proliferation.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -1- DOMAIN: Composed of two homologous domains.
CC -1- SIMILARITY: Belongs to the transferrin family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

EMBL, AF40692; AA33453.1; -
EMBL, AK085754; BAC39532.1; -
EMBL, BC012313; AA112313.1; -

```

DR EMBL, BC022986; AAH22986.1; -.
DR EMBL, BC008559; AAH08559.1; -.
DR EMBL, AF027336; AAB84034.1; -.
DR EMBL, M23014; AAA40489.1; -.
DR EMBL, M23015; AAA40490.1; -.
DR EMBL, M23016; AAA40491.1; -.
DR EMBL, S67217; AAB28966.2; -.
DR EMBL, J03299; AAA39438.1; -.
DR PIR, A28446; A28446.
DR MGD; MGI:96821; Tf.
DR GO; GO:0030139; C:cytosolic vesicle; IDA.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW Glycoprotein; Iron transport; Metal-binding; Repeat; signal;
transport.
FT SIGNAL 1 19 By similarity.
FT CHAIN 20 697 Serotransferrin.
FT REPEAT 20 355 1.
FT REPEAT 356 697 2.
FT DISULFID 28 67 By similarity.
FT DISULFID 38 58 By similarity.
FT DISULFID 137 213 By similarity.
FT DISULFID 156 350 By similarity.
FT DISULFID 177 350 By similarity.
FT DISULFID 180 196 By similarity.
FT DISULFID 190 198 By similarity.
FT DISULFID 246 260 By similarity.
FT DISULFID 363 395 By similarity.
FT DISULFID 373 386 By similarity.
FT DISULFID 420 692 By similarity.
FT DISULFID 435 655 By similarity.
FT DISULFID 472 683 By similarity.
FT DISULFID 496 683 By similarity.
FT DISULFID 506 520 By similarity.
FT DISULFID 517 526 By similarity.
FT DISULFID 583 597 By similarity.
FT DISULFID 633 638 By similarity.
FT METAL 82 82 Iron 1 (By similarity).
FT METAL 114 114 Iron 1 (By similarity).
FT METAL 207 207 Iron 1 (By similarity).
FT METAL 268 268 Iron 1 (By similarity).
FT METAL 410 410 Iron 2 (By similarity).
FT METAL 448 448 Iron 2 (By similarity).
FT METAL 537 537 Iron 2 (By similarity).
FT METAL 605 605 Iron 2 (By similarity).
FT BINDING 139 139 Carbonate 1 (By similarity).
FT BINDING 143 143 Carbonate 1 (via amide nitrogen) (By similarity).
FT BINDING 145 145 Carbonate 1 (via amide nitrogen) (By similarity).
FT BINDING 146 146 Carbonate 1 (via amide nitrogen) (By similarity).
FT BINDING 474 474 Carbonate 2 (By similarity).
FT BINDING 478 478 Carbonate 2 (By similarity).
FT BINDING 480 480 Carbonate 2 (via amide nitrogen) (By similarity).
FT BINDING 481 481 Carbonate 2 (via amide nitrogen) (By similarity).
FT CARBOHYD 513 513 N-linked (GlcNAc...) (Potential).
FT CONFLICT 3 4 LT -> FA (in Ref. 1).
FT CONFLICT 71 74 ISAS -> HASG (in Ref. 3; AAH08559).
FT CONFLICT 283 283 W -> L (in Ref. 6).
FT CONFLICT 307 307 P -> L (in Ref. 6).
FT CONFLICT 350 351 CP -> SA (in Ref. 7).
FT CONFLICT 487 487 G -> C (in Ref. 5).
Query Match Score 92; DB 1; Length 697;
Best Local Similarity 81.8%; Pred. No. 2; e-05;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

OY 1 TTEDSIKINNGEADAMSLDGG 22
Db 391 TTEDCIKIVNGEADAMTLDDGG 412

RESULT 7
TRFE_BOVIN STANDARD; PRT; 704 AA.
ID TRFE_BOVIN 029443;
AC 029443;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal
binding globulin).
GN Name:TF;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RX MEDLINE=96132861; PubMed=8557646; DOI=10.1074/jbc.271.2.1166;
RA Retzer M.D., Kabani A., Button L.J., Yu R.H., Schryvers A.B.;
RT "Production and characterization of chimeric transferrins for the
determination of the binding domains for bacterial transferrin
receptors.";
RL J. Biol. Chem. 271:1166-1173(1996).
CC -!- FUNCTION: Transferrins are iron binding transport proteins which
can bind two atoms of ferric iron in association with the binding
of an anion, usually bicarbonate. It is responsible for the
transport of iron from sites of absorption and heme degradation to
those of storage and utilization. Serum transferrin may also have
a further role in stimulating cell proliferation.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -!- DOMAIN: Composed of two homologous domains.
CC -!- SIMILARITY: Belongs to the transferrin family.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
DR EMBL, U02564; AAA96735.1; -.
DR HSSP; P09571; 1H76.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
KW Glycoprotein; Iron transport; Metal-binding; Repeat; Signal;
transport.
FT SIGNAL 1 19 By similarity.
FT CHAIN 20 704 Serotransferrin.
FT REPEAT 20 359 1.
FT REPEAT 360 704 2.
FT DISULFID 28 66 By similarity.
FT DISULFID 38 57 By similarity.
FT DISULFID 136 217 By similarity.
FT DISULFID 176 192 By similarity.
FT DISULFID 179 200 By similarity.
FT DISULFID 189 202 By similarity.
FT DISULFID 250 264 By similarity.
FT DISULFID 362 622 By similarity.
FT DISULFID 367 399 By similarity.

```

```

FT DISUPID 377 390 By similarity.
FT DISUPID 424 699 By similarity.
FT DISUPID 441 663 By similarity.
FT DISUPID 473 549 By similarity.
FT DISUPID 497 690 By similarity.
FT DISUPID 507 521 By similarity.
FT DISUPID 518 532 By similarity.
FT DISUPID 589 603 By similarity.
FT DISUPID 641 646 By similarity.
FT METAL 81 81 Iron 1 (By similarity).
FT METAL 113 113 Iron 1 (By similarity).
FT METAL 211 211 Iron 1 (By similarity).
FT METAL 272 272 Iron 1 (By similarity).
FT METAL 414 414 Iron 2 (By similarity).
FT METAL 449 449 Iron 2 (By similarity).
FT METAL 543 543 Iron 2 (By similarity).
FT METAL 611 611 Iron 2 (By similarity).
FT BINDING 138 138 Carbonate 1 (By similarity).
FT BINDING 142 142 Carbonate 1 (By similarity).
FT BINDING 144 144 Carbonate 1 (via amide nitrogen) (By similarity).
FT BINDING 145 145 Carbonate 1 (via amide nitrogen) (By similarity).
FT BINDING 475 475 Carbonate 2 (By similarity).
FT BINDING 479 479 Carbonate 2 (By similarity).
FT BINDING 481 481 Carbonate 2 (via amide nitrogen) (By similarity).
FT BINDING 482 482 Carbonate 2 (via amide nitrogen) (By similarity).
FT CARBOHYD 514 514 N-linked (GlcNAc...) (Potential).
FT SEQUENCE 704 AA; 77753 MW; D87BB2AFE46C708D CRC64;

```

```

Query Match 80.0%; Score 92; DB 1; Length 704;
Best Local Similarity 81.8%; Pred. No. 2; Le-05;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 2 TEDSIKIMNGBADAMSLDGGF 23
Db 396 TECCIANKIMGEBDAMSLDGGY 417

```

```

RESULT 8
TRFL_PIG STANDARD; PRT; 704 AA.
AC P14632; 029557;
DT 01-APR-1990 (Rel. 14, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin).
GN Name-LTF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxId=9823;
OX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92379101; PubMed=1511016; DOI=10.1016/0167-4781(92)90061-4;
RA Lyndon J.P., O'Malley B.R., Saucedo O., Lee T., Headon D.R.,
RA Connolly O.M.;
RT "Nucleotide and primary amino acid sequence of porcine lactoferrin.";
RL Blochim. Biophys. Acta 1132:97-99(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92367939; PubMed=1503259;
RA Alexander L.J., Levine W.B., Teng C.T., Beattie C.W.;
RT "Cloning and sequencing of the porcine lactoferrin cDNA.";
RL Anim. Genet. 23:251-256(1992).
RN [3]
RP SEQUENCE OF 20-49.
RX MEDLINE=90105538; PubMed=2605266;
RA Hutcheon T.W., Magnuson J.S., Yip T.-T.;
RT "Rapid purification of porcine colostrum whey lactoferrin by affinity
chromatography on single-stranded DNA-agarose. Characterization, amino

```

```

RT acid composition and N-terminal amino acid sequence.";
RL Blochim. Biophys. Acta 999:323-329(1989).
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC can bind two atoms of ferric iron in association with the binding
CC of an anion, usually bicarbonate.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: Composed of two homologous domains.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M92089; AAA31102.1; -.
DR EMBL; M81327; AAA31059.1; -.
DR PIR; A45543; A45543.
DR HSSP; Q9TUM0; 1DTZ.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin_2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER_2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
KM Direct protein sequencing; Glycoprotein; Iron transport;
KM Metal-binding; Repeat; Signal; Transport.
FT STGNAL 1 19
FT CHAIN 20 704
FT REPEAT 20 359
FT 360 704
FT DISUPID 28 52 By similarity.
FT DISUPID 38 63 By similarity.
FT DISUPID 130 213 By similarity.
FT DISUPID 172 188 By similarity.
FT DISUPID 185 196 By similarity.
FT DISUPID 246 260 By similarity.
FT DISUPID 363 395 By similarity.
FT DISUPID 373 386 By similarity.
FT DISUPID 420 699 By similarity.
FT DISUPID 472 547 By similarity.
FT DISUPID 496 690 By similarity.
FT DISUPID 506 520 By similarity.
FT DISUPID 517 530 By similarity.
FT DISUPID 588 602 By similarity.
FT DISUPID 640 645 By similarity.
FT METAL 77 77 Iron 1 (By similarity).
FT METAL 107 107 Iron 1 (By similarity).
FT METAL 207 207 Iron 1 (By similarity).
FT METAL 268 268 Iron 1 (By similarity).
FT METAL 410 410 Iron 2 (By similarity).
FT METAL 448 448 Iron 2 (By similarity).
FT METAL 541 541 Iron 2 (By similarity).
FT METAL 610 610 Iron 2 (By similarity).
FT BINDING 132 132 Carbonate 1 (By similarity).
FT BINDING 136 136 Carbonate 1 (By similarity).
FT BINDING 138 138 Carbonate 1 (via amide nitrogen) (By similarity).
FT BINDING 139 139 Carbonate 1 (via amide nitrogen) (By similarity).
FT BINDING 474 474 Carbonate 2 (By similarity).
FT BINDING 478 478 Carbonate 2 (By similarity).
FT BINDING 480 480 Carbonate 2 (via amide nitrogen) (By similarity).
FT BINDING 481 481 Carbonate 2 (via amide nitrogen) (By similarity).
FT CARBOHYD 385 385 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 491 491 N-linked (GlcNAc...) (Potential).
FT CONFLICT 12 12 G -> W (in Ref. 1).

```

```
FT CONFLICT 46 48 RRT -> TTR (in Ref. 3).
FT CONFLICT 51 51 M -> I (in Ref. 1).
FT CONFLICT 85 85 D -> G (in Ref. 1).
FT CONFLICT 121 121 Missing (in Ref. 2).
FT CONFLICT 132 132 T -> I (in Ref. 1).
FT CONFLICT 284 284 E -> S (in Ref. 1).
FT CONFLICT 573 573 B -> Q (in Ref. 1).
FT CONFLICT 590 590 D -> N (in Ref. 1).
FT CONFLICT 623 623 V -> M (in Ref. 1).
FT CONFLICT 662 662 V -> C (in Ref. 1).
FT CONFLICT 704 704 NUKCVSPLKCAFMW -> T (in Ref. 1).
SQ SEQUENCE 704 AA; 77625 MW; 93261EPD608AD358 CRC64;

Query Match
Best Local Similarity 73.9%; Score 92; DB 1; Length 704;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTEDSIKINGEADAMSIDGDF 23
DB 391 TTEDCIVQVLKGEADAMSIDGDF 413

RESULT 9
Q8WMNB PRELIMINARY; PRT; 704 AA.
AC Q8WMNB;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lactoferrin (Fragment).
GN Name=LTF;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Wang S.-R., Lin T.-Y., Weng C.-N.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC bind ferric iron in association with the binding of an anion,
CC usually bicarbonate (By similarity).
CC -1- DOMAIN: Composed of two homologous domains (By similarity).
CC -1- SIMILARITY: Belongs to the transferrin family.
DR EMBL: L77887; AAL40161.1; -.
DR HSSP: P24627; INKX.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0008199; F:ferric iron binding; IEA.
DR GO: GO:0006879; P:iron ion homeostasis; IEA.
DR GO: GO:0006826; P:iron ion transport; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR Pfam: PF00405; Transferrin_2.
DR PRINTS: PR00422; TRANSFERRIN.
DR SMART: SM00094; TR_FER; 2.
DR PROSITE: PS00205; TRANSFERRIN_1; 2.
DR PROSITE: PS00206; TRANSFERRIN_2; 2.
DR PROSITE: PS00207; TRANSFERRIN_3; 1.
DR Iron transport; Metal-binding; Transport.
KW NON_TER
FT SEQUENCE 704 AA; 77681 MW; 64EE769F7503CC32 CRC64;

Query Match
Best Local Similarity 80.0%; Score 92; DB 2; Length 704;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTEDSIKINGEADAMSIDGDF 23
DB 391 TTEDCIVQVLKGEADAMSIDGDF 413

RESULT 10
Q6Y739 PRELIMINARY; PRT; 704 AA.
AC Q6Y739;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Lactotransferrin.
GN Name=LTF;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Shikai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC bind ferric iron in association with the binding of an anion,
CC usually bicarbonate (By similarity).
CC -1- DOMAIN: Composed of two homologous domains (By similarity).
CC -1- SIMILARITY: Belongs to the transferrin family.
DR EMBL: AP06185; BAD08651.1; -.
DR HSSP: Q29477; LWT1.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0008199; F:ferric iron binding; IEA.
DR GO: GO:0006879; P:iron ion homeostasis; IEA.
DR GO: GO:0006826; P:iron ion transport; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR001156; Peptidase_S60.
DR Pfam: PF00405; Transferrin_2.
DR PRINTS: PR00422; TRANSFERRIN.
DR SMART: SM00094; TR_FER; 2.
DR PROSITE: PS00205; TRANSFERRIN_1; 2.
DR PROSITE: PS00206; TRANSFERRIN_2; 2.
DR PROSITE: PS00207; TRANSFERRIN_3; 1.
DR Iron transport; Metal-binding; Transport.
KW SEQUENCE 704 AA; 77611 MW; 10DFEA3C136D5DA CRC64;

Query Match
Best Local Similarity 80.0%; Score 92; DB 2; Length 704;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTEDSIKINGEADAMSIDGDF 23
DB 391 TTEDCIVQVLKGEADAMSIDGDF 413

RESULT 11
Q7YS20 PRELIMINARY; PRT; 704 AA.
AC Q7YS20;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lactoferrin.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Pecorini C., Fogher C., Baldi A.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC bind ferric iron in association with the binding of an anion,
CC usually bicarbonate (By similarity).
CC -1- DOMAIN: Composed of two homologous domains (By similarity).
CC -1- SIMILARITY: Belongs to the transferrin family.
DR EMBL: AY306198; AAP70487.1; -.
DR HSSP: P24627; INKX.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0008199; F:ferric iron binding; IEA.
DR GO: GO:0006879; P:iron ion homeostasis; IEA.
```

```
ID Q6Y739 PRELIMINARY; PRT; 704 AA.
AC Q6Y739;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Lactotransferrin.
GN Name=LTF;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Shikai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC bind ferric iron in association with the binding of an anion,
CC usually bicarbonate (By similarity).
CC -1- DOMAIN: Composed of two homologous domains (By similarity).
CC -1- SIMILARITY: Belongs to the transferrin family.
DR EMBL: AP06185; BAD08651.1; -.
DR HSSP: Q29477; LWT1.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0008199; F:ferric iron binding; IEA.
DR GO: GO:0006879; P:iron ion homeostasis; IEA.
DR GO: GO:0006826; P:iron ion transport; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR001156; Peptidase_S60.
DR Pfam: PF00405; Transferrin_2.
DR PRINTS: PR00422; TRANSFERRIN.
DR SMART: SM00094; TR_FER; 2.
DR PROSITE: PS00205; TRANSFERRIN_1; 2.
DR PROSITE: PS00206; TRANSFERRIN_2; 2.
DR PROSITE: PS00207; TRANSFERRIN_3; 1.
DR Iron transport; Metal-binding; Transport.
KW SEQUENCE 704 AA; 77611 MW; 10DFEA3C136D5DA CRC64;

Query Match
Best Local Similarity 80.0%; Score 92; DB 2; Length 704;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTEDSIKINGEADAMSIDGDF 23
DB 391 TTEDCIVQVLKGEADAMSIDGDF 413

RESULT 11
Q7YS20 PRELIMINARY; PRT; 704 AA.
AC Q7YS20;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lactoferrin.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Pecorini C., Fogher C., Baldi A.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC bind ferric iron in association with the binding of an anion,
CC usually bicarbonate (By similarity).
CC -1- DOMAIN: Composed of two homologous domains (By similarity).
CC -1- SIMILARITY: Belongs to the transferrin family.
DR EMBL: AY306198; AAP70487.1; -.
DR HSSP: P24627; INKX.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0008199; F:ferric iron binding; IEA.
DR GO: GO:0006879; P:iron ion homeostasis; IEA.
```

```

DR GO: GO:0006826; P:iron ion transport; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR001156; Peptidase_S60.
DR Pfam: PF00405; Transferrin_2.
DR SMART: SM00094; TR_FER_2.
DR PROSITE: PS00205; TRANSFERRIN_1; 2.
DR PROSITE: PS00206; TRANSFERRIN_2; 1.
DR PROSITE: PS00207; TRANSFERRIN_3; 1.
DR Itron transport; Metal-binding; transport.
KW SEQUENCE 704 AA; 77522 MW; AAC8B1767E56BFE6A CRC64;

Query Match 80.0%; Score 92; DB 2; Length 704;
Best Local Similarity 73.9%; Pred. No. 2; E-05;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTEDSIKINMGADAMSLDGGF 23
Db 391 TTEDCIYQVLKGEADAMSLDGGF 413

RESULT 12
TRFE_RAT STANDARD; PRF; 698 AA.
AC P12346; Q63602; Q64628; Q64630;
DT 01-OCT-1989 (Rel. 12, Created)
DT 15-JUN-1999 (Rel. 38, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Sero transferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal
DE binding globulin).
GN Name=TF;
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=Mistar; TISSUE=Mammary gland;
RX MEDLINE=95234054; PubMed=7717992;
RA Bescriva H., Pierce A., Coddeville B., Gonzalez F., Benaisa M.,
RA Legey D., Wernyszeki J.M., Spik G., Pamblanco M.;
RT "rat mammary-gland transferrin: nucleotide sequence, phylogenetic
RT analysis and glycan structure.";
RL Biochem. J. 307:47-55(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=Mistar; TISSUE=Liver;
RX MEDLINE=96208933; PubMed=8829802; DOI=10.1016/0305-0491(95)02068-3;
RA Hosino A., Hisayasu S., Shimada T.;
RT "Complete sequence analysis of rat transferrin and expression of
RT transferrin but not lactoferrin in the digestive glands.";
RL Comp. Biochem. Physiol. 113B:491-497(1996).
RN [3]
RP SEQUENCE OF 7-295 FROM N.A. (ISOFORM 2).
RX MEDLINE=84307580; PubMed=6236811;
RA Aldred A.R., Howlett G.J., Schreiber G.;
RT "Synthesis of rat transferrin in Escherichia coli containing a
RT recombinant bacteriophage.";
RL Biochem. Biophys. Res. Commun. 122:960-965(1984).
RN [4]
RP SEQUENCE OF 521-698 FROM N.A.
RX MEDLINE=87053639; PubMed=3023031;
RA Huggenvik J.I., Idzerda R.L., Haywood L., Lee D.C., McKnight G.S.,
RA Griebold M.D.;
RT "Transferrin messenger ribonucleic acid: molecular cloning and
RT hormonal regulation in rat Sertoli cells.";
RL Endocrinology 120:332-340(1987).
RN [5]
RP SEQUENCE OF 20-47.
RX MEDLINE=80049855; PubMed=500689;
RA Schreiber G., Dryburgh H., Millership A., Matsuda Y., Inglis A.,
RA Phillips J., Edwards K., Mages J.;
RT "The synthesis and secretion of rat transferrin.";
RL J. Biol. Chem. 254:12013-12019(1979).

RN [6]
RP SEQUENCE OF 20-30 AND 642-653.
RX PubMed=3046565;
RA Purves L.R., Purves M., Linton N., Brandt W., Johnson G., Jacobs P.;
RT "Properties of the transferrin associated with rat intestinal
RT mucosa.";
RL Biochim. Biophys. Acta 966:318-327(1988).
RN [7]
RP SEQUENCE OF 89-102, 232-243 AND 404-411.
RX PubMed=1791188;
RA Cavanaugh P.G., Nicolson G.L.;
RT "Lung-derived growth factor that stimulates the growth of lung-
RT metastasizing tumor cells: identification as transferrin.";
RL J. Cell. Biochem. 47:261-271(1991).
CC -1- FUNCTION: Transferrin are iron binding transport proteins which
CC can bind two atoms of ferric iron in association with the binding
CC of an anion, usually bicarbonate. It is responsible for the
CC transport of iron from sites of absorption and heme degradation to
CC those of storage and utilization. Serum transferrin may also have
CC a further role in stimulating cell proliferation.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P12346-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P12346-2; Sequence=VSP_011840;
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -1- DOMAIN: Composed of two homologous domains.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ch/announce/
CC or send an email to license@ebi.ebi.ch).
CC -----
DR EMBL: X77158; CAA54403.1; -
DR EMBL: D38380; BAA07458.1; -
DR EMBL: M26113; AAA42266.1; -
DR EMBL: M27965; AAA42267.1; -
DR PIR: S49163; S49163.
DR HSP: P19134; ITFD.
DR GlycoSuiteDB: P12346; -
DR InterPro: IPR001156; Peptidase_S60.
DR Pfam: PF00405; Transferrin_2.
DR PRINTS: PR00422; TRANSFERRIN.
DR SMART: SM00094; TR_FER_2.
DR PROSITE: PS00205; TRANSFERRIN_1; 1.
DR PROSITE: PS00206; TRANSFERRIN_2; 2.
DR PROSITE: PS00207; TRANSFERRIN_3; 2.
KW Alternative splicing; Direct protein sequencing; Glycoprotein;
KW Itron transport; Metal-binding; Repeat; Signal; Transport.
FT SIGNAL 1 19
FT CHAIN 20 698 Sero transferrin.
FT REPEAT 20 355 1.
FT REPEAT 356 698 2.
FT DISULFID 28 67 By similarity.
FT DISULFID 38 58 By similarity.
FT DISULFID 137 213 By similarity.
FT DISULFID 156 350 By similarity.
FT DISULFID 177 193 By similarity.
FT DISULFID 180 196 By similarity.
FT DISULFID 190 198 By similarity.
FT DISULFID 246 260 By similarity.
FT DISULFID 363 395 By similarity.
FT DISULFID 373 386 By similarity.
FT DISULFID 420 693 By similarity.
FT DISULFID 435 656 By similarity.
FT DISULFID 471 542 By similarity.

```



```

FT DISULFID 495 684 By similarity.
FT DISULFID 505 519 By similarity.
FT DISULFID 516 525 By similarity.
FT DISULFID 582 536 By similarity.
FT DISULFID 634 639 By similarity.
FT METAL 82 82 Iron 1 (By similarity).
FT METAL 114 114 Iron 1 (By similarity).
FT METAL 207 207 Iron 1 (By similarity).
FT METAL 268 268 Iron 2 (By similarity).
FT METAL 410 410 Iron 2 (By similarity).
FT METAL 447 447 Iron 2 (By similarity).
FT METAL 536 536 Iron 2 (By similarity).
FT METAL 604 604 Iron 2 (By similarity).
FT BINDING 139 143 Carbonate 1 (By similarity).
FT BINDING 143 143 Carbonate 1 (By similarity).
FT BINDING 145 145 Carbonate 1 (via amide nitrogen) (By similarity).
FT BINDING 146 146 Carbonate 1 (via amide nitrogen) (By similarity).
FT BINDING 473 473 Carbonate 2 (By similarity).
FT BINDING 477 477 Carbonate 2 (By similarity).
FT BINDING 479 479 Carbonate 2 (via amide nitrogen) (By similarity).
FT BINDING 480 480 Carbonate 2 (via amide nitrogen) (By similarity).
FT CARBOHYD 512 512 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 65 266 Missing (in isoform 2).
FT CONFLICT 57 57 A -> P (in Ref. 1).
FT CONFLICT 110 110 P -> R (in Ref. 1).
FT CONFLICT 318 354 AFCCYVPPRMDELRYLGHSYVTAIRNREGVCPEAS -> RFLRLAPKDGLOAVRPOLCHCHSKSGSCPDPA (in Ref. 1).
FT CONFLICT 380 380 S -> G (in Ref. 1).
FT CONFLICT 691 691 E -> D (in Ref. 4).
FT CONFLICT 696 697 HK -> YA (in Ref. 4).
SQ SEQUENCE 698 AA; 76363 MW; DDF2C1918E2A1B0E CRC64;

Query Match 78.3%; Score 90; DB 1; Length 698;
Best Local Similarity 81.8%; Pred. No. 4.3e-05;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTEDSIKIMNGEADAMSIDGG 22
:|||||:|||||:|||||:
Db 391 STEDCIDKIVNGEADAMSIDGG 412

RESULT 13
O7TNXO PRELIMINARY; PRT; 698 AA.
AC O7TNXO;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Liver regeneration-related protein LRRG03.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu C.S., Li W.Q., Li Y.C., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,
RA Yang K.J., Yan H.M., Chang C.F., Zhao L.F., Ma H., Wang L., Wang S.F.,
RA Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC bind ferric iron in association with the binding of an anion,
CC usually bicarbonate (By similarity).
CC -1- DOMAIN: Composed of two homologous domains (By similarity).
CC -1- SIMILARITY: Belongs to the transferrin family.
DR EMBL; AY327504; AAP97736.1; -.
DR HSP; P02787; I8P5.
DR GO; GO:0005576; C:extracellular; IEA.

```

```

DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006825; P:iron ion transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin_2.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW Iron transport; Metal-binding; Transport.
SQ SEQUENCE 698 AA; 76395 MW; B91AB841CA447194 CRC64;

Query Match 78.3%; Score 90; DB 2; Length 698;
Best Local Similarity 81.8%; Pred. No. 4.3e-05;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 391 STEDCIDKIVNGEADAMSIDGG 412

RESULT 14
TRFL_HUMAN STANDARD; PRT; 711 AA.
AC P02788; O00756; Q16780; Q16785; Q16786; Q16789; Q81U92; Q81ZH6;
AC O8TCD2; Q96K24; Q96K25; Q9H123;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Lactoferrin precursor (Lactoferrin) [Contains: Kallistocin-1;
DE Lactoferron A; Lactoferron B; Lactoferron C].
GN Name=Lf; Synonyms=LF;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=90384839; PubMed=2402455;
RA Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;
RT "Complete nucleotide sequence of human mammary gland lactoferrin.";
RL Nucleic Acids Res. 18:5288-5288 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Cho Y.Y.;
RL Theils (1994), Genetic Engineering Research Institute / Taejon, Korea.
RN [3]
RP SEQUENCE FROM N.A.
RA Conneely O.M.;
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Liang Q., Jimenez-Piorea R., Richardson T.;
RT "Molecular cloning and sequence analysis of human lactoferrin.";
RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=bone marrow;
RA Wei X., Han J., Rado T.A.;
RT "Human neutrophil lactoferrin coding and 5' flanking region DNA
RT sequences.";
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Cheng H., Chen X., Huan L.;
RT "cDNA cloning and sequence analysis of human lactoferrin.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [7]

```


RP SEQUENCE FROM N.A., AND VARIANTS THR-30 AND ARG-48.
RA Kaplan J.B., Fine D.H.; amino acid polymorphism in the antibacterial
RT "characterization of an amino acid polymorphism in the antibacterial
RL domain of human lactoferrin.";
RN Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A., AND VARIANTS THR-30, ARG-48 AND ASP-580.
RC TISSUE=Mammary gland;
RA Shi Y.-Q., Zhang Y., Zheng Y.-M.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A., AND VARIANTS THR-30; ARG-48 AND ASP-580.
RC TISSUE=Seminal vesicle;
RA Baekar Singh S., Saravanan K., Paramasivam M., Srinivasan A.,
RL Singh T.P.;
RN Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Krausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huljck S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S., Sanchez
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skaleka U., Smallue D.E.,
RA Scheraga J.E., Scheraga J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [11]
RP SEQUENCE OF 1-15 FROM N.A.
RX MEDLINE=9315571; PubMed=1480183; DOI=10.1210/me.6.11.1969;
RA Teng C.T., Liu Y., Yang N., Walmer D., Panella T.;
RT "Differential molecular mechanism of the estrogen action that
RT regulates lactoferrin gene in human and mouse.";
RL Mol. Endocrinol. 6:1969-1981(1992).
RN [12]
RP SEQUENCE OF 3-711 FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=90326549; PubMed=2374734;
RA Powell M.J., Ogden J.E.;
RT "Nucleotide sequence of human lactoferrin cDNA.";
RL Nucleic Acids Res. 18:4013-4013(1990).
RN [13]
RP SEQUENCE OF 20-711.
RX MEDLINE=85076667; PubMed=6510420;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
RA Legend D., Spik G., Montreuil J., Jolles P.;
RT "Human lactoferrin: amino acid sequence and structural
RT comparisons with other transferrins.";
RL Eur. J. Biochem. 145:659-666(1984).
RN [14]
RP PRELIMINARY SEQUENCE OF 20-73; 134-171, 257-278 AND 347-530.
RX MEDLINE=92046817; PubMed=6796460; DOI=10.1016/0005-2795(81)90016-7;
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
RA Jolles P.;
RT "The present state of the human lactoferrin sequence. Study and
RT alignment of the cyanogen bromide fragments and characterization of N-
RL Biochim. Biophys. Acta 670:243-254(1981).
RN [15]
RP SEQUENCE OF 609-711.
RX MEDLINE=82262043; PubMed=7049727; DOI=10.1016/0014-5793(82)80229-9;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
RA Jolles P.;
RT "An 88 amino acid long C-terminal sequence of human
RT lactoferrin.";
RL FEBS Lett. 142:107-110(1982).
RN [16]
RP SEQUENCE OF 436-711 FROM N.A.
RX MEDLINE=88001031; PubMed=3477300;
RA Rado T.A., Wei X., Benz E.J. Jr.;
RT "Isolation of lactoferrin cDNA from a human myeloid library and
RT expression of mRNA during normal and leukemic myelopoiesis.";
RL Blood 70:989-993(1987).
RN [17]
RP SEQUENCE OF 237-711 FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Gao L., La Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
RA Sagripanti J.L.;
RN Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [18]
RP SYNTHESIS OF 172-202 (KALIOCIN-1).
RX PubMed=12693969; DOI=10.1023/A:1022657630698;
RA Viejo-Diaz M., Andres M.T., Perez-Gil J., Sanchez M., Pierra J.F.;
RT "Potassium efflux induced by a new lactoferrin-derived peptide
RT mimicking the effect of native human lactoferrin on the bacterial
RT cytoplasmic membrane.";
RL Biochimica 68:217-227(2003).
RN [19]
RP CHARACTERIZATION OF LACTOFERROXINS.
RX MEDLINE=9166929; PubMed=1369293;
RA Tani F., Ito K., Chiba H., Yoshikawa M.;
RT "Isolation and characterization of oploid antagonist peptides derived
RT from human lactoferrin.";
RL Agric. Biol. Chem. 54:1803-1810(1990).
RN [20]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
RX MEDLINE=90064528; PubMed=2585506;
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
RT "Structure of human lactoferrin: crystallographic structure analysis
RT and refinement at 2.8-A resolution.";
RL J. Mol. Biol. 209:711-734(1989).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX PubMed=15299793;
RA Haridas M., Anderson B.F., Baker E.N.;
RT "Structure of human lactoferrin refined at 2.2-A
RT resolution.";
RL Acta Crystallogr. D 51:629-646(1995).
RN [22]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
RX MEDLINE=97156796; PubMed=9003186; DOI=10.1021/bj961908y;
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
RA Baker E.N.;
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron
RT binding properties and crystal structure of the histidine-
RT 253-->methionine mutant.";
RL Biochemistry 36:341-346(1997).
RN [23]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=99190892; PubMed=10089347; DOI=10.1107/S0907444998011226;
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
RT "Structure of recombinant human lactoferrin expressed in Aspergillus
RT awamori.";
RL Acta Crystallogr. D 55:403-407(1999).
RN [24]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=99192677; PubMed=10089508; DOI=10.1107/S0907444998004417;
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement and

RT analysis of ligand-induced conformational change."
 RL Acta Crystallogr. D 54:1319-1335 (1998).
 RL [25]
 RP VARIANTS THR-30 AND ARG-48.
 RX MEDLINE=9091914; PubMed=9873069;

Query Match 78.3%; Score 90; DB 1; Length 711;
 Best Local Similarity 73.9%; Pred. No. 4.3e-05;
 Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTEDSIAKIMGADAMSJDGGF 23
 Db 396 TTEDCIALYKGEADAMSJDGGY 418

RESULT 15

ID 07TMC7 PRELIMINARY; PRT; 979 AA.
 AC 07TMC7;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Ab2-417 (Cc1-8).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Xu C.S., Li W.Q., Li Y.C., Chang C.F., Zhao L.F., Ma H., Wang L.,
 RA Wang S.F., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y., Yang K.J.,
 RA Yan H.M., Shi J.B., Rahman S., Rahman S., Wang Q.N., Zhang J.B.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RA Xu C.S., Li W.Q., Li Y.C., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,
 RA Yang K.J., Yan H.M., Chang C.F., Zhao L.F., Ma H., Wang L., Wang S.F.,
 RA Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Transferrins are iron binding transport proteins which
 bind ferric iron in association with the binding of an anion,
 usually bicarbonate (By similarity).
 CC -!- DOMAIN: Composed of two homologous domains (By similarity).
 CC -!- SIMILARITY: Belongs to the transferrin family.
 DR EMBL; AY325214; AAP92615.1; -;
 DR EMBL; AY325241; AAP92642.1; -;
 DR HSSP; P02787; 1B3E.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008199; F:ferric iron binding; IEA.
 DR GO; GO:0006879; P:iron ion homeostasis; IEA.
 DR GO; GO:0006826; P:iron ion transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001156; Peptidase_S60.
 DR Pfam; PF00405; Transferrin; 2.
 DR SMART; SM00094; TR_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN_1; 1.
 DR PROSITE; PS00206; TRANSFERRIN_2; 2.
 DR PROSITE; PS00207; TRANSFERRIN_3; 2.
 SQ Iron transport; Metal-binding; Transport.
 SQ SEQUENCE 979 AA; 107411 MW; 5BE80A6A1DD67D09 CRC64;

Query Match 78.3%; Score 90; DB 2; Length 979;
 Best Local Similarity 81.8%; Pred. No. 6.2e-05;
 Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTEDSIAKIMGADAMSJDGG 22
 Db 377 TTEDCIDLKINGADAMSJDGG 398

Search completed: November 1, 2005, 12:54:30
 Job time : 113.632 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 13:32:37 ; Search time 162 Seconds
(without alignments)
54.910 Million cell updates/sec

Title: US-10-612-162A-2

Perfect score: 115

Sequence: 1 TTEDSIAKIMNGEADMSLDGCR 23

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 750623

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	115	100.0	23	8	ADG46076	Adg46076 Human CDT
2	77	67.0	21	6	ABP74737	Abp74737 Proteome
3	77	67.0	21	8	ADR15960	Adr15960 Transferr
4	77	67.0	21	8	ADR15901	Adr15901 Transferr
5	68	59.1	13	8	ADG46093	Adg46093 Human CDT
6	67	58.3	19	2	AAR71072	Aar71072 Draculin
7	65	56.5	13	8	ADG46092	Adg46092 Human CDT
8	62	53.9	13	8	ADG46090	Adg46090 Human CDT
9	62	53.9	13	8	ADG46091	Adg46091 Human CDT
10	59	51.3	18	8	ADR19359	Adr19359 TRPI derl
11	36	31.3	7	8	ADR15885	Adr15885 Transferr
12	34	29.6	12	4	AU68027	Au68027 Human Bre
13	34	29.6	12	4	AU68103	Au68103 Human Bre
14	34	29.6	12	4	AU68052	Au68052 Human Bre
15	34	29.6	12	4	AA884372	Aa884372 Splice-va
16	34	29.6	12	6	ABP98991	Abp98991 Et082 cel
17	34	29.6	12	6	ABP72825	Abp72825 Human lac
18	34	29.6	12	8	ADH89361	Adh89361 Human tcr
19	34	29.6	12	8	ADL15871	Adl15871 Neutrophil
20	34	29.6	12	8	ADL70737	Adl70737 Neutrophil
21	34	29.6	12	8	ADL24415	Adl24415 Neutrophil
22	34	29.6	17	2	AA891738	Aa891738 HBK4 immu
23	33	28.7	14	8	ADR15908	Adr15908 Transferr
24	33	28.7	15	8	ADS13210	Adsl3210 Human rbe
25	33	28.7	16	8	ADR15849	Adr15849 Transferr

ALIGNMENTS

RESULT 1
ID ADG46076 standard; peptide; 23 AA.
XX
AC ADG46076;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human CDT peptide fragment #2.
XX
KW antibody; carbohydrate-deficient transferrin; CDT;
KM non-glycosylated transferrin; alcoholism; alcoholic; diagnosis; human.
XX
OS Homo sapiens.
XX
XX BP1378521-A1.
XX
PD 07-JAN-2004.
XX
PF 19-MAY-2003; 2003EP-00011334.
XX
XX 05-JUL-2002; 2002DE-01030550.
XX
PA (DADE-) DADE BEHRING MAREBURG GMBH.
XX
PI Althaus H;
XX
DR WPI; 2004-073743/08.
XX
PT New antibody specific for carbohydrate-deficient transferrin, useful for
PT diagnosis of alcoholism, can bind its target in solution, eliminating
PT need for immobilization.
XX
PS Claim 4; SEQ ID NO 2; 21pp; German.
XX
XX This invention describes a novel antibody that, in aqueous solution,
XX binds selectively to carbohydrate-deficient transferrin (CDT) without
XX having to bind CDT to a solid phase. The invention also describes an
XX antibody that binds selectively to CDT at regions containing the
XX sequences VVARSMGSGEDLIWEL, TTEDSIAKIMNGEADMSLDGCR, SKLSMGSLNSEEPN and
XX YEKYIGEBYKXAV (ADG46075-ADG46078) and an immunoassay for detecting CDT
XX using the antibodies of the invention. The antibodies of the invention
XX are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
XX antibodies are obtained by immunisation with non-glycosylated
XX transferrin, or a fragment, then generation of hybridomas by standard
XX fusion of spleen and myeloma cells. Hybridomas are then selected for
XX production of antibodies that specifically bind CDT from the aqueous
XX phase. The antibodies are useful for diagnosis of alcoholism, CDT, which

CC lacke glycosylation at Asn413 and/or Asn 611, is present only in
CC alcohols. The antibodies allow direct detection of CDT in solution,
CC eliminating the need for immobilising it on a solid phase (as required
CC when using known antibodies). ADG45075-ADG46094 represent CDT peptide
CC fragments used in the method of the invention.

CC Sequence 23 AA;

Query Match 100.0%; Score 115; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 4e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTEDSIAKIMNGEADAMSIDGCF 23
Db 1 TTEDSIAKIMNGEADAMSIDGCF 23

RESULT 2

ABP74737 standard; peptide; 21 AA.

AC ABP74737;

DT 03-FEB-2003 (first entry)

DE Proteome analysis related peptide #22.

KM Proteome analysis; isolation; determination; diagnostic assay; detection;
KM protein marker; identification; metastatic; invasive cancer;
KM differential expression; signalling pathway; chromatography.

OS Homo sapiens.

OS Synthetic.

PN WO200277016-A2.

PD 03-OCT-2002.

PF 22-MAR-2002; 2002WO-EP003368.

PR 22-MAR-2001; 2001US-0278171P.

PR 12-SEP-2001; 2001US-0318749P.

PR 20-SEP-2001; 2001US-0323999P.

(VLA-) VLAAWS INTERUNIVERSITAIR INST BIOTECHNOG.

PI Vandekerckhove J, Gevaert K;

DR WPI; 2003-067379/06.

PT Method for isolation of peptides from complex mixture of peptides
PT involves specific chemical and/or enzymatic alteration of at least one
PT type of peptide.

PS Example 19; Page 138; 193pp; English.

CC The present invention describes a method (M1) for the isolation of a
CC subset of peptides from a protein peptide mixture (P1). M1 involves: (a)
CC separating the protein peptide mixture into fractions of peptides via
CC chromatography; (b) chemically, or enzymatically, or chemically and
CC enzymatically, altering at least one amino acid of at least one of the
CC peptides; and (c) isolating the altered (flagged) peptides out of each
CC fraction via chromatography, where the chromatography of steps (a) and
CC (c) is performed with the same type of chromatography. M1 can be used for
CC the isolation and determination of peptides from protein peptide
CC mixtures. M1 can also be used in diagnostic assays for detection of the
CC presence, the absence or a variation in expression level of at least one
CC protein marker or a specific set of proteins indicative of a disease
CC state. M1 can be used for identifying target proteins present in
CC metastatic and invasive cancers, in differential expression of proteins
CC in transgenic mice, identification of proteins that are upregulated or
CC down regulated in disease tissues, in identification of intracellular

CC changes in cells with physiological changes such as metabolic shift, in
CC the identification of biomarkers in cancers and in the identification of
CC signalling pathways. The method is gel-free methodology for qualitative
CC and quantitative proteome analysis without the need for multidimensional
CC chromatography and without the use of affinity tags. ABP74714 to ABP75190
CC represent peptide sequences used in the exemplification of the present
CC invention

CC Sequence 21 AA;

Query Match 67.0%; Score 77; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 INNGEADAMSIDGCF 23
Db 1 INNGEADAMSIDGCF 15

RESULT 3

ADR15960 standard; peptide; 21 AA.

AC ADR15960;

DT 04-NOV-2004 (first entry)

DE Transferrin peptide fragment #118.

KM glycosylation; proteolytic enzyme; proteolysis; detection; transferrin.

OS Synthetic.

PN WO2004070389-A1.

PD 19-AUG-2004.

PF 06-FEB-2004; 2004WO-GB000480.

PR 06-FEB-2003; 2003GB-00002740.

PA (AXIS-) AXIS-SHIELD ASA.

PI Rye PD;

DR WPI; 2004-625547/60.

PT Assay for differentiating protein isoforms to determine their
PT concentrations in sample e.g. blood, involves contacting the sample with
PT proteolytic enzyme to produce peptide fragment by proteolysis followed by
PT detecting.

PS Disclosure; Page 17; 30pp; English.

CC The present invention describes an assay for a protein having at least
CC two isoforms with different glycosylation patterns. The assay involves
CC contacting a sample containing the protein with a proteolytic enzyme,
CC followed by detecting the content or relative content of at least one
CC peptide fragment produced by proteolysis. Also described is a kit for the
CC assay method comprising the proteolytic enzyme and a substrate bound
CC specific binding partner (S1) for at least 2 of the isoforms of the
CC proteins. The method can be used for assaying isoforms of proteins
CC according to their glycosylation pattern to determine their concentration
CC or relative concentration in the sample or material (e.g. blood). The
CC method avoids use of antibodies for distinguishing between glycosylated
CC isoforms of the proteins. The present sequence represents a transferrin
CC peptide fragment which is used in the exemplification of the present
CC invention.

CC Sequence 21 AA;

Query Match 67.0%; Score 77; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 INNGEADAMSJDGF 23
| | | | | | | | | |
DB 1 INNGEADAMSJDGF 15

RESULT 4

ADRI5901 standard; peptide; 21 AA.

ADRI5901;

04-NOV-2004 (first entry)

Transferrin peptide fragment #59.

glycosylation; proteolytic enzyme; proteolysis; detection; transferrin.

Synthetic.

WO2004070389-A1.

19-AUG-2004.

06-FEB-2004; 2004WO-GB000480.

06-FEB-2003; 2003GB-00002740.

(AXIS-) AXIS-SHIELD ASA.

Rye PD;

WPI; 2004-625547/60.

Assay for differentiating protein isoforms to determine their

concentrations in sample e.g. blood. Involves contacting the sample with

proteolytic enzyme to produce peptide fragment by proteolysis followed by

detecting.

Disclosure; Page 15; 30pp; English.

The present invention describes an assay for a protein having at least

two isoforms with different glycosylation patterns. The assay involves

contacting a sample containing the protein with a proteolytic enzyme,

followed by detecting the content or relative content of at least one

peptide fragment produced by proteolysis. Also described is a kit for the

assay method comprising the proteolytic enzyme and a substrate bound

specific binding partner (SI) for at least 2 of the isoforms of the

proteins. The method can be used for assaying isoforms of proteins

according to their glycosylation pattern to determine their concentration

or relative concentration in the sample or material (e.g. blood). The

method avoids use of antibodies for distinguishing between glycosylated

isoforms of the proteins. The present sequence represents a transferrin

peptide fragment which is used in the exemplification of the present

invention.

Sequence 21 AA;

Query Match 67.0%; Score 77; DB 8; Length 21;

Best Local Similarity 100.0%; Pred. No. 4.4e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 INNGEADAMSJDGF 23
| | | | | | | | | |
DB 1 INNGEADAMSJDGF 15

RESULT 5

ADG46093 standard; peptide; 13 AA.

ADG46093;

XX 25-MAR-2004 (first entry)

XX Human CDT peptide fragment #19.

XX antibody; carbohydrate-deficient transferrin; CDT;

XX non-glycosylated transferrin; alcoholism; alcoholic; diagnosis; human.

XX Homo sapiens.

XX BP1378521-A1.

XX 07-JAN-2004.

XX 19-MAY-2003; 2003EP-00011334.

XX 05-JUL-2002; 2002DE-01030550.

XX (DADE-) DADE BEHRING MARBURG GMBH.

XX Althaus H;

XX WPI; 2004-073743/08.

XX New antibody specific for carbohydrate-deficient transferrin, useful for

diagnosis of alcoholism, can bind its target in solution, eliminating

need for immobilization.

XX Example 7; Page 15; 21pp; German.

XX This invention describes a novel antibody that, in aqueous solution,

binds selectively to carbohydrate-deficient transferrin (CDT) without

having to bind CDT to a solid phase. The invention also describes an

antibody that binds selectively to CDT at regions containing the

sequences VVARSWGKEDDIWEL, TTEDSIKINNGEADAMSJDGF, SLSMSGGLNSEPN and

CC YERYLDEEVKAV (ADG46075-ADG46078) and an immunoassay for detecting CDT

using the antibodies of the invention. The antibodies of the invention

are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The

antibodies are obtained by immunisation with non-glycosylated

transferrin, or a fragment, then generation of hybridomas by standard

fusion of spleen and myeloma cells. Hybridomas are then selected for

production of antibodies that specifically bind CDT from the aqueous

CC phase. The antibodies are useful for diagnosis of alcoholism, CDT, which

lacks glycosylation at Asn413 and/or Asn 611, is present only in

CC alcoholics. The antibodies allow direct detection of CDT in solution,

CC eliminating the need for immobilising it on a solid phase (as required

CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide

XX fragments used in the method of the invention.

Sequence 13 AA;

Query Match 59.1%; Score 68; DB 8; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.00069;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 NGEADAMSJDGF 23
| | | | | | | | | |
DB 1 NGEADAMSJDGF 13

RESULT 6

AAR71072 standard; peptide; 19 AA.

AAR71072;

25-MAR-2003 (revised)

15-NOV-1995 (first entry)

Draculin peptide #35.

Anticoagulant; Draculin; saliva; vampire bat; inhibition; factor IX;

factor X; blood coagulation cascade; serine protease inhibitor; PMFS;

KW acute myocardial infarction; deep vein thrombosis; pulmonary embolism;
 KW unstable angina; transient ischemic attack; peripheral vascular; DPE;
 KW bypass occlusion; disseminated intravascular coagulation.
 XX
 OS Desmodus rotundus.
 XX
 PN WO9505836-A1.
 XX
 PD 02-MAR-1995.
 XX
 XX
 PF 22-AUG-1994; 94WO-US009488.
 XX
 PR 20-AUG-1993; 93US-00109807.
 XX
 PA (RHON) RHONE-POULENC RORER PHARM INC.
 XX
 PI Hemker H, Aplitz-Castro R, Beguin S;
 XX
 DR WPI; 1995-106668/14.
 XX
 XX
 PT New anticoagulant protein, draculin, from vampire bat saliva - and
 PT related nucleic acid, vectors, transformed cells and probes, for treating
 PT myocardial infarction, etc.
 XX
 XX
 PS Example 8; Page 35; 107pp; English.
 XX
 CC The sequences given in AAR71038-84 represent peptide fragments derived
 CC from the anticoagulant protein, Draculin. Draculin is isolated from the
 CC saliva of vampire bats and is distinct from other known anticoagulants in
 CC that it inhibits both factors IX and X of the blood coagulation cascade.
 CC The anticoagulant activity is not inhibited by serine protease inhibitors
 CC such as PMFS or DPP. The molecular weight of Draculin ranges from 75-90
 CC kD and may be used in treatment of acute myocardial infarction, deep vein
 CC thrombosis, pulmonary embolism, unstable angina, transient ischemic
 CC attacks, peripheral vascular or bypass occlusions and disseminated
 CC intravascular coagulation. These peptide fragments were derived from
 CC Draculin by cleavage with chymotrypsin and overlapping peptide fragments
 CC were compared to determine the complete amino acid sequence of Draculin.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 SO Sequence 19 AA;
 Query Match 58.3%; Score 67; DB 2; Length 19;
 Best Local Similarity 80.0%; Pred. No. 0.0016;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 9 INNGEADAMSLDGCF 23
 DB 1 VLKGEADAMSLDGCF 15
 RESULT 7
 ADG46092
 ID ADG46092 standard; peptide; 13 AA.
 XX
 AC ADG46092;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Human CDT peptide fragment #18.
 XX
 KW antibody; carbohydrate-deficient transferrin; CDT;
 KW non-glycosylated transferrin; alcoholism; diagnosis; human.
 XX
 OS Homo sapiens.
 XX
 PN EP1378521-A1.
 XX
 PD 07-JAN-2004.
 XX
 PF 19-MAY-2003; 2003EP-00011334.
 XX
 PR 05-JUL-2002; 2002DE-01030550.

XX
 PA (DADE-) DADE BEHRING MARBURG GMBH.
 XX
 PI Althaus H;
 XX
 DR WPI; 2004-073743/08.
 XX
 XX
 PT New antibody specific for carbohydrate-deficient transferrin, useful for
 PT diagnosis of alcoholism, can bind its target in solution, eliminating
 PT need for immobilization.
 XX
 PS Example 7; Page 15; 21pp; German.
 XX
 CC This invention describes a novel antibody that, in aqueous solution,
 CC binds selectively to carbohydrate-deficient transferrin (CDT) without
 CC having to bind CDT to a solid phase. The invention also describes an
 CC antibody that binds selectively to CDT at regions containing the
 CC sequences VVARSWGKEDLIWEL, ITEDSIKIMNGEADAMSLDGCF, SKUSWGSGLNDEPN and
 CC YEKYLGEYKAV (ADG46075-ADG46078) and an immunoassay for detecting CDT
 CC using the antibodies of the invention. The antibodies of the invention
 CC are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
 CC antibodies are obtained by immunisation with non-glycosylated
 CC transferrin, or a fragment, then generation of hybridomas by standard
 CC fusion of spleen and myeloma cells. Hybridomas are then selected for
 CC production of antibodies that specifically bind CDT from the aqueous
 CC phase. The antibodies are useful for diagnosis of alcoholism, CDT, which
 CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
 CC alcoholics. The antibodies allow direct detection of CDT in solution,
 CC eliminating the need for immobilising it on a solid phase (as required
 CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
 CC fragments used in the method of the invention.
 XX
 SO Sequence 13 AA;
 Query Match 56.5%; Score 65; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 INNGEADAMSLDG 21
 DB 1 INNGEADAMSLDG 13
 RESULT 8
 ADG46090
 ID ADG46090 standard; peptide; 13 AA.
 XX
 AC ADG46090;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Human CDT peptide fragment #16.
 XX
 KW antibody; carbohydrate-deficient transferrin; CDT;
 KW non-glycosylated transferrin; alcoholism; diagnosis; human.
 XX
 OS Homo sapiens.
 XX
 PN EP1378521-A1.
 XX
 PD 07-JAN-2004.
 XX
 PF 19-MAY-2003; 2003EP-00011334.
 XX
 PR 05-JUL-2002; 2002DE-01030550.
 XX
 PA (DADE-) DADE BEHRING MARBURG GMBH.
 XX
 PI Althaus H;
 XX
 DR WPI; 2004-073743/08.
 XX
 PT New antibody specific for carbohydrate-deficient transferrin, useful for

PT diagnosis of alcoholism, can bind its target in solution, eliminating
PT need for immobilization.
XX
PS Example 7; Page 15; 21pp; German.
XX
CC This invention describes a novel antibody that, in aqueous solution,
CC binds selectively to carbohydrate-deficient transferrin (CDT) without
CC having to bind CDT to a solid phase. The invention also describes an
CC antibody that binds selectively to CDT at regions containing the
CC sequence VVARSMGKEDLWEL, TTEDSIKIMNGEADMSLDGF, SLSMSGSLNSEPN and
CC YKRYGEEYVKAV (ADG46075-ADG46078) and an immunoassay for detecting CDT
CC using the antibodies of the invention. The antibodies of the invention
CC are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
CC antibodies are obtained by immunisation with non-glycosylated
CC transferrin, or a fragment, then generation of hybridomas by standard
CC fusion of spleen and myeloma cells. Hybridomas are then selected for
CC production of antibodies that specifically bind CDT from the aqueous
CC phase. The antibodies are useful for diagnosis of alcoholism, CDT, which
CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
CC alcoholics. The antibodies allow direct detection of CDT in solution,
CC eliminating the need for immobilising it on a solid phase (as required
CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
CC fragments used in the method of the invention.
SO
XX
SO Sequence 13 AA;
Query Match 53.9%; Score 62; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 SIAKIMNGEADAM 17
DB 1 SIAKIMNGEADAM 13
RESULT 9
ADG46091
ID ADG46091 standard; peptide; 13 AA.
XX
AC ADG46091;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human CDT peptide fragment #17.
XX
KW antibody; carbohydrate-deficient transferrin; CDT;
XX non-glycosylated transferrin; alcoholism; alcoholic; diagnosis; human.
OS Homo sapiens.
XX
PN EPI378521-A1.
XX
PD 07-JAN-2004.
XX
PF 19-MAY-2003; 2003EP-00011334.
XX
PR 05-JUL-2002; 2002DE-01030550.
XX
PA (DADE-) DADE BEHRING MARBURG GMBH.
XX
PI Althaus H,
XX
DR WPI; 2004-073743/08.
XX
PT New antibody specific for carbohydrate-deficient transferrin, useful for
PT diagnosis of alcoholism, can bind its target in solution, eliminating
PT need for immobilization.
XX
PS Example 7; Page 15; 21pp; German.
XX
CC This invention describes a novel antibody that, in aqueous solution,
CC binds selectively to carbohydrate-deficient transferrin (CDT) without
CC having to bind CDT to a solid phase. The invention also describes an

CC antibody that binds selectively to CDT at regions containing the
CC sequence VVARSMGKEDLWEL, TTEDSIKIMNGEADMSLDGF, SLSMSGSLNSEPN and
CC YKRYGEEYVKAV (ADG46075-ADG46078) and an immunoassay for detecting CDT
CC using the antibodies of the invention. The antibodies of the invention
CC are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
CC antibodies are obtained by immunisation with non-glycosylated
CC transferrin, or a fragment, then generation of hybridomas by standard
CC fusion of spleen and myeloma cells. Hybridomas are then selected for
CC production of antibodies that specifically bind CDT from the aqueous
CC phase. The antibodies are useful for diagnosis of alcoholism, CDT, which
CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
CC alcoholics. The antibodies allow direct detection of CDT in solution,
CC eliminating the need for immobilising it on a solid phase (as required
CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
CC fragments used in the method of the invention.
SO
XX
SO Sequence 13 AA;
Query Match 53.9%; Score 62; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 AKIMNGEADAMSL 19
DB 1 AKIMNGEADAMSL 13
RESULT 10
ADRI9359
ID ADRI9359 standard; peptide; 18 AA.
XX
AC ADRI9359;
XX
DT 04-NOV-2004 (first entry)
XX
DE TRPI derived human tryptic digest peptide, SEQ ID 21.
XX
KW Tissue damage; chronic; tissue repair-associated protein isoform; TRPI;
XX antitumor; vulnery; chronic dermal ulcer; human; tryptic digest;
XX proteolysis; trypsin.
OS Homo sapiens.
XX
PN WO2004069795-A2.
XX
PD 19-AUG-2004.
XX
PF 02-FEB-2004; 2004MO-US002881.
XX
PR 03-FEB-2003; 2003US-0444600P.
XX
PA (PFIZ) PFIZER PROD INC.
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Butt R, Rumpel K, Williams-Jones BI, Herath HMAC, Rohlf C,
PI Bruce JA, Patel TP;
XX
DR WPI; 2004-604404/58.
XX
PT Diagnosing, or monitoring the effect of therapy of, chronic tissue damage
PT (e.g. chronic dermal ulcer) comprises detecting and/or quantifying tissue
PT repair-associated protein isoform in a sample (e.g. wound exudate) from
PT the subject.
XX
PS Claim 7; SEQ ID NO 21; 107pp; English.
XX
CC The invention relates to a novel method for assessing, screening,
CC diagnosing or prognosing chronic tissue damage in a subject, identifying
CC a subject at risk of developing chronic tissue damage, or monitoring the
CC effect of therapy administered to a subject having chronic tissue damage.
CC The method comprises detecting and/or quantifying in a biological sample
CC from the subject a tissue repair-associated protein isoform (TRPI), given
CC in the specification. The invention further comprises: an isolated or

Matches 5, Conservative 4, Mismatches 2, Indels 0, Gaps 0;

QY 12 GEADAMSLOG 22
|:|:|:|:|
Db 1 GQELALQVDG 11

RESULT 13

AAU68103
ID AAU68103 standard; peptide; 12 AA.

AC AAU68103;

DT 16-JAN-2002 (first entry)

DE Human Breast cancer-associated protein isoform, BPI-7 peptide #2.

KW Human; Breast cancer-associated protein isoform; breast cancer;

KM Immunogen; cytosolic; BPI; tryptic digest peptide.

OS Homo sapiens.

PN WO200171357-A2.

PD 27-SEP-2001.

PF 20-MAR-2001; 2001WO-GB001219.

PR 20-MAR-2000; 2000GB-00006695.

PR 24-MAR-2000; 2000GB-00007265.

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Herath HMAc, O'hare MJ, Page MJ, Parekh RB, Waterfield MD;

DR WPI; 2001-611532/70.

PT Identifying proteins for clinical screening, diagnosis and prognosis of breast cancer, comprises detecting Breast Cancer-Associated Protein isoforms (BPIs) using two-dimensional electrophoresis.

PS Claim 9; Page 44; 197bp; English.

CC The invention relates to diagnosing, determining the stage or severity, or identifying the risk of a subject developing cancer (especially breast cancer), or monitoring the effect of therapy on a subject with cancer, comprising analysing a test sample using two-dimensional electrophoresis and detecting Breast Cancer-Associated Protein isoforms (BPIs). The methods disclosed are used for the diagnosis and prognosis of breast cancer, for determining the severity of breast cancer, and for identifying a subject at risk of developing breast cancer, and for the effect of therapy administered to a subject. Antibodies raised against the binding domain of a BPI, the binding domain of a BPI, a nucleic acid encoding a BPI, or a nucleic acid that inhibits the function of a BPI can be incorporated into a pharmaceutical composition for treating or preventing breast cancer. The methods use sensitive and specific biomarkers provide early diagnosis of breast cancer, and the compositions are more potent, specific, and has a more rapid effect with fewer side effects than other prior art methods. The present sequence is a tryptic digest peptide from a BPI of the invention

SO Sequence 12 AA;

Query Match 29.6%; Score 34; DB 4; Length 12;

Best Local Similarity 45.5%; Pred. No. 1.7e+02; Mismatches 2; Indels 0; Gaps 0;

QY 12 GEADAMSLOG 22
|:|:|:|:|
Db 1 GQELALQVDG 11

RESULT 14

AAU68052
ID AAU68052 standard; peptide; 12 AA.

AC AAU68052;

DT 16-JAN-2002 (first entry)

DE Human Breast cancer-associated protein isoform, BPI-3 peptide #1.

KW Human; Breast cancer-associated protein isoform; breast cancer;

KM Immunogen; cytosolic; BPI; tryptic digest peptide.

OS Homo sapiens.

PN WO200171357-A2.

PD 27-SEP-2001.

PF 20-MAR-2001; 2001WO-GB001219.

PR 20-MAR-2000; 2000GB-00006695.

PR 24-MAR-2000; 2000GB-00007265.

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Herath HMAc, O'hare MJ, Page MJ, Parekh RB, Waterfield MD;

DR WPI; 2001-611532/70.

PT Identifying proteins for clinical screening, diagnosis and prognosis of breast cancer, comprises detecting Breast Cancer-Associated Protein isoforms (BPIs) using two-dimensional electrophoresis.

PS Claim 9; Page 43; 197bp; English.

CC The invention relates to diagnosing, determining the stage or severity, or identifying the risk of a subject developing cancer (especially breast cancer), or monitoring the effect of therapy on a subject with cancer, comprising analysing a test sample using two-dimensional electrophoresis and detecting Breast Cancer-Associated Protein isoforms (BPIs). The methods disclosed are used for the diagnosis and prognosis of breast cancer, for determining the severity of breast cancer, and for identifying a subject at risk of developing breast cancer, and for the effect of therapy administered to a subject. Antibodies raised against the binding domain of a BPI, the binding domain of a BPI, a nucleic acid encoding a BPI, or a nucleic acid that inhibits the function of a BPI can be incorporated into a pharmaceutical composition for treating or preventing breast cancer. The methods use sensitive and specific biomarkers provide early diagnosis of breast cancer, and the compositions are more potent, specific, and has a more rapid effect with fewer side effects than other prior art methods. The present sequence is a tryptic digest peptide from a BPI of the invention

SO Sequence 12 AA;

Query Match 29.6%; Score 34; DB 4; Length 12;

Best Local Similarity 45.5%; Pred. No. 1.7e+02; Mismatches 2; Indels 0; Gaps 0;

QY 12 GEADAMSLOG 22
|:|:|:|:|
Db 1 GQELALQVDG 11

RESULT 15

AAU64372
ID AAU64372 standard; peptide; 12 AA.

AC AAU64372;

DT 22-AUG-2001 (first entry)

DE Splice-variance region of a human transferrin.

```

XX Human; transferrin; autoimmune disease; rheumatoid arthritis;
KM hyperproliferative disorder; neoplasia; cardiovascular disorder;
LW cardiac arrest; cerebrovascular disorder; cerebral ischemia;
KM angiogenesis; nervous system disorder; Alzheimer's disease; infection;
KM ocular disorder; corneal infection; wound healing;
KM epithelial cell proliferation; aging; organ transplant.
XX
OS Homo sapiens.
XX
PN WO200146254-A1.
XX
PD 28-JUN-2001.
XX
PF 21-DEC-2000; 2000MO-US034769.
XX
PR 23-DEC-1999; 99US-0171595P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Shi Y, Choi GH;
XX
DR WPI; 2001-381910/40.
XX
PT Isolated nucleic acid molecule encoding a human transferrin protein is
PT used in preventing, treating or ameliorating a medical condition.
XX
PS Disclosure; Page 11; 290pp; English.
XX
XX The present sequence is a splice-variance region of a transferrin.
CC Transferrin polypeptides and polynucleotides are used to prevent, treat
CC or ameliorate a medical condition in e.g. humans, mice, rabbits, goats,
CC horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or
CC treated include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and
CC ocular disorders e.g. corneal infection. The polypeptides can also be
CC used to aid wound healing and epithelial cell proliferation, to prevent
CC skin aging due to sunburn, to maintain organs before transplantation, for
CC supporting cell culture of primary tissues, to regenerate tissues and in
CC chemotaxis. The polypeptides can also be used as a food additive or
CC preservative to increase or decrease storage capabilities
XX
SQ Sequence 12 AA;

```

```

Query Match          29.6%; Score 34; DB 4; Length 12;
Best Local Similarity 64.3%; Pred. No. 1.7e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
QY 3 EDSIAKINNGEADA 16
   |||||:|||||
DB 1 EDCIA--LKGEDA 12

```

Search completed: November 1, 2005, 13:48:43
 Job time : 164 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 13:43:13, Search time 41 Seconds

(Without alignment)
41.876 Million cell updates/sec

Title: US-10-612-162a-2

Sequence: 1 TTEDSLAKIMNGEADMSLDGCF 23

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 211522

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

1: /cgn2_6/prodata/1/aa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/aa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/aa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/aa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/aa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	29.6	17	2	US-08-484-438-31
2	33	28.7	23	1	US-08-568-147B-14
3	31	27.0	16	1	US-08-487-890A-134
4	31	27.0	16	2	US-08-478-435-134
5	31	27.0	16	2	US-08-337-483-134
6	31	27.0	16	2	US-08-478-373-134
7	31	27.0	16	3	US-08-474-671-134
8	31	27.0	16	3	US-08-483-577A-134
9	31	27.0	16	3	US-08-897-438-134
10	31	27.0	16	3	US-08-637-654-134
11	31	27.0	16	3	US-08-649-818-134
12	31	27.0	17	1	US-08-487-890A-133
13	31	27.0	17	2	US-08-478-435-133
14	31	27.0	17	2	US-08-337-483-133
15	31	27.0	17	2	US-08-478-373-133
16	31	27.0	17	3	US-08-474-671-133
17	31	27.0	17	3	US-08-483-577A-133
18	31	27.0	17	3	US-08-897-438-133
19	31	27.0	17	3	US-08-637-654-133
20	31	27.0	17	3	US-08-649-818-133
21	31	27.0	20	1	US-08-440-861-48
22	30	26.1	13	3	US-09-155-941-23
23	30	26.1	17	5	PCT-US96-01600-26
24	29	25.2	12	4	US-09-462-118-27
25	29	25.2	13	4	US-09-155-941-15
26	29	25.2	20	1	US-08-241-054-79
27	29	25.2	20	1	US-08-241-054-79

28	29	25.2	20	1	US-08-241-054-93	Sequence 93, Appl
29	29	25.2	20	1	US-08-390-156A-37	Sequence 37, Appl
30	29	25.2	20	1	US-08-390-156A-44	Sequence 44, Appl
31	29	25.2	20	1	US-08-439-817-59	Sequence 59, Appl
32	29	25.2	20	1	US-08-439-817-73	Sequence 73, Appl
33	29	25.2	20	1	US-08-485-508-79	Sequence 79, Appl
34	29	25.2	20	1	US-08-485-508-93	Sequence 93, Appl
35	29	25.2	22	3	US-08-256-747C-41	Sequence 41, Appl
36	29	25.2	22	3	US-08-334-130A-41	Sequence 41, Appl
37	28	24.3	16	2	US-08-334-122-127	Sequence 127, Appl
38	28	24.3	16	2	US-08-333-402-127	Sequence 127, Appl
39	28	24.3	16	2	US-09-207-621-127	Sequence 127, Appl
40	28	24.3	16	2	US-08-532-818-127	Sequence 127, Appl
41	28	24.3	16	3	US-09-231-797-127	Sequence 127, Appl
42	28	24.3	16	3	US-08-534-224-127	Sequence 127, Appl
43	28	24.3	16	3	US-08-533-843-127	Sequence 127, Appl
44	28	24.3	16	3	US-08-534-223-127	Sequence 127, Appl
45	28	24.3	16	3	US-09-413-492-127	Sequence 127, Appl

ALIGNMENTS

RESULT 1
US-08-484-438-31
Sequence 31, Application US/08484438
Patent No. 5811098
Patent No. 5811098 5780031
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory D.
APPLICANT: Culouscou, Jean-Michel
APPLICANT: Shoyab, Mohammed
APPLICANT: Siegall, Clay B.
APPLICANT: Hellstr m, Ingegerd
APPLICANT: Hellstr m, Karl E.
TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,438
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,442
FILING DATE: 14-OCT-1994
APPLICATION NUMBER: US 08/150,704
FILING DATE: 10-NOV-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/981,165
FILING DATE: 24-NOV-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-2310
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-8090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-484-438-31

Query Match 29.6%; Score 34; DB 2; Length 17;
Best Local Similarity 29.4%; Pred. No. 41;
Matches 5; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 6 IAKINGEADAMSLDGG 22
Db 1 LARLEGEDEKEYNADGG 17

RESULT 2
US-08-568-147B-14
Sequence 14, Application US/08568147B
Patent No. 5763422

GENERAL INFORMATION:
APPLICANT: Sumitani, Yoshinori
APPLICANT: Kato, Hiroshi
APPLICANT: Sekiguchi, Kiyoshi
APPLICANT: Takeda, Kazumichi
TITLE OF INVENTION: DNA FRAGMENT CODING FOR SQUAMOUS CELL
TITLE OF INVENTION: CARCINOMA-ASSOCIATED ANTIGEN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
ZIP: 11530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,147B
FILING DATE:
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 800,952
FILING DATE: 02-DEC-1991

ATTORNEY/AGENT INFORMATION:
NAME: Digilio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8425
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-568-147B-14

Query Match 28.7%; Score 33; DB 1; Length 23;
Best Local Similarity 46.2%; Pred. No. 86;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 9 INNGEADAMSLDGG 21
Db 5 IFNGDADLSGWTG 17

RESULT 3

US-08-487-890A-134
Sequence 134, Application US/08487890A
Patent No. 5708149

GENERAL INFORMATION:
APPLICANT: Loomore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Wang, Yan-ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,890A
FILING DATE: 07-JUN-1993
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-466 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
US-08-487-890A-134

Query Match 27.0%; Score 31; DB 1; Length 16;
Best Local Similarity 60.0%; Pred. No. 12e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 14 ADAMSLDGGF 23
Db 3 ASTSLBGGF 12

RESULT 4
US-08-478-435-134

Sequence 134, Application US/08478435
Patent No. 5922323

GENERAL INFORMATION:
APPLICANT: Loomore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele

APPLICANT: Gray-Owen, Scott
APPLICANT: Wang, Yan-ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel

TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,435
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-462 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-478-435-134

Query Match 27.0%; Score 31; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 14 ADAMSJGCF 23
DB 3 ASSTSLGCF 12

RESULT 5
US-08-337-483-134
Sequence 134, Application US/08337483
Patent No. 5922562
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-ping
APPLICANT: Mordin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada

ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-337-483-134

Query Match 27.0%; Score 31; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 14 ADAMSJGCF 23
DB 3 ASSTSLGCF 12

RESULT 6
US-08-478-373-134
Sequence 134, Application US/08478373
Patent No. 5922841
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-ping
APPLICANT: Mordin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,373
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-463 MIS:Vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-478-373-134

Query Match 27.0%; Score 31; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 14 ADAMSIDGCF 23
DB 3 AASTSLGCF 12

RESULT 7
US-08-474-671-134
Sequence 134, Application US/08474671
Patent No. 6008326
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,671
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-465 MIS:Vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155

TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-474-671-134

Query Match 27.0%; Score 31; DB 3; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 14 ADAMSIDGCF 23
DB 3 AASTSLGCF 12

RESULT 8
US-08-483-577A-134
Sequence 134, Application US/08483577A
Patent No. 6015688
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,577A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-511
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-483-577A-134

Query Match 27.0%; Score 31; DB 3; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 14 ADAMSJDGGF 23
DB 3 ASTTSLGGF 12

RESULT 9
US-08-897-438-134
; Sequence 134, Application US/08897438
; Patent No. 6262016
; GENERAL INFORMATION:
; APPLICANT: Loomore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murlin, Andrew
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897,438
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,577
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-897-438-134

DB 3 ASTTSLGGF 12

RESULT 10
US-08-637-654-134
; Sequence 134, Application US/08637654
; Patent No. 6368727
; GENERAL INFORMATION:
; APPLICANT: Loomore, Sheena M
; APPLICANT: Harkness, Robin E
; APPLICANT: Schryvers, Anthony B
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murlin, Andrew D
; TITLE OF INVENTION: HAEMOPHILUS TRANSFERRIN RECEPTOR GENES
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,654
; FILING DATE: 05-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/CA94/00616
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-637-654-134

Query Match 27.0%; Score 31; DB 3; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 14 ADAMSJDGGF 23
DB 3 ASTTSLGGF 12

RESULT 11
US-08-649-518-134
; Sequence 134, Application US/08649518
; Patent No. 6361779
; GENERAL INFORMATION:
; APPLICANT: Loomore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murlin, Andrew


```

/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/337,483
/ FILING DATE: 08-NOV-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/175,116
/ FILING DATE: 29-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/148,968
/ FILING DATE: 08-NOV-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Stewart, Michael I
/ REGISTRATION NUMBER: 24,973
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (416) 595-1155
/ TELEFAX: (416) 595-1163
/ INFORMATION FOR SEQ ID NO: 133:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-08-478-435-133

Query Match      27.0%; Score 31; DB 2; Length 17;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      14 ADAMSJDGF 23
DB      3 ASTTSLEGGF 12

RESULT 14
US-08-337-483-133
/ Sequence 133, Application US/08337483
/ Patent No. 5922562
/ GENERAL INFORMATION:
/ APPLICANT: Loomore, Sheena
/ APPLICANT: Harkness, Robin
/ APPLICANT: Schryvers, Anthony
/ APPLICANT: Chong, Pele
/ APPLICANT: Gray-Owen, Scott
/ APPLICANT: Yang, Yan-Ping
/ APPLICANT: Murlin, Andrew
/ APPLICANT: Klein, Michel
/ TITLE OF INVENTION: Transferrin Receptor Genes
/ NUMBER OF SEQUENCES: 147
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sim & McBurney
/ STREET: Suite 701, 330 University Avenue
/ CITY: Toronto
/ STATE: Ontario
/ COUNTRY: Canada
/ ZIP: M5G 1R7
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Releasee #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/337,483
/ FILING DATE: 08-NOV-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Stewart, Michael I
/ REGISTRATION NUMBER: 24,973
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (416) 595-1155
/ TELEFAX: (416) 595-1163
```

```

/ INFORMATION FOR SEQ ID NO: 133:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-08-337-483-133

Query Match      27.0%; Score 31; DB 2; Length 17;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      14 ADAMSJDGF 23
DB      3 ASTTSLEGGF 12

RESULT 15
US-08-478-373-133
/ Sequence 133, Application US/08478373
/ Patent No. 5922841
/ GENERAL INFORMATION:
/ APPLICANT: Loomore, Sheena
/ APPLICANT: Harkness, Robin
/ APPLICANT: Schryvers, Anthony
/ APPLICANT: Chong, Pele
/ APPLICANT: Gray-Owen, Scott
/ APPLICANT: Yang, Yan-Ping
/ APPLICANT: Murlin, Andrew
/ APPLICANT: Klein, Michel
/ TITLE OF INVENTION: Transferrin Receptor Genes
/ NUMBER OF SEQUENCES: 147
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sim & McBurney
/ STREET: Suite 701, 330 University Avenue
/ CITY: Toronto
/ STATE: Ontario
/ COUNTRY: Canada
/ ZIP: M5G 1R7
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Releasee #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/478,373
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/337,483
/ FILING DATE: 08-NOV-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/175,116
/ FILING DATE: 29-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/148,968
/ FILING DATE: 08-NOV-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Stewart, Michael I
/ REGISTRATION NUMBER: 24,973
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (416) 595-1155
/ TELEFAX: (416) 595-1163
/ INFORMATION FOR SEQ ID NO: 133:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-08-478-373-133
```

Query Match 27.0%; Score 31; DB 2; Length 17;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 14 ADAMSLDGGF 23
| | | | |
Db 3 ASTTSLGGF 12

Search completed: November 1, 2005, 13:53:07
Job time : 42 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: November 1, 2005, 13:49:34 ; Search time 163 Seconds

(Without alignments)
58.988 Million cell updates/sec

Title: US-10-612-162A-2

Perfect score: 115
Sequence: 1 TTEDSIKIMNGEADMSLDGGR 23

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 400862

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubppa/PCT_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB.pep:*
6: /cgn2_6/prodata/1/pubppa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/prodata/1/pubppa/US08_NEW_PUB.pep:*
8: /cgn2_6/prodata/1/pubppa/US08_PUBCOMB.pep:*
9: /cgn2_6/prodata/1/pubppa/US09A_PUBCOMB.pep:*
10: /cgn2_6/prodata/1/pubppa/US09B_PUBCOMB.pep:*
11: /cgn2_6/prodata/1/pubppa/US09C_PUBCOMB.pep:*
12: /cgn2_6/prodata/1/pubppa/US09_NEW_PUB.pep:*
13: /cgn2_6/prodata/1/pubppa/US10_PUBCOMB.pep:*
14: /cgn2_6/prodata/1/pubppa/US10B_PUBCOMB.pep:*
15: /cgn2_6/prodata/1/pubppa/US10C_PUBCOMB.pep:*
16: /cgn2_6/prodata/1/pubppa/US10D_PUBCOMB.pep:*
17: /cgn2_6/prodata/1/pubppa/US10E_PUBCOMB.pep:*
18: /cgn2_6/prodata/1/pubppa/US10_NEW_PUB.pep:*
19: /cgn2_6/prodata/1/pubppa/US11A_PUBCOMB.pep:*
20: /cgn2_6/prodata/1/pubppa/US11_NEW_PUB.pep:*
21: /cgn2_6/prodata/1/pubppa/US60_NEW_PUB.pep:*
22: /cgn2_6/prodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	100.0	23	15	US-10-612-162-2
2	77	67.0	21	15	US-10-394-980-20
3	77	67.0	21	18	US-10-952-557-20
4	34	29.6	12	9	US-09-891-126-6
5	34	29.6	12	10	US-09-988-493-10
6	34	29.6	12	14	US-10-266-745-6
7	34	29.6	12	15	US-10-378-094-5
8	34	29.6	12	15	US-10-384-060-4
9	34	29.6	12	15	US-10-231-494-8
10	34	29.6	12	16	US-10-700-330-101
11	33	28.7	15	17	US-10-801-990-1

12	32	27.8	12	17	US-10-801-990-12	Sequence 12, App1
13	31	27.0	14	15	US-10-432-422-88	Sequence 86, App1
14	31	27.0	16	14	US-10-043-344-134	Sequence 134, App
15	31	27.0	17	14	US-10-043-344-133	Sequence 133, App
16	31	27.0	20	11	US-09-855-604-138	Sequence 138, App
17	31	27.0	20	12	US-09-855-604-138	Sequence 138, App
18	30	26.1	15	16	US-10-416-249-415	Sequence 415, App
19	30	26.1	17	10	US-09-880-748-3151	Sequence 3151, App
20	30	26.1	17	15	US-10-293-418-3151	Sequence 3151, App
21	30	26.1	23	18	US-10-862-195-357	Sequence 357, App
22	29	25.2	12	18	US-10-937-042-28	Sequence 28, App1
23	29	25.2	12	14	US-10-247-946-27	Sequence 27, App1
24	29	25.2	12	14	US-10-251-526-27	Sequence 27, App1
25	29	25.2	13	16	US-10-700-330-164	Sequence 164, App
26	29	25.2	13	18	US-10-789-4948-8	Sequence 8, App1
27	29	25.2	13	18	US-10-789-4948-8	Sequence 8, App1
28	29	25.2	20	14	US-10-115-072-18	Sequence 68, App1
29	29	25.2	20	16	US-10-679-033-56	Sequence 18, App1
30	29	25.2	20	18	US-10-862-195-2151	Sequence 2151, App
31	28.5	24.8	19	9	US-09-734-417-4	Sequence 4, App1
32	28	24.3	10	10	US-09-572-4048-448	Sequence 448, App
33	28	24.3	13	15	US-10-469-837-58	Sequence 58, App1
34	28	24.3	13	16	US-10-488-671-51	Sequence 51, App1
35	28	24.3	13	16	US-10-488-671-52	Sequence 52, App1
36	28	24.3	13	16	US-10-488-671-53	Sequence 53, App1
37	28	24.3	13	16	US-10-488-671-54	Sequence 54, App1
38	28	24.3	14	16	US-10-813-638-1337	Sequence 1237, App
39	28	24.3	14	16	US-10-813-638-1298	Sequence 1298, App
40	28	24.3	15	9	US-09-826-290-144	Sequence 144, App
41	28	24.3	15	15	US-10-264-309-193	Sequence 193, App
42	28	24.3	15	16	US-10-416-249-417	Sequence 417, App
43	28	24.3	15	18	US-10-264-309-193	Sequence 193, App
44	28	24.3	16	9	US-09-073-009-41	Sequence 41, App1
45	28	24.3	16	9	US-09-023-588-41	Sequence 41, App1

ALIGNMENTS

RESULT 1
US-10-612-162-2
; Sequence 2, App1
; Publication No. US20040014145A1
; GENERAL INFORMATION:
; APPLICANT: Dade Behring Marburg GmbH
; TITLE OF INVENTION: Carbohydrate deficient transferrin (CDT)-specific
; FILE REFERENCE: 2002/B001
; CURRENT APPLICATION NUMBER: US/10/612,162
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 10230550.1
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 03011334.4
; PRIOR FILING DATE: 2003-05-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-162-2

Query Match 100.0%; Score 115; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 5,5e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEADMSLDGGR 23
|||||
Db 1 TTEDSIKIMNGEADMSLDGGR 23
|||||

RESULT 2
US-10-394-980-20

DB 1 GQLEALQVDSG 11

```
RESULT 6
US-10-266-745-6
; Sequence 6, Application US/10266745
; Publication No. US20030149256A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Transferrin Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT035PI
; CURRENT APPLICATION NUMBER: US/10/266,745
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/891,126
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: PCT/US00/34769
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/171,595
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-266-745-6
```

Query Match 29.6%; Score 34; DB 14; Length 12;
Best Local Similarity 64.3%; Pred. No. 1.6e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 3 EDSIAKIMGEADA 16
DB 1 EDCIA--LKGEADA 12

```
RESULT 7
US-10-378-094-5
; Sequence 5, Application US/10378094
; Publication No. US20030221201A1
; GENERAL INFORMATION:
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: LAI, Char-Huei
; APPLICANT: SADEGH, Homayoun
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN FUSION PROTEINS
; FILE REFERENCE: 54710-5001-01-US
; CURRENT APPLICATION NUMBER: US/10/378,094
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentln version 3.2
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Neutrophil lactoferrin splice variant
US-10-378-094-5
```

Query Match 29.6%; Score 34; DB 15; Length 12;
Best Local Similarity 64.3%; Pred. No. 1.6e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 3 EDSIAKIMGEADA 16
DB 1 EDCIA--LKGEADA 12

```
RESULT 8
US-10-384-060-4
; Sequence 4, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGH, Homayoun
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patentln version 3.2
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Neutrophil splice variant sequence
US-10-384-060-4
```

Query Match 29.6%; Score 34; DB 15; Length 12;
Best Local Similarity 64.3%; Pred. No. 1.6e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 3 EDSIAKIMGEADA 16
DB 1 EDCIA--LKGEADA 12

```
RESULT 9
US-10-231-494-8
; Sequence 8, Application US/10231494
; Publication No. US2004002334A1
; GENERAL INFORMATION:
; APPLICANT: PRIOR, Christopher P.
; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
; FILE REFERENCE: 54710-5001-US
; CURRENT APPLICATION NUMBER: US/10/231,494
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 8
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Lactoferrin splice variant sequence
US-10-231-494-8
```

Query Match 29.6%; Score 34; DB 15; Length 12;
Best Local Similarity 64.3%; Pred. No. 1.6e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 3 EDSIAKIMGEADA 16
DB 1 EDCIA--LKGEADA 12

RESULT 10
US-10-700-330-101
; Sequence 101, Application US/10700330
; Publication No. US20040203022A1
; GENERAL INFORMATION:
; APPLICANT: Heratch, Mudiyanselage Athula Chandrasiri Heratch
; APPLICANT: Page, Martin John
; TITLE OF INVENTION: Proteins and Genes For Diagnosis And Treatment of ErbB2-Related C
; FILE REFERENCE: 2543-1-031
; CURRENT APPLICATION NUMBER: US/10/700,330
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: GB 0110886.9
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: GB 0128183.1
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-700-330-101

Query Match 29.6%; Score 34; DB 16; Length 12;
Best Local Similarity 45.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 12 G6ADAMSLSGG 22
|:|:|:|
DB 1 GQLEALQVDGG 11

RESULT 11
US-10-801-990-1
; Sequence 1, Application US/10801990
; Publication No. US20050048574A1
; GENERAL INFORMATION:
; APPLICANT: Kantor, Aaron B.
; APPLICANT: Schulman, Howard
; APPLICANT: Becker, Christopher
; TITLE OF INVENTION: BIOMARKERS FOR RHEUMATOID ARTHRITIS
; FILE REFERENCE: SURR.121
; CURRENT APPLICATION NUMBER: US/10/801,990
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US 60/455,037
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-801-990-1

Query Match 28.7%; Score 33; DB 17; Length 15;
Best Local Similarity 87.5%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIAX 8
|:|:|:|
DB 8 TTEDCIAX 15

RESULT 12
US-10-801-990-12
; Sequence 12, Application US/10801990
; Publication No. US20050048574A1
; GENERAL INFORMATION:
; APPLICANT: Kantor, Aaron B.
; APPLICANT: Schulman, Howard
; APPLICANT: Becker, Christopher
; TITLE OF INVENTION: BIOMARKERS FOR RHEUMATOID ARTHRITIS
; FILE REFERENCE: SURR.121

; CURRENT APPLICATION NUMBER: US/10/801,990
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US 60/455,037
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-801-990-12

Query Match 27.8%; Score 32; DB 17; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 SLDDGF 23
|:|:|:|
DB 1 SLDDGF 6

RESULT 13
US-10-432-422-88
; Sequence 88, Application US/10432422
; Publication No. US20040076981A1
; GENERAL INFORMATION:
; APPLICANT: Syngenta Participations AG
; APPLICANT: Cornell Research Foundation, Inc.
; APPLICANT: Yoder, Olen
; APPLICANT: Turgeon, Barbara G.
; APPLICANT: Lu, Shen-wen
; TITLE OF INVENTION: Fungal Iron Reductase Gene
; FILE REFERENCE: 1360.017MO1
; CURRENT APPLICATION NUMBER: US/10/432,422
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: US 60/252,732
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/252,649
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Cochliobolus heterostrophus
US-10-432-422-88

Query Match 27.0%; Score 31; DB 15; Length 14;
Best Local Similarity 66.7%; Pred. No. 5.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 15 DAMSLDGGF 23
|:|:|:|
DB 6 DSPSLSGF 14

RESULT 14
US-10-043-344-134
; Sequence 134, Application US/10043344
; Publication No. US20030080806A1
; GENERAL INFORMATION:
; APPLICANT: Loomore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Mordin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSPERLIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518

; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 134
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-134

Query Match 27.0%; Score 31; DB 14; Length 16;
Best Local Similarity 60.0%; Pred. No. 6.8e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 14 ADAMSLDGGF 23
| |||||
Db 3 ASTTSLEGGF 12

RESULT 15
US-10-043-344-133
; Sequence 133. Application US/10043344
; Publication No. US20030088086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Mordin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 133
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-133

Query Match 27.0%; Score 31; DB 14; Length 17;
Best Local Similarity 60.0%; Pred. No. 7.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 14 ADAMSLDGGF 23
| |||||
Db 3 ASTTSLEGGF 12

Search completed: November 1, 2005, 14:05:54
Job time : 167 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 13:40:49 ; Search time 38 seconds

(without alignments)
58.236 Million cell updates/sec

Title: US-10-612-162A-2

Perfect score: 115

Sequence: 1 TTEDSTAKINNGEADMSLDGCF 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4495

Minimum DB seq length: 0
Maximum DB seq length: 23Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79: *
2: PIR1: *
3: PIR2: *
4: PIR3: *
5: PIR4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	31	27.0	16	2	A44823	synaptosomal-assoc
2	28	24.3	23	2	S54339	cytochrome P450 CYP
3	27	23.5	22	2	H83991	hypothetical prote
4	26	22.6	16	2	A29501	fibrinopeptide A -
5	26	22.6	16	2	B24180	fibrinogen alpha c
6	26	22.6	16	2	A24180	fibrinogen alpha c
7	26	22.6	16	2	B28854	fibrinopeptide A -
8	26	22.6	16	2	C28854	fibrinopeptide A -
9	26	22.6	16	2	A28854	fibrinopeptide A -
10	25	21.7	11	2	CS3652	rhlr protein - Pse
11	25	21.7	13	2	S03879	6-phosphofructokin
12	25	21.7	20	4	IS3672	somatotropin - syn
13	25	21.7	21	2	SI6073	alanine-tRNA ligase
14	24	20.9	11	4	SI19015	hypothetical prote
15	24	20.9	12	2	PH1172	T-cell receptor al
16	24	20.9	12	2	E64573	hypothetical prote
17	24	20.9	15	2	S26516	T-cell receptor al
18	24	20.9	16	2	PH1453	T-cell receptor al
19	24	20.9	18	2	S30346	4-hydroxybenzoate-
20	23	20.0	12	2	FQ0730	unidentified 5.4/3
21	23	20.0	15	2	PH1807	T cell receptor al
22	23	20.0	16	2	D83794	hypothetical prote
23	23	20.0	17	2	A44896	heat shock protein
24	23	20.0	18	2	S09086	proteasome chain 5
25	23	20.0	19	2	A43192	transferrin - bu
26	23	20.0	19	2	A39504	octamer-binding pr
27	23	20.0	20	2	S65135	xanthine dehydroge
28	23	20.0	21	2	S09088	proteasome chain 7
29	23	20.0	22	2	S08990	calcimedlin, 67K -

30	22	19.1	10	2	PT0309	Ig heavy chain CRD
31	22	19.1	10	2	C39572	sperm-activating p
32	22	19.1	11	2	A35594	buccalin - Cal1for
33	22	19.1	18	2	PH1349	Ig heavy chain DJ
34	22	19.1	18	2	I78841	thrombopoietin rec
35	22	19.1	20	2	B61333	chymotrypsin (EC 3
36	22	19.1	20	2	S53440	glutathione-bindin
37	22	19.1	20	2	AS6899	serum heterodimer,
38	22	19.1	21	2	S33868	quinolinate acid 4-o
39	22	19.1	22	2	S06487	glycine cleavage s
40	21	18.3	10	2	E41946	T-cell receptor ga
41	21	18.3	10	2	C60787	sperm-activating p
42	21	18.3	13	2	PC2369	unidentified 85K p
43	21	18.3	15	2	PA0075	fructose-bisphosph
44	21	18.3	16	2	H29501	fibrinopeptide A -
45	21	18.3	16	2	S01669	RNA N-glycosidase

ALIGNMENTS

RESULT 1

A44823

N:Altername names: superprotein peptide 10B - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996

C/Accession: A44823

R:Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.

J. Neurosci. 11, 3412-3421, 1991

A>Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is

A/Accession: A44823; MUID:92044785; PMID:1941090

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-16 <LOB>

A/Experimental source: visual tissue

A/Note: sequence extracted from NCBI backbone (NCBIRP:64256)

C/Keywords: membrane trafficking

Query Match 27.0%; Score 31; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 13 EADMSLDGCF 23

DB 4 ERSQMAISGCF 14

RESULT 2

S54339

cytochrome P450 CYP2A7AS - human

C/Species: Homo sapiens (man)

C/Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999

C/Accession: S54339

R: Ding, S.; Lake, B.G.; Friedberg, T.; Wolf, C.R.

Biochem. J. 306, 161-166, 1995

A>Title: Expression and alternative splicing of the cytochrome P-450 CYP2A7.

A/Reference number: S54338; MUID:95169049; PMID:7864805

A/Accession: S54339

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-23 <DIN>

Query Match 24.3%; Score 28; DB 2; Length 23;
Best Local Similarity 54.5%; Pred. No. 6e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 DSTAKINNGEA 14

DB 6 DSTIKVSGGVA 16

Query Match 22.6%; Score 26; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 8.2e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 12 G6ADAMSLDGS 22
DB 4 G6GDPLAEGGS 14

RESULT 9
A28854
Fibrinopeptide A - olive baboon
C/Species: Papio anubis, Papio hamadryas anubis (olive baboon)
C/Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C/Accession: A28854
R/Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A/Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropit
A/Reference number: A91973; MUID:64161822; PMID:6423621
A/Accession: A28854
A/Molecule type: protein
A/Residues: 1-16 <NA>
A/Cross-references: UNIPROT:P12803
C/Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 22.6%; Score 26; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 8.2e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 12 G6ADAMSLDGS 22
DB 4 G6GDPLAEGGS 14

RESULT 10
C53652
rhlr protein - Pseudomonas aeruginosa (fragment)
C/Species: Pseudomonas aeruginosa
C/Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
C/Accession: C53652
R/Ochener, U.A.; Flechter, A.; Reiser, J.
J. Biol. Chem. 269, 19787-19795, 1994
A/Title: Isolation, characterization, and expression in Escherichia coli of the Pseudom
A/Reference number: A53652; MUID:94321521; PMID:8051059
A/Accession: C53652
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-11 <OCH>
A/Cross-references: UNIPROT:P54292; GB:I28170
C/Superfamily: edla regulatory protein

Query Match 21.7%; Score 25; DB 2; Length 11;
Best Local Similarity 71.4%; Pred. No. 7.7e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 17 MSUDGCF 23
DB 1 MRNDGCF 7

RESULT 11
S03879
6-phosphofructokinase (EC 2.7.1.11) B - rabbit (fragment)
N/Alternate names: phosphofructo-1-kinase B
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C/Accession: S03879
R/Valaitis, A.P.; Poe, L.G.; Kwiatkowski, D.; Latshaw, S.P.; Kemp, R.G.
Biochim. Biophys. Acta 995, 187-194, 1989
A/Title: The sites of phosphorylation of rabbit brain phosphofructo-1-kinase by cyclic A
A/Reference number: S03878; MUID:89194250; PMID:2539199
C/Accession: S03879

A/Molecule type: protein
A/Residues: 1-13 <VAL>
A/Cross-references: UNIPROT:Q7M3F5
A/Note: the sequence from the summary is inconsistent with that from table 1 and Fig. 4
C/Keywords: glycolysis; phosphotransferase

Query Match 21.7%; Score 25; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 16 AMSUDGCF 23
DB 6 SLMDKCF 13

RESULT 12
I53672
somatotropin - synthetic
C/Species: synthetic
C/Date: 07-Jun-1996 #sequence_revision 31-Jul-1997 #text_change 19-May-2000
C/Accession: I53672
R/Bogostan, G.; Bilyeu, K.; O'Neill, J.P.
Gene 133, 17-22, 1993
A/Title: Genome rearrangements by residual IS10 elements in strains of Escherichia coli
A/Reference number: I53672; MUID:94040791; PMID:8224890
A/Accession: I53672
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-20 <BOG>
A/Cross-references: GB:S67119; NID:9455674; PIDN:AA82847.1; PID:9455675
A/Note: partial sequence of bovine somatotropin synthesized and expressed in Escherichi

Query Match 21.7%; Score 25; DB 4; Length 20;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 AMSUDGCF 23
DB 4 AMSLSGLF 11

RESULT 13
S16073
alanine-tRNA ligase (EC 6.1.1.7) - rat (fragment)
N/Alternate names: alanyl-tRNA synthetase
C/Species: Rattus norvegicus (Norway rat)
C/Date: 19-Mar-1997 #sequence_revision 24-Oct-1998 #text_change 09-Jul-2004
C/Accession: S16073
R/Dignam, J.D.; Dignam, S.S.; Brumley, L.L.
Eur. J. Biochem. 198, 201-210, 1991
A/Title: Alanyl-tRNA synthetase from Escherichia coli, Bombyx mori and Rattus rattus. Exi
A/Reference number: S16072; MUID:91249799; PMID:2040280
A/Accession: S16073
A/Molecule type: protein
A/Residues: 1-21 <DIG>
A/Cross-references: UNIPROT:P50475
C/Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis

Query Match 21.7%; Score 25; DB 2; Length 21;
Best Local Similarity 55.6%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 G6ADAMSLD 20
DB 3 G6EDLIMLD 11

RESULT 14
S19015
hypothetical protein 11 ruvc-yebc intergenic region - Escherichia coli
C/Species: Escherichia coli
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: S19015

R:Sharples, G.J.; Lloyd, R.G.
J. Bacteriol. 173, 7711-7715, 1991
A>Title: Resolution of Holliday junctions in Escherichia coli: identification of the ruv
A/Reference number: S19013; MUID:92041688; PMID:1657895
A/Accession: S19015
A/Molecule type: DNA
A/Residues: 1-11 <SHA>
A/Cross-references: UNIPROT:Q47420; EMBL:X59551; NID:942172; PIDN:CAA42127.1; PID:942174
C/Comment: This is the hypothetical translation of a sequence that was not reported as a

Query Match 20.9%; Score 24; DB 4; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 AKINGEA 14
DB 4 AKQONGDA 11

RESULT 15

PH1172
T-cell receptor alpha chain V region (Cw3/Cas15) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1172
R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A>Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A/Reference number: S26512; MUID:92364546; PMID:1380061
A/Accession: PH1172
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>

Query Match 20.9%; Score 24; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DGGF 23
DB 5 DGGF 8

Search completed: November 1, 2005, 13:49:26
Job time : 39 secs


```
RL Mol. Biol. Evol. 19:1272-1287(2002).
DR EMBL; AF488855; AANI17030.1; -.
DR EMBL; AF488871; AANI17040.1; -.
DR EMBL; AF488879; AANI17045.1; -.
DR EMBL; AF488887; AANI17050.1; -.
DR EMBL; AF488895; AANI17055.1; -.
DR EMBL; AF488903; AANI17060.1; -.
DR EMBL; AF488911; AANI17065.1; -.
DR EMBL; AF488919; AANI17071.1; -.
DR EMBL; AF488927; AANI17076.1; -.
DR EMBL; AF488935; AANI17081.1; -.
DR EMBL; AF488943; AANI17086.1; -.
DR EMBL; AF488951; AANI17091.1; -.
DR EMBL; AF488959; AANI17095.1; -.
DR EMBL; AF488967; AANI17101.1; -.
DR EMBL; AF488975; AANI17106.1; -.
DR EMBL; AF488983; AANI17111.1; -.
DR EMBL; AF488991; AANI17116.1; -.
DR EMBL; AF488999; AANI17121.1; -.
DR EMBL; AF489007; AANI17126.1; -.
DR EMBL; AF489015; AANI17131.1; -.
DR EMBL; AF489023; AANI17136.1; -.
DR EMBL; AF489031; AANI17141.1; -.
DR EMBL; AF489039; AANI17146.1; -.
DR EMBL; AF489047; AANI17151.1; -.
DR EMBL; AF489055; AANI17156.1; -.
DR EMBL; AF489063; AANI17161.1; -.
DR EMBL; AF489071; AANI17166.1; -.
DR EMBL; AF489079; AANI17171.1; -.
DR EMBL; AF489087; AANI17176.1; -.
DR EMBL; AF489095; AANI17181.1; -.
DR EMBL; AF488863; AANI17035.1; -.
FT NON_TER
SQ SEQUENCE 12 AA; 1231 MW; 8C2833524BA05DDA CRC64;

Query Match          34.8%; Score 40; DB 2; Length 12;
Best Local Similarity 70.0%; Pred. No. 31;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 13 EADAMSLDGG 22
DB 3 EADAITVDGG 12

RESULT 3
Q38573 PRELIMINARY; PRT; 18 AA.
ID Q38573;
AC Q38573;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Coat protein (fragment).
OS Bacteriophage KUI.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Levivirinae.
OX NCB1_TaxID=12021;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96207403; PubMed=8615017; DOI=10.1006/viro.1996.0174;
RA Groenewald H., Oudot F., van Duin J.V.;
RA "RNA phage KUI has an insertion of 18 nucleotides in the start codon
RT of its lysate gene.";
RL Virology 218:141-147(1996).
DR EMBL; S81763; AADI4371.1; -.
DR HSSP; P07238; IUNA..
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
KW Coat protein.
FT NON_TER
SQ SEQUENCE 18 AA; 1825 MW; 2D4092DC26D8904 CRC64;

Query Match          32.2%; Score 37; DB 2; Length 18;
```

```
Best Local Similarity 56.2%; Pred. No. 1.4e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 8 KIMGEADAMSLDGGF 23
DB 1 KIGNPVDAISQSGF 16

RESULT 4
Q9QVF4 PRELIMINARY; PRT; 8 AA.
ID Q9QVF4;
AC Q9QVF4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE TRANSFERRIN=PEPTIDE 60 (fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCB1_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92165927; PubMed=1791188;
RA Cavanaugh P.G., Nicolson G.L.;
RT "Lung-derived growth factor that stimulates the growth of lung-
RT metastasizing tumor cells: identification as transferrin.";
RL J. Cell. Biochem. 47:261-271(1991).
FT NON_TER
SQ SEQUENCE 8 AA; 778 MW; 9D744735B69DDAAD CRC64;

Query Match          29.6%; Score 34; DB 2; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.6e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 ADAMSLDG 21
DB 1 ADAMSLING 8

RESULT 5
Q9UCF6 PRELIMINARY; PRT; 18 AA.
ID Q9UCF6;
AC Q9UCF6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE LOW-affinity Interleukin-4 receptor (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93271485; PubMed=8499634;
RA Benschow W.C., Spriggs M.K., Rauch C.T., Clifford K.N., Macduff B.M.,
RA Ziegler S.F., Schooley K.A., Mohler K.M., March C.J., Armitage R.J.;
RT "Identification of a distinct low-affinity receptor for human
RT interleukin-4 on pre-B cells.";
RL Blood 81:2998-3005(1993).
SQ SEQUENCE 18 AA; 1853 MW; F047PBA0F773B5A5 CRC64;

Query Match          24.3%; Score 28; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 3.6e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 14 ADAMSLDG 21
DB 11 SDLSLDG 18

RESULT 6
Q6S8FO
```

```

ID 0688F0 PRELIMINARY; PRT; 21 AA.
AC 0688F0;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Putative 26S proteasome regulatory subunit 8 (Fragment).
OS Musa acuminata (Banana).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
OC Musa.
OC NCBI_TaxID=4641;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pulp;
RA Baezot W.A., do Nascimento J.R.O., Lajolo F.M., Purgatto E.;
RA Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY63021; AAR88784.1; -
DR GO; GO:0005829; Cytoisol; IEA.
KM Proteasome.
FT NON TER
SQ SEQUENCE 21 AA; 2519 MW; E877B80AC269BA4E CRC64;

Query Match 23.9%; Score 27.5; DB 2; Length 21;
Best Local Similarity 43.8%; Pred. No. 5.1e+03;
Matches 7; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 5 SIANKNGEADA-MSL 19
DB 1 AVAKVMKETEKNMSL 16

RESULT 7
ID 06PAJ9 PRELIMINARY; PRT; 12 AA.
AC 06PAJ9;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE D1Wsu47e protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywicki M.I., Skelton U., Smalins D.E., Schenck A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RA Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RA EMBL; BC060257; AAH60257.1; -

```

```

SQ SEQUENCE 12 AA; 1262 MW; DFE49D95A4D33DC2 CRC64;

Query Match 23.5%; Score 27; DB 2; Length 12;
Best Local Similarity 54.5%; Pred. No. 3.3e+03;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 9 IMGEADAMSL 19
DB 1 MLNSVAKAMSL 11

RESULT 8
ID 07RLN8 PRELIMINARY; PRT; 19 AA.
AC 07RLN8;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
OS Name=PY02502;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OC NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XN1;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Anguioni S.V., Suh B.B., Kool J.T.W., Perlea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmiller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabli A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAL0100686; EAA21950.1; -
KM Hypothetical protein.
FT NON TER
SQ SEQUENCE 19 AA; 2174 MW; 42DBA0B172A783F CRC64;

Query Match 23.5%; Score 27; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 5.5e+03;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTEDSIKANG 12
DB 2 TTTEAIKANG 13

RESULT 9
ID 09K9B3 PRELIMINARY; PRT; 22 AA.
AC 09K9B3;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE BH2736 protein.
GN OrderedLocNames=BH2736;
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC NCBI_TaxID=8665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125;
RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;

```

RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaaki R., Masui N.,
 RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium *Bacillus*
 RT *halodurans* and genomic sequence comparison with *Bacillus subtilis*.";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL; AF001516; BAB06455.1; -.
 DR PIR; H83991; H83991.
 KM Complete proteome.
 SQ SEQUENCE 22 AA; 2527 MW; 471D4FD20D09C39 CRC64;

Query Match 23.5%; Score 27; DB 2; Length 22;
 Best Local Similarity 31.2%; Pred. No. 6.4e+03;
 Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 DSIKXIMGEADMSL 19
 DB 7 ETIKKLMEGIFDVATI 22

RESULT 10
 ID Q801G7 PRELIMINARY; PRT; 12 AA.
 AC Q801G7;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Mini-cistron protein.
 OS *Choristoneura fumiferana* nuclear polyhedrosis virus (CFNPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=208973;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX Pubmed=14671115; DOI=10.1128/JVI.78.1.329-339.2004;
 RA Chen T., Sahni D., Carstens E.B.;
 RT "Characterization of the interaction between P143 and Lef-3 from two
 RT different baculovirus species: *Choristoneura fumiferana*
 RT nucleopolyhedrovirus Lef-3 can complement *Autographa californica*
 RT nucleopolyhedrovirus Lef-3 in supporting DNA replication.";
 RL J. Virol. 78:329-339(2004).
 DR EMBL; AF127530; AAF36457.1; -.
 SQ SEQUENCE 12 AA; 1252 MW; C878D87A88B2CDD9 CRC64;

Query Match 22.6%; Score 26; DB 2; Length 12;
 Best Local Similarity 80.0%; Pred. No. 4.7e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 19 LDGDF 23
 DB 1 MDGDF 5

RESULT 11
 ID Q798V0 PRELIMINARY; PRT; 14 AA.
 AC Q798V0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE g1PT and g1PQ genes for glycerol 3-phosphate permease and
 DE glycerophosphoryl diester phosphodiesterase (Fragment).
 OS *Bacillus subtilis*.
 OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BR95;
 RX MEDLINE=94282317; Pubmed=8012593;
 RA Nilsson R.P., Beijer L., Rutberg B.;
 RT "The g1PT and g1PQ genes of the glycerol regulon in *Bacillus*
 RT *subtilis*.";
 RL Microbiology 140:723-730(1994).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BR95;
 RA Nilsson R.;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ database.
 DR EMBL; Z26522; CAA81293.1; -.
 DT NON TER 1
 SQ SEQUENCE 14 AA; 1416 MW; 801FFDSFF58E05 CRC64;

Query Match 22.6%; Score 26; DB 2; Length 14;
 Best Local Similarity 33.3%; Pred. No. 5.6e+03;
 Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 8 KIMGEADA 16
 DB 1 QILNGSEA 9

RESULT 12
 ID FIBA_CERAE STANDARD; PRT; 16 AA.
 AC P681I2; P12803;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
 GN Name=FGA;
 OS *Cercopithecus aethiops* (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE.
 RA Blomback B., Blomback M., Gron Dahl N.J., Guthrie C., Hinton M.;
 RT "Studies on fibrinopeptides from primates.";
 RL Acta Chem. Scand. 19:1788-1789(1965).
 CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
 CC polymerize into fibrin and acting as a cofactor in platelet
 CC aggregation.
 CC SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
 CC (alpha, beta and gamma), linked to each other by disulfide bonds.
 CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 CC which cleaves fibrinopeptides A and B from alpha and beta chains,
 CC and thus exposes the N-terminal polymerization sites responsible
 CC for the formation of the soft clot.
 KW Blood coagulation; Direct protein sequencing; Plasma.
 FT NON TER 16
 FT PEPTIDE 1
 FT FIBRINOPEPTIDE A.
 SQ SEQUENCE 16 AA; 1551 MW; 49E8CBB63EA04DD3 CRC64;

Query Match 22.6%; Score 26; DB 1; Length 16;
 Best Local Similarity 45.5%; Pred. No. 6.5e+03;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 12 GEADMSLDG 22
 DB 4 GEGDFLAEGG 14

RESULT 13
 ID FIBA_ERYPA STANDARD; PRT; 16 AA.
 AC P681I2; P12803;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
 GN Name=FGA;
 OS *Erythrocybus patas* (Red guenon) (Cercopithecus patas).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Erythrocybus.

OX NCBI_TaxID=9538;
RP SEQUENCE
RX MEDLINE=85289140; Pubmed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.,
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas
monkey (Erythrocebus patas): their amino acid sequences, restricted
RT mutations, and a molecular phylogeny for macaques, guenons, and
baboons";
RL Blochem. 97:1487-1492(1985).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC (alpha, beta and gamma), linked to each other by disulfide bonds.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
DR PIR; B24180; B24180.
KM Blood coagulation; Direct protein sequencing; Plasma.
FT PEPTIDE 1 16 Fibrinopeptide A.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1551 MW; 4988CB63EA04DD3 CRC64;

Query Match 22.6%; Score 26; DB 1; Length 16;
Best local Similarity 45.5%; Pred. No. 6.5e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 12 GEADAMSLDGG 22
Db 4 GEGDPLAEGGG 14

RESULT 14
FIBA_MACFA STANDARD; PRT; 16 AA.
AC P68109; P12803;
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN Name=FGA;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN 1)
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
RT "Studies on fibrinopeptides from primates.";
RL Acta Chem. Scand. 19:1788-1789(1965).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC (alpha, beta and gamma), linked to each other by disulfide bonds.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
KM Blood coagulation; Direct protein sequencing; Plasma.
FT PEPTIDE 1 16 Fibrinopeptide A.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1551 MW; 4988CB63EA04DD3 CRC64;

Query Match 22.6%; Score 26; DB 1; Length 16;
Best local Similarity 45.5%; Pred. No. 6.5e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 12 GEADAMSLDGG 22

Db 4 GEGDPLAEGGG 14

RESULT 15
FIBA_MACFU STANDARD; PRT; 16 AA.
AC P68109; P12803;
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN Name=FGA;
OS Macaca fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9543;
RN 1)
RP SEQUENCE.
RX MEDLINE=85289140; Pubmed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.,
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas
monkey (Erythrocebus patas): their amino acid sequences, restricted
RT mutations, and a molecular phylogeny for macaques, guenons, and
baboons";
RL Blochem. 97:1487-1492(1985).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
CC (alpha, beta and gamma), linked to each other by disulfide bonds.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
DR PIR; A24180; A24180.
KM Blood coagulation; Direct protein sequencing; Plasma.
FT PEPTIDE 1 16 Fibrinopeptide A.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1551 MW; 4988CB63EA04DD3 CRC64;

Query Match 22.6%; Score 26; DB 1; Length 16;
Best local Similarity 45.5%; Pred. No. 6.5e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 12 GEADAMSLDGG 22
Db 4 GEGDPLAEGGG 14

Search completed: November 1, 2005, 13:52:20
Job time : 169 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:28:13 ; Search time 85.8088 Seconds
(without alignments)
67.608 Million cell updates/sec

Title: US-10-612-162A-3

Perfect score: 74

Sequence: 1 SKLSMGSGLNLESPN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	15	8	ADG46077 Human CDT
2	65	87.8	13	8	ADG46094 Human CDT
3	60	81.1	42	8	ADH89392 Human tra
4	60	81.1	42	8	ADK15881 Human tra
5	60	81.1	328	4	AAB84371 Human tra
6	60	81.1	575	6	ABR82321 Human met
7	60	81.1	609	8	ABM83782 Human dia
8	60	81.1	627	8	ABM83781 Human dia
9	60	81.1	628	8	ABM83779 Human dia
10	60	81.1	643	8	ABM83778 Human dia
11	60	81.1	645	8	ABM83783 Human dia
12	60	81.1	646	4	AAU02938 Angiogens
13	60	81.1	646	4	ABM83780 Human dia
14	60	81.1	665	4	AAU02937 Angiogens
15	60	81.1	679	6	ABP72820 Human tra
16	60	81.1	679	8	ADH89360 Human tra
17	60	81.1	679	8	ADK15869 Mature hu
18	60	81.1	679	8	ADL17032 Human tra
19	60	81.1	679	8	ADL24413 Human tra
20	60	81.1	698	2	AAR12499 Human tra
21	60	81.1	698	2	AAR66492 Human tra
22	60	81.1	698	2	AAW54354 Secretans
23	60	81.1	698	3	AAI50717 Human ser
24	60	81.1	698	6	ABP72819 Human tra
25	60	81.1	698	7	ADD45282 Human Pro

ALIGNMENTS

26	60	81.1	698	7	ADP74796	ADP74796 Human NOV
27	60	81.1	698	7	ADP74800	ADP74800 Human NOV
28	60	81.1	698	8	ADH34559	ADH34559 Human tra
29	60	81.1	698	8	ADH89359	ADH89359 Human tra
30	60	81.1	698	8	ADK15868	ADK15868 Human tra
31	60	81.1	698	8	ADL70731	ADL70731 Human tra
32	60	81.1	698	8	ADL24412	ADL24412 Human tra
33	60	81.1	698	8	ADP21259	ADP21259 Human tra
34	60	81.1	1074	2	AAW07621	AAW07621 LDR/TF c
35	60	81.1	1418	4	AAU32831	AAU32831 Novel hum
36	60	81.1	1418	6	ABU04138	ABU04138 Human exp
37	57	77.0	1410	2	AAW07622	AAW07622 LDR/TF c
38	57	77.0	1410	6	ABU04139	ABU04139 Human exp
39	55	74.3	15	8	ADR15909	ADR15909 Transferr
40	55	74.3	15	8	ADR15970	ADR15970 Transferr
41	55	74.3	15	8	ADS13393	ADS13393 Human the
42	55	74.3	15	8	ADS13389	ADS13389 Human the
43	55	74.3	26	8	ADS13223	ADS13223 Human the
44	52	70.3	696	1	AAW0384	AAW0384 Sequence
45	46	62.2	823	6	ABR43160	ABR43160 Candida a

RESULT 1
ADG46077 standard; peptide, 15 AA.
ID ADG46077;
AC ADG46077;
AC ADG46077;
DT 25-MAR-2004 (first entry)
XX XX
DE Human CDT peptide fragment #3.
XX XX
KW antibody; carbohydrate-deficient transferrin; CDT;
KM non-glycosylated transferrin; alcoholic; diagnosis; human.
XX XX
OS Homo sapiens.
XX XX
PN EP1378521-A1.
XX XX
PD 07-JAN-2004.
XX XX
PF 19-MAY-2003; 2003EP-00011334.
XX XX
PR 05-JUL-2002; 2002DE-01030550.
XX XX
PA (DADE-) DADE BEHRING MARBURG GMBH.
XX XX
PI Althaus H;
XX XX
DR WPI; 2004-073743/08.
XX XX
PT New antibody specific for carbohydrate-deficient transferrin, useful for
PT diagnosis of alcoholism, can bind its target in solution, eliminating
PT need for immobilization.
XX XX
PS Claim 4; SEQ ID NO 3; 21pp; German.
XX XX
XX This invention describes a novel antibody that, in aqueous solution,
XX binds selectively to carbohydrate-deficient transferrin (CDT) without
XX having to bind CDT to a solid phase. The invention also describes an
XX antibody that binds selectively to CDT at regions containing the
XX sequences VVARSMGKEDILWELL, TTEDSIKAKIMNGEADAWSLDGGF, SKLSMGSGLNLESPN and
XX YEKYGEDEVKAV (ADG46075-ADG46078) and an immunoassay for detecting CDT
XX using the antibodies of the invention. The antibodies of the invention
XX are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
XX antibodies are obtained by immunisation with non-glycosylated
XX transferrin, or a fragment, then generation of hybridomas by standard
XX fusion of spleen and myeloma cells. Hybridomas are then selected for
XX production of antibodies that specifically bind CDT from the aqueous
XX phase. The antibodies are useful for diagnosis of alcoholism, CDT, which

CC lacks glycosylation at Asn413 and/or Asn 611. is present only in
CC alcohols. The antibodies allow direct detection of CDT in solution,
CC eliminating the need for immobilising it on a solid phase (as required
CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
CC fragments used in the method of the invention.

CC Sequence 15 AA;

Query Match 100.0%; Score 74; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLSMGSLNLSSEPN 15
| | | | | | | | | | | | | | | | |
Db 1 SKLSMGSLNLSSEPN 15

RESULT 2
ADG46094
ID ADG46094 standard; peptide; 13 AA.

AC ADG46094;

DT 25-MAR-2004 (first entry)

DE Human CDT peptide fragment #20.

KM antibody; carbohydrate-deficient transferrin; CDT;
KW non-glycosylated transferrin; alcoholism; alcoholic; diagnosis; human.

OS Homo sapiens.

PN EPI378521-A1.

PD 07-JAN-2004.

PF 19-MAY-2003; 2003EP-00011334.

PR 05-JUL-2002; 2002DE-01030550.

PA (DADE-) DADE BEHRING MAREBURG GMBH.

PI Althaus H;

DR WPI; 2004-073743/08.

PT New antibody specific for carbohydrate-deficient transferrin, useful for
PT diagnosis of alcoholism, can bind its target in solution, eliminating
PT need for immobilization.

PS Example 7; Page 15; 21pp; German.

CC This invention describes a novel antibody that, in aqueous solution,
CC binds selectively to carbohydrate-deficient transferrin (CDT) without
CC having to bind CDT to a solid phase. The invention also describes an
CC antibody that binds selectively to CDT at regions containing the
CC sequences VVARSMGKEDIVL, TTEDSYAKINMGADMSLDGF, SKLSMGSLNLSSEPN and
CC YKRTGSEYVAV (ADG46075-ADG46078) and an immunoassay for detecting CDT
CC using the antibodies of the invention. The antibodies of the invention
CC are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
CC antibodies are obtained by immunisation with non-glycosylated
CC transferrin, or a fragment, then generation of hybridomas by standard
CC fusion of spleen and myeloma cells. Hybridomas are then selected for
CC production of antibodies that specifically bind CDT from the aqueous
CC phase. The antibodies are useful for diagnosis of alcoholism, CDT, which
CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
CC alcohols. The antibodies allow direct detection of CDT in solution,
CC eliminating the need for immobilising it on a solid phase (as required
CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
CC fragments used in the method of the invention.

XX Sequence 13 AA;

Query Match 87.8%; Score 65; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LSMGSLNLSSEPN 15
| | | | | | | | | | | | | | | | |
Db 1 LSMGSLNLSSEPN 13

RESULT 3
ADH89392
ID ADH89392 standard; protein; 42 AA.

AC ADH89392;

DT 15-APR-2004 (first entry)

DE Human transferrin protein domain SegID36.

KM fusion protein; transferrin protein; glycosylation;
KW antibody variable region; cytotatic; antibacterial; virucide;
KW antiparasitic; immunosuppressive; antiarthritic; gene therapy;
KW septic shock; endotoxic shock; cachexia syndrome; bacterial infection;
KW viral infection; parasitic infection; neoplasm; autoimmune disease;
KW arthritis; graft rejection; human.

OS Homo sapiens.

PN US2003226155-A1.

PD 04-DEC-2003.

PF 10-MAR-2003; 2003US-00384060.

PR 30-AUG-2001; 2001US-0315745P.

PR 30-NOV-2001; 2001US-0334059P.

PR 30-AUG-2002; 2002US-00231494.

PR 30-AUG-2002; 2002US-0406977P.

PA (BIOR-) BIOREXIS PHARM CORP.

PI Sadeghi H, Prior CP, Turner A;

DR WPI; 2004-022093/02.

PT New fusion protein comprising a transferrin protein exhibiting reduced
PT glycosylation fused to at least one antibody variable region, useful for
PT preparing a composition for treating e.g., septic shock, neoplasm or
PT autoimmune disease.

PS Example 2; SEQ ID NO 36; 82pp; English.

CC This invention relates to a novel fusion protein which comprises a
CC transferrin protein exhibiting reduced glycosylation fused to at least
CC one antibody variable region. The invention may be useful for the
CC development of compounds with cytostatic, antibacterial, virucide,
CC antiparasitic, immunosuppressive or antiarthritic activity. In addition,
CC the sequences disclosed may be useful for gene therapy. The fusion
CC protein is useful for preparing a composition for treating a disease or
CC disease symptom in a patient for example septic shock, endotoxic shock,
CC cachexia syndrome associated with bacterial, viral or parasitic
CC infections, neoplasm, autoimmune disease, arthritis or adverse effects
CC associated with treatment for preventing graft rejection. The present
CC sequence is that of a domain of the human transferrin protein which was
CC used in the exemplification of the invention.

XX Sequence 42 AA;

Query Match 81.1%; Score 60; DB 8; Length 42;
Best Local Similarity 85.7%; Pred. No. 0.0035;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMGSLNLSSEPN 15

Db 25 KLCWGSGLNLCERN 38

RESULT 4
ADK15881
ID ADK15881 standard; protein: 42 AA.

XX ADK15881,
XX
XX
XX 06-MAY-2004 (first entry)

XX Human transferrin (Tf) protein fragment #3.

XX fusion protein; transferrin; Tf; beta-interferon; beta-IFN;
XX glucagon-like peptide; GLP-1; erythropoietin mimetic peptide; EMP1;
XX T-20; soluble toxin receptor; epitope tagging; human.

XX Homo sapiens.

XX US2003221201-A1.

XX 27-NOV-2003.

XX 04-MAR-2003; 2003US-00378094.

XX 30-AUG-2001; 2001US-0315745P.

XX 30-NOV-2001; 2001US-0314059P.

XX 30-AUG-2002; 2002US-00231494.

XX 30-AUG-2002; 2002US-0406977P.

XX (BIOREX-) BIOREXIS PHARM CORP.

XX Prior CP, Lai C, Sadeghi H, Turner A;

XX WPI; 2004-010899/01.

XX New fusion protein comprising a modified transferrin (Tf) protein fused
XX to a therapeutic protein or peptide, useful for epitope tagging.

XX Example 5; SEQ ID NO 15; 70pp; English.

XX The invention comprises a fusion protein that contains a modified
XX transferrin (Tf) protein fused to a therapeutic protein/peptide (e.g.

XX beta-interferon - IFN, glucagon-like peptide - GLP-1, erythropoietin
XX mimetic peptide - EMP1, T-20 and soluble toxin receptor). The fusion
XX protein of the invention is useful for epitope tagging. The present amino
XX acid sequence represents a fragment of the human Tf protein.

XX Sequence 42 AA;

Query Match 81.1%; Score 60; DB 8; Length 42;
Best Local Similarity 85.7%; Pred. No. 0.0035;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLCWGSGLNLCERN 15
DB 25 KLCWGSGLNLCERN 38

RESULT 5
AAB84371
ID AAB84371 standard; protein: 328 AA.

XX AAB84371;

XX 22-AUG-2001 (first entry)

XX Amino acid sequence of a human transferrin.

XX Human; transferrin; autoimmune disease; rheumatoid arthritis;

XX hyperproliferative disorder; neoplasm; cardiovascular disorder;

XX cardiac arrest; cerebrovascular disorder; cerebral ischemia;

KW angiogenesis; nervous system disorder; Alzheimer's disease; infection;
KW ocular disorder; corneal infection; wound healing;
KW epithelial cell proliferation; aging; organ transplant.

XX Homo sapiens.

XX WO200146254-A1.

XX 28-JUN-2001.

XX 21-DEC-2000; 2000WO-US034769.

XX 23-DEC-1999; 99US-0171595P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Shi Y, Choi GH;

XX WPI; 2001-381910/40.

XX N-PSDB; AAH25190.

XX Isolated nucleic acid molecule encoding a human transferrin protein is
XX used in preventing, treating or ameliorating a medical condition.

XX Claim 11; Page 286-287; 290pp; English.

XX The present sequence represents human transferrin polypeptide.

XX Transferrin polypeptides and polynucleotides are used to prevent, treat
XX or ameliorate a medical condition in e.g. humans, mice, rabbits, goats,
XX horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or
XX treated include autoimmune diseases e.g. rheumatoid arthritis,

XX hyperproliferative disorders e.g. neoplasms of the breast or liver,
XX cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
XX e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.

XX Alzheimer's disease, infections caused by bacteria, viruses and fungi and
XX ocular disorders e.g. corneal infection. The polypeptides can also be
XX used to aid wound healing and epithelial cell proliferation, to prevent

XX skin aging due to sunburn, to maintain organs before transplantation, for
XX supporting cell culture of primary tissues, to regenerate tissues and in
XX chemotaxis. The polypeptides can also be used as a food additive or

XX preservative to increase or decrease storage capabilities

XX Sequence 328 AA;

Query Match 81.1%; Score 60; DB 4; Length 328;
Best Local Similarity 85.7%; Pred. No. 0.035;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLCWGSGLNLCERN 15
DB 179 KLCWGSGLNLCERN 192

RESULT 6
ABR82321
ID ABR82321 standard; protein: 575 AA.

XX ABR82321;

XX 06-NOV-2003 (first entry)

XX Human metalloprotein (MEPR) polypeptide (td-7509328CD1).

XX MEPR; metalloprotein; anti-HIV; antiallergic; antiinflammatory; human;

XX antianemic; antiparkinsonian; nootropic; anticonvulsant; cytoskeletal;

XX antiarteriosclerotic; antiaschemic; immunosuppressive; antithyroid;

XX hepatotropic; dermatological; antidiabetic; nephrotropic; antigout;

XX thymotropic; neuroprotective; osteoprotective; antiarthritic; uropathic;

XX antiparasitic; antihelminthic; antiparasitic; ophthalmological; vitruclide;

XX antineumatic; haemostatic; antibacterial; protozoacide; fungicide;

XX gene therapy; transgenic.

XX Homo sapiens.

```

XX PN WO2003060089-A2.
XX XX
XX PD 24-JUL-2003.
XX XX
XX PF 14-JAN-2003; 2003WO-US001485.
XX XX
XX PR 14-JAN-2002; 2002US-0348769P.
XX PR 18-JAN-2002; 2002US-0350701P.
XX PR 19-MAR-2002; 2002US-0366059P.
XX PR 10-MAY-2002; 2002US-0379907P.
XX PA
XX PA (INCY-) INCYTE GENOMICS INC.
XX XX
XX PI Kable AE, Griffin JA, Gorvad AE, Becha SD, Richardson TW;
XX PI Emerling BM, Chien D, Jin P, Chawla NK, Yue H, Khare R, Margulis JP;
XX PI Tang YT;
XX DR WPI; 2003-598523/56.
XX DR N-PSDB; ACF35812.
XX XX
XX PT New human metalloproteins and polynucleotides, useful for diagnosing,
XX PT treating or preventing autoimmune or inflammatory disorders (e.g. AIDS,
XX PT allergy or anemia), multiple sclerosis, osteoarthritis, cancer or
XX PT hepatitis.
XX PS Claim 1; Page 146-148; 153pp; English.
XX XX
XX CC The invention relates to novel human metalloproteins (MEPR) and encoding
XX CC polynucleotides. The human MEPR polypeptides, polynucleotides and
XX CC modulators are useful for diagnosing, treating or preventing disorders
XX CC associated with aberrant expression of MEPR, particularly cell
XX CC proliferative disorders (e.g. arteriosclerosis, atherosclerosis,
XX CC cirrhosis, hepatitis, paroxysmal nocturnal hemoglobinuria, polycythemia
XX CC vera, porphyria, primary thrombocytopenia or cancer), developmental
XX CC disorders (e.g. renal tubular acidosis, anemia or mental retardation),
XX CC neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or
XX CC epilepsy), autoimmune/inflammatory disorders (e.g. AIDS, allergies,
XX CC asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease,
XX CC diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout,
XX CC Graves' disease, Hashimoto's thyroiditis, irritable bowel syndrome,
XX CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's
XX CC syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,
XX CC bacterial, fungal, parasitic, protozoan or helminthic infections. The
XX CC polynucleotides encoding MEPR are useful for creating transgenic animals
XX CC to model human disease. Sequences ABR82316-323 represent the human MEPR
XX CC polypeptides of the invention
XX SQ
XX Sequence 575 AA;
XX
XX Query Match 81.1%; Score 60; DB 6; Length 575;
XX Best Local Similarity 85.7%; Pred. No. 0.065;
XX Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 KLSMGSGLNLSEPN 15
XX Db 392 KLCMGSGLNLCEPN 405
XX
XX RESULT 7
XX ABR83782
XX ID ABR83782 standard; protein; 609 AA.
XX XX
XX AC ABR83782;
XX XX
XX DT 18-NOV-2004 (first entry)
XX XX
XX DE Human diagnostic and therapeutic pproteins SEQ ID NO:4031.
XX XX
XX KM gene therapy; human diagnostic and therapeutic polynucleotide; dthp.
XX XX
XX OS Homo sapiens.
XX XX

```

```

PN PN WO2004023973-A2.
XX XX
XX PD 25-MAR-2004.
XX XX
XX PF 12-SEP-2003; 2003WO-US028227.
XX XX
XX PR 12-SEP-2002; 2002US-0410259P.
XX PR 12-SEP-2002; 2002US-0410260P.
XX XX
XX PA (INCY-) INCYTE CORP.
XX XX
XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
XX PI Harshborne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV;
XX PI Mooney EM, Deleagane AM, Panesar IS, Banville SC, Reddy TP;
XX PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gershin EH;
XX PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve IL;
XX PI Lagae RE, Spiro PA, Stewart EA, Wingrove J, Viltz UA, Kirton ES;
XX PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
XX PI Patury S, Shi X, Suarez CJ;
XX DR WPI; 2004-329368/30.
XX DR N-PSDB; ACN42434.
XX XX
XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
XX PT in diagnosing a condition, disease or disorder associated with human
XX PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
XX PT in gene mapping.
XX PS Claim 27; Page; 190pp; English.
XX XX
XX CC The invention relates to novel diagnostic and therapeutic polynucleotides
XX CC selected from one of the 2722 sequences defined in the specification. A
XX CC polynucleotide of the invention may have a use in gene therapy. The human
XX CC polynucleotide and therapeutic polynucleotides (dthp) or polypeptides may be
XX CC used to diagnose a particular condition, disease or disorder associated
XX CC with human molecules, e.g. cell proliferative disorders,
XX CC autoimmune/inflammatory disorder, developmental disorder, endocrine
XX CC disorder, neurological disorders, gastrointestinal disorders, or
XX CC infections caused by virus, bacteria, fungi or parasite. The dthp
XX CC molecules may also be used in genetic mapping, in identifying individuals
XX CC from minute biological samples, in detecting single nucleotide
XX CC polymorphisms, as molecular weight markers, and for somatic or germline
XX CC gene therapy. The present sequence represents a dthp protein of the
XX CC invention. Note: The sequence data for this patent is not represented in
XX CC the printed specification, but was obtained in electronic format directly
XX CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX SQ
XX Sequence 609 AA;
XX
XX Query Match 81.1%; Score 60; DB 8; Length 609;
XX Best Local Similarity 85.7%; Pred. No. 0.07;
XX Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 KLSMGSGLNLSEPN 15
XX Db 444 KLCMGSGLNLCEPN 457
XX
XX RESULT 8
XX ABR83781
XX ID ABR83781 standard; protein; 627 AA.
XX XX
XX AC ABR83781;
XX XX
XX DT 18-NOV-2004 (first entry)
XX XX
XX DE Human diagnostic and therapeutic pproteins SEQ ID NO:4030.
XX XX
XX KM gene therapy; human diagnostic and therapeutic polynucleotide; dthp.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO2004023973-A2.
XX PN

```

XX 25-MAR-2004.
 PD 12-SEP-2003; 2003MO-US028227.
 XX 12-SEP-2002; 2002US-0410259P.
 PR 12-SEP-2002; 2002US-0410260P.
 XX (INCY-) INCYTE CORP.
 PA Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
 PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV,
 PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP,
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH,
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL,
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kitron ES,
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,
 PI Patury S, Shi X, Suarez CJ;
 XX WPI; 2004-329368/30.
 DR N-PSDB; ACN42433.
 XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 PS Claim 27, Page; 190pp; English.
 XX The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorder, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dithp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/11sting.htm
 CC SQ
 XX Sequence 627 AA;
 SQ
 Query Match 81.1%; Score 60; DB 8; Length 627;
 Best Local Similarity 85.7%; Pred. No. 0.072; Mismatches 2; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 KLSMGSGNLNLEPN 15
 Db 444 KLCMGSGNLNLEPN 457
 RESULT 9
 ABM83779
 ID ABM83779 standard; protein; 628 AA.
 XX
 AC ABM83779;
 DT 18-NOV-2004 (first entry)
 XX
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4028.
 XX
 KM gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
 XX
 OS Homo sapiens.
 XX
 PN WO2004023973-A2.
 XX

PD 25-MAR-2004.
 XX 12-SEP-2003; 2003MO-US028227.
 XX 12-SEP-2002; 2002US-0410259P.
 PR 12-SEP-2002; 2002US-0410260P.
 XX (INCY-) INCYTE CORP.
 PA Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
 PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV,
 PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP,
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH,
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL,
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kitron ES,
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,
 PI Patury S, Shi X, Suarez CJ;
 XX WPI; 2004-329368/30.
 DR N-PSDB; ACN42431.
 XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 PS Claim 27, Page; 190pp; English.
 XX The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorder, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dithp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/11sting.htm
 CC SQ
 XX Sequence 628 AA;
 SQ
 Query Match 81.1%; Score 60; DB 8; Length 628;
 Best Local Similarity 85.7%; Pred. No. 0.072; Mismatches 2; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 KLSMGSGNLNLEPN 15
 Db 463 KLCMGSGNLNLEPN 476
 RESULT 10
 ABM83778
 ID ABM83778 standard; protein; 643 AA.
 XX
 AC ABM83778;
 DT 18-NOV-2004 (first entry)
 XX
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4027.
 XX
 KM gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
 XX
 OS Homo sapiens.
 XX
 PN WO2004023973-A2.
 XX
 PD 25-MAR-2004.

XX 12-SEP-2003; 2003WO-US028227.
PF 12-SEP-2002; 2002US-0410259P.
XX 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
XX (INCY-) INCYTE CORP.
PA
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV,
PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP,
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH,
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL,
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Valt UA, Kirtton ES,
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,
PI Patursky S, Shi X, Suarez CJ,
XX
XX WPI; 2004-329368/30.
DR N-PSDB; ACN42430.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
XX Claim 27; Page; 190pp; English.
PS
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 643 AA;
Query Match 81.1%; Score 60; DB 8; Length 643;
Best Local Similarity 85.7%; Pred. No. 0.074;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 KLSMGSGLNLSEPN 15
Db 478 KLCMGSGLNLCEPN 491

RESULT 11
ABM83783
ID ABM83783 standard; protein; 645 AA.
XX
XX ABM83783;
AC
XX
XX 18-NOV-2004 (first entry)
DT
XX
XX Human diagnostic and therapeutic pproetin SEQ ID NO:4032.
DE
XX
XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
KM
XX
XX Homo sapiens.
OS
XX
XX MO2004023973-A2.
PN
XX
XX 25-MAR-2004.
PD
XX

PF 12-SEP-2003; 2003WO-US028227.
XX 12-SEP-2002; 2002US-0410259P.
XX 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
XX (INCY-) INCYTE CORP.
PA
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV,
PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP,
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH,
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL,
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Valt UA, Kirtton ES,
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,
PI Patursky S, Shi X, Suarez CJ,
XX
XX WPI; 2004-329368/30.
DR N-PSDB; ACN42435.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
XX Claim 27; Page; 190pp; English.
PS
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 645 AA;
Query Match 81.1%; Score 60; DB 8; Length 645;
Best Local Similarity 85.7%; Pred. No. 0.074;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 KLSMGSGLNLSEPN 15
Db 462 KLCMGSGLNLCEPN 475

RESULT 12
AAU02938
ID AAU02938 standard; protein; 646 AA.
XX
XX AAU02938;
AC
XX
XX 12-SEP-2001 (first entry)
DT
XX
XX Angiotensin converting enzyme (ACEV) splice variant protein #38.
DE
XX
XX Angiotensin converting enzyme splice variant; ACEV, interleukin 6;
KM granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KM platelet-derived endothelial cell growth factor; cardiovascular disease;
KM cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
KM vasorelaxant intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KM myocardial infarction; coronary arterial thrombosis; renal disease;
KM diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KM multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KM nonaroidotic pulmonary granulomatous disease; endothelial abnormality;
KM

KW vascular disorder; asbestosis.
 XX
 OS Homo sapiens.
 XX
 FN WO200136632-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 17-NOV-2000; 2000WO-IL000766.
 XX
 PR 17-NOV-1999; 99IL-00132978.
 PR 10-DEC-1999; 99IL-00133455.
 XX
 PA (COMP-) COMPUGEN LTD.
 XX
 PI Levine Z, David A, Azar I, Khosravi R, Bernstein J;
 XX
 DR WPI; 2001-336004/35.
 DR N-PSDB; AAS06038.
 XX
 PT Novel alternative splicing variants e.g. variant of angiotensin
 PT converting enzyme (ACEV), useful in identifying candidate compounds
 PT capable of binding to the variant and to detect anti-variant antibodies.
 XX
 PS Claim 4; Fig 38; 519pp; English.
 XX
 CC The sequence represents an angiotensin converting enzyme splice variant
 CC (ACEV) polypeptide. The polypeptides of the invention include variants of
 CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
 CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
 CC inhibitor 1C, cellular tumour antigen p53, and vasoactive intestinal
 CC polypeptide receptor 2. The polypeptides and their associated nucleic
 CC acids are useful for identification of variant sequences and detection of
 CC candidate compounds capable of binding the molecules. The sequences of
 CC the invention can be used in the treatment and diagnosis of various
 CC disorders including cardiovascular diseases such as arteriosclerosis,
 CC myocardial infarction and coronary arterial thrombosis, renal diseases
 CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
 CC immune disorders such as immune complex nephritis, multiple sclerosis,
 CC cancer, sarcoidosis, nonatrophic pulmonary granulomatous diseases such
 CC as asbestosis and vascular pathologies involving an endothelial
 CC abnormality such as deep vein thrombosis
 CC
 SO Sequence 646 AA;
 XX
 QY Query Match 81.1%; Score 60; DB 4; Length 646;
 Best Local Similarity 85.7%; Pred. No. 0.075;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 DB 2 KLSWGSGLINSEPN 15
 463 KLCWGSGLINCEPN 476

RESULT 13
 ABM83780
 ID ABM83780 standard; protein; 646 AA.
 XX
 AC ABM83780;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human diagnostic and therapeutic protein SEQ ID NO:4029.
 XX
 KW gene therapy; human diagnostic and therapeutic polynucleotide; dthp.
 XX
 OS Homo sapiens.
 XX
 PN WO2004023973-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 12-SEP-2003; 2003WO-US028227.

XX
 PR 12-SEP-2002; 2002US-0410259P.
 PR 12-SEP-2002; 2002US-0410260P.
 XX
 XX (INCY-) INCYTE CORP.
 XX
 PI Schmidt JP, Wright RJ, Brune CM, Marjanovic MM, Shen F;
 PI Harthorn TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV;
 PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
 PI Peralta CH, Anderson SB, Rieux P, Shen EJ, Wu MC, Stuve LU;
 PI Lagace RE, Spito PA, Stewart EA, Wingrove J, Vitt UA, Kirton BS;
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gierzen D;
 PI Patury S, Shi X, Suarez CJ;
 XX
 XX WPI; 2004-329368/30.
 DR N-PSDB; ACN42432.
 XX
 PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 XX
 PS Claim 27; Page; 190pp; English.
 XX
 CC The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders, endocrine
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorder, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dthp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dthp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/11sting.htm
 CC
 SO Sequence 646 AA;
 XX
 QY Query Match 81.1%; Score 60; DB 8; Length 646;
 Best Local Similarity 85.7%; Pred. No. 0.075;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 DB 2 KLSWGSGLINSEPN 15
 463 KLCWGSGLINCEPN 476

RESULT 14
 AAU02937
 ID AAU02937 standard; protein; 665 AA.
 XX
 AC AAU02937;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Angiotensin converting enzyme (ACEV) splice variant protein #37.
 XX
 KW Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
 KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
 KW platelet-derived endothelial cell growth factor; cardiovascular disease;
 KW cellular tumour antigen p53; cyclin-dependent kinase inhibitor 1C;
 KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
 KW myocardial infarction; coronary arterial thrombosis; renal disease;
 KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
 KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
 KW nonatrophic pulmonary granulomatous disease; endothelial abnormality;
 KW vascular disorder; asbestosis.

XX	OS	Homo sapiens.
XX	OS	WO200136632-A2.
XX	PN	
XX	PD	25-MAY-2001.
XX	PF	17-NOV-2000; 2000WO-IL000766.
XX	PR	17-NOV-1999; 99IL-00132978.
XX	PR	10-DEC-1999; 99IL-00133455.
XX	PA	(COMP-) COMPUGEN LTD.
XX	PI	Levine Z, David A, Azar I, Khosravi R, Bernstein J;
XX	DR	WPI; 2001-336004/35.
XX	DR	N-PSDB; AAS06037.
XX	PT	Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies.
XX	PT	
XX	PS	Claim 4; Fig 37; 519p; English.
XX	CC	The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen p53, and vasoreactive intestinal
XX	CC	inhibitor 2 receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding to the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases
XX	CC	such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, noncardiotoxic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial abnormality such as deep vein thrombosis
XX	CC	
XX	SQ	Sequence 665 AA;
XX		
XX	Query Match	81.1%; Score 60; DB 4; Length 665;
XX	Best Local Similarity	85.7%; Pred. No. 0.077;
XX	Matches 12; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
XX	QY	2 KLSMGSGLNLSFNN 15
XX		
XX	DB	515 KLSMGSGLNLSFNN 528
XX		
XX	RESULT 15	
XX	ABP72820	
XX	ID	ABP72820 standard; protein; 679 AA.
XX	XX	
XX	AC	ABP72820;
XX	DT	11-AUG-2003 (first entry)
XX	XX	
XX	DE	Human transferrin (mature polypeptide).
XX	XX	
XX	KW	Human; transferrin; neuroprotective; cerebroprotective; vasotropic; antiparkinsonian; nootropic; anti-HIV; antisthmatic; antiallergic; cytostatic; immunosuppressive; antithrombotic; cardiant;
XX	KW	gynaecological; immunostimulant; antinaeemic; haemostatic;
XX	KW	antiinflammatory; dermatological; antibacterial; virucide; antiparasitic; fungicide; hepatotropic; antirheumatic; antiarthritic; antignout;
XX	KW	craniallifer; vulnerary; antidiabetic; nephrotropic; antipyretic;
XX	KW	gastrointestinal; gene therapy; transgenic animal.
XX	OS	Homo sapiens

XX	Key	Location/Qualifiers
FH	Binding-site	63
FT		/note= "Iron binding site"
FT	Region	94. .96
FT		/note= "Hinge region"
FT	Binding-site	95
FT		/note= "Iron binding site"
FT	Binding-site	120
FT		/note= "Carbonate ion binding site"
FT	Binding-site	124
FT		/note= "Carbonate ion binding site"
FT	Binding-site	126
FT		/note= "Carbonate ion binding site"
FT	Binding-site	127
FT		/note= "Carbonate ion binding site"
FT	Binding-site	188
FT		/note= "Iron binding site"
FT	Region	245. .247
FT		/note= "Hinge region"
FT	Binding-site	249
FT		/note= "Iron binding site"
FT	Region	316. .318
FT		/note= "Hinge region"
FT	Binding-site	392
FT		/note= "Iron binding site"
FT	Modified-site	413
FT		/note= "N-glycosylated"
FT	Region	425. .427
FT		/note= "Hinge region"
FT	Binding-site	426
FT		/note= "Iron binding site"
FT	Binding-site	452
FT		/note= "Carbonate ion binding site"
FT	Binding-site	456
FT		/note= "Carbonate ion binding site"
FT	Binding-site	458
FT		/note= "Carbonate ion binding site"
FT	Binding-site	459
FT		/note= "Carbonate ion binding site"
FT	Binding-site	514
FT		/note= "Iron binding site"
FT	Binding-site	517
FT		/note= "Iron binding site"
FT	Region	581. .582
FT		/note= "Hinge region"
FT	Binding-site	585
FT		/note= "Iron binding site"
FT	Modified-site	611
FT		/note= "N-glycosylated"
FT	Region	652. .658
FT		/note= "Hinge region"
XX		
XX	WO2003020746-A1.	
XX		
PD	13-MAR-2003.	
XX		
PF	30-AUG-2002; 2002WO-US027637.	
XX		
PR	30-AUG-2001; 2001US-0315745P.	
PR	30-NOV-2001; 2001US-0334059P.	
XX		
PA	(BIOREXIS PHARM CORP.	
XX		
XX	Prior CP;	
PI		
XX		
DR	WPI; 2003-332916/31.	
XX		
PT	New fusion protein, useful in the diagnosis and treatment of diseases on	
PT	disorders relating to the respiratory, cardiovascular and digestive	
PT	systems, comprises a transferrin protein fused to a therapeutic protein.	
PS	Disclosure; Page 280-281; 298pp; English.	

XX The present sequence is the protein sequence of human transferrin (Tf),
 CC minus the signal peptide. The invention relates to modified Tf fusion
 CC proteins comprising at least one therapeutic protein, polypeptide or
 CC peptide, in which the Tf portion is engineered to extend the serum half-
 CC life or bioavailability of the molecule. The modified Tf fusion protein
 CC preferably comprises a human Tf moiety that has been modified to reduce
 CC or prevent glycosylation, iron binding and/or transferrin receptor
 CC binding, having at least one amino acid substitution, deletion or
 CC addition in the hinge region, or at residues Asp-63, Gly-65, Tyr-95, Tyr-
 CC 188, Lys-206, His-207, His-249, Asp-392, Tyr-426, Tyr-514, Tyr-517, His-
 CC 585, Thr-120, Arg-124, Ala-126, Gly-127, Thr-452, Arg-456, Ala-458 and
 CC Gly-459, or a mutation which prevents glycosylation at Asn-413 or Asn-611
 CC (all claimed). Nucleic acids encoding such fusion proteins, vectors, host
 CC cells and transgenic animals which produce the fusion protein in their
 CC serum or milk are also claimed. The modified fusion protein is useful for
 CC treating a disease or disease symptom, or for delivering a therapeutic
 CC agent complexed to the ferric iron of transferrin to the inside of a cell
 CC or across the blood-brain barrier. The modified fusion protein, or a
 CC nucleic acid encoding it, can be used in the diagnosis, prognosis, or a
 CC prevention and/or treatment of diseases and/or disorders of the
 CC endocrine, nervous, immune, respiratory, cardiovascular, reproductive and
 CC digestive systems, diseases and/or disorders relating to the blood or to
 CC cell proliferation, inflammatory conditions, and to treat viral, fungal,
 CC bacterial or parasitic infection
 CC
 XX
 SQ Sequence 679 AA;

Query Match 81.1%; Score 60; DB 6; Length 679;
 Best Local Similarly 85.7%; Pred. No. 0.079;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 KLSMGSGLNSEPN 15
 |||||||||
 DB 496 KLCMGSGLNLCPPN 509

Search completed: November 1, 2005, 12:48:53
 Job time : 86.8088 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:37:09 ; Search time 22.0588 Seconds
(without alignments)
50.761 Million cell updates/sec

Title: US-10-612-162A-3

Perfect score: 74

Sequence: 1 SKLMSGGLNLSEPN 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodaca/1/1aa/5A COMB pep:*
- 2: /cgn2_6/ptodaca/1/1aa/5B COMB pep:*
- 3: /cgn2_6/ptodaca/1/1aa/6A COMB pep:*
- 4: /cgn2_6/ptodaca/1/1aa/6B COMB pep:*
- 5: /cgn2_6/ptodaca/1/1aa/PTUS COMB pep:*
- 6: /cgn2_6/ptodaca/1/1aa/backfile1 pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	81.1	698	2	US-08-175-158A-2
2	60	81.1	698	4	US-09-439-740-2
3	60	81.1	1074	2	US-08-470-058-2
4	60	81.1	1074	3	US-09-037-188-2
5	60	81.1	1074	3	US-09-285-310-2
6	60	81.1	1410	2	US-08-470-058-4
7	60	81.1	1410	3	US-09-037-188-4
8	60	81.1	1410	3	US-09-285-310-4
9	52	70.3	696	6	5262177-4
10	52	70.3	696	6	5262177-4
11	46	62.2	439	4	US-09-248-796A-15968
12	43	58.1	1969	4	US-09-418-710-72
13	43	58.1	1969	4	US-09-839-479-71
14	43	58.1	1972	4	US-09-418-710-21
15	43	58.1	1972	4	US-09-839-479-21
16	41	55.4	148	4	US-09-711-164-464
17	41	55.4	884	4	US-09-248-796A-20574
18	40.5	54.7	504	4	US-09-469-039A-11966
19	40	54.1	125	3	US-08-480-173A-50
20	40	54.1	125	3	US-08-484-408A-50
21	40	54.1	170	2	US-08-683-262B-49
22	40	54.1	170	3	US-09-361-707-49
23	40	54.1	174	2	US-08-683-262B-38
24	40	54.1	174	2	US-08-683-262B-39
25	40	54.1	174	2	US-08-683-262B-42
26	40	54.1	174	2	US-08-683-262B-43
27	40	54.1	174	2	US-08-683-262B-44

28	40	54.1	174	2	US-08-683-262B-45	Sequence 45, Appl
29	40	54.1	174	2	US-08-683-262B-46	Sequence 46, Appl
30	40	54.1	174	2	US-08-683-262B-47	Sequence 47, Appl
31	40	54.1	174	2	US-08-683-262B-48	Sequence 48, Appl
32	40	54.1	174	3	US-08-480-173A-48	Sequence 48, Appl
33	40	54.1	174	3	US-08-484-408A-48	Sequence 48, Appl
34	40	54.1	174	3	US-09-361-707-48	Sequence 38, Appl
35	40	54.1	174	3	US-09-361-707-39	Sequence 39, Appl
36	40	54.1	174	3	US-09-361-707-42	Sequence 42, Appl
37	40	54.1	174	3	US-09-361-707-43	Sequence 43, Appl
38	40	54.1	174	3	US-09-361-707-44	Sequence 44, Appl
39	40	54.1	174	3	US-09-361-707-45	Sequence 45, Appl
40	40	54.1	174	3	US-09-361-707-46	Sequence 46, Appl
41	40	54.1	174	3	US-09-361-707-47	Sequence 47, Appl
42	40	54.1	174	3	US-09-361-707-48	Sequence 48, Appl
43	40	54.1	174	6	5204096-5	Patent No. 5204096
44	40	54.1	174	6	5204096-5	Patent No. 5204096
45	40	54.1	358	4	US-09-328-352-7579	Sequence 7579, Ap

ALIGNMENTS

RESULT 1
US-08-175-158A-2

Sequence 2, Application US/08175158A
Patent No. 5986067

GENERAL INFORMATION:

APPLICANT: FUNK, Walter D.
APPLICANT: MAGGILLIVRAY, Rose T.A.

APPLICANT: WOODWORTH, Robert C.
TITLE OF INVENTION: RECOMBINANT TRANSFERRINS, TRANSFERRIN HALF-

NUMBER OF SEQUENCES: 7
TITLE OF INVENTION: MOLECULES AND MUTANTS THEREOF

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510

CITY: Boston
STATE: Massachusetts

COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,158A

FILING DATE: 28-DEC-1993
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/832,029

FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:

NAME: Deconati, Giulio A.
REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: UVI-005CP2
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 698 amino acids
TYPES: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein

Query Match 81.1%; Score 60; DB 2; Length 698;

Best Local Similarity 85.7%; Pred. No. 0.018;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMGSGLNLSERN 15
DB 515 KLCMGSGLNLSERN 528

RESULT 2

US-09-439-740-2
Sequence 2, Application US/09439740
Patent No. 6825037
GENERAL INFORMATION:
APPLICANT: FUNK, Walter D.
APPLICANT: MACGILLIVRAY, Ross T.A.
APPLICANT: MASON, Anne B.
APPLICANT: WOODWORTH, Robert C.
TITLE OF INVENTION: RECOMBINANT TRANSFERRIN HALF-
TITLE OF INVENTION: MOLECULES AND MUTANTS THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/439,740
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/175,158
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: UVI-0050CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 698 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-439-740-2

Query Match 81.1%; Score 60; DB 4; Length 698;
Best Local Similarity 85.7%; Pred. No. 0.018;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 KLSMGSGLNLSERN 15
DB 515 KLCMGSGLNLSERN 528

RESULT 3

US-08-470-058-2
Sequence 2, Application US/08470058
Patent No. 5817789
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
TITLE OF INVENTION: Chimeric Proteins For Use in Transport
TITLE OF INVENTION: of a Selected Substance Into Cells
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TKT93-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-058-2

Query Match 81.1%; Score 60; DB 2; Length 1074;
Best Local Similarity 85.7%; Pred. No. 0.029;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMGSGLNLSERN 15
DB 891 KLCMGSGLNLSERN 904

RESULT 4

US-09-037-188-2
Sequence 2, Application US/09037188
Patent No. 6027921
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,188
FILING DATE: 02-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-037-188-2

Query Match 81.1%; Score 60; DB 3; Length 1074;
Best Local Similarity 85.7%; Pred. No. 0.029;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 KLSMGSGLNCEPN 15
Db 891 KLCMGSGLNCEPN 904

RESULT 5
US-09-285-310-2
Sequence 2, Application US/09285310
Patent No. 6262026
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,310
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/037,188
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-285-310-2

Query Match 81.1%; Score 60; DB 3; Length 1074;
Best Local Similarity 85.7%; Pred. No. 0.029;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 KLSMGSGLNCEPN 15
Db 891 KLCMGSGLNCEPN 904

RESULT 6
US-08-470-058-4
Sequence 4, Application US/08470058
Patent No. 5817789
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
TITLE OF INVENTION: Chimeric Proteins For Use in Transport
of a Selected Substance into Cells
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TKT93-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-058-4

Query Match 81.1%; Score 60; DB 2; Length 1410;
Best Local Similarity 85.7%; Pred. No. 0.04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 KLSMGSGLNCEPN 15
Db 1227 KLCMGSGLNCEPN 1240

RESULT 7
US-09-037-188-4
Sequence 4, Application US/09037188
Patent No. 6027921
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

Query Match 81.1%; Score 60; DB 2; Length 1410;
Best Local Similarity 85.7%; Pred. No. 0.04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 KLSMGSGLNCEPN 15
Db 1227 KLCMGSGLNCEPN 1240

OPERATING SYSTEM: windows95
SOFTWARE: FASTSEQ for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,188
FILING DATE: 02-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-037-188-4

Query Match 81.1%; Score 60; DB 3; Length 1410;
Best Local Similarity 85.7%; Pred. No. 0.04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMGSGLNLSEPN 15
DB 1227 KLCMPSGLNLCEPN 1240

RESULT 8
US-09-285-310-4
Sequence 4: Application US/09285310
Patent No. 6262026
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: windows95
SOFTWARE: FASTSEQ for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,310
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/037,188
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids

TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-285-310-4

Query Match 81.1%; Score 60; DB 3; Length 1410;
Best Local Similarity 85.7%; Pred. No. 0.04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMGSGLNLSEPN 15
DB 1227 KLCMPSGLNLCEPN 1240

RESULT 9
5262177-4
Patent No. 5262177
APPLICANT: BROWN, J. OSEPH P.; ESTIN, CHARLES D.; PLOWMAN, GREGORY
D.; HELSTROM, KARL E.; ROSE, TIMOTHY M.; HELSTROM, INGEGARD;
PURCHIO, ANTHONY F.; HU, SHU-LOK; PENNATHUR, SRIDHAR
TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HHUMAN
MELANOMA-ASSOCIATED ANTIGEN
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/7230
FILING DATE: 27-JAN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 827,313
FILING DATE: 07-FEB-1986
SEQ ID NO: 4:
LENGTH: 696

Query Match 70.3%; Score 52; DB 6; Length 696;
Best Local Similarity 78.6%; Pred. No. 0.5;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KLSMGSGLNLSEPN 15
DB 514 KLCMPSGLNLCEPN 527

RESULT 10
5262177-4
Patent No. 5262177
APPLICANT: BROWN, J. OSEPH P.; ESTIN, CHARLES D.; PLOWMAN, GREGORY
D.; HELSTROM, KARL E.; ROSE, TIMOTHY M.; HELSTROM, INGEGARD;
PURCHIO, ANTHONY F.; HU, SHU-LOK; PENNATHUR, SRIDHAR
TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HHUMAN
MELANOMA-ASSOCIATED ANTIGEN
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/7230
FILING DATE: 27-JAN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 827,313
FILING DATE: 07-FEB-1986
SEQ ID NO: 4:
LENGTH: 696

Query Match 70.3%; Score 52; DB 6; Length 696;
Best Local Similarity 78.6%; Pred. No. 0.5;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KLSMGSGLNLSEPN 15
DB 514 KLCMPSGLNLCEPN 527

RESULT 11
US-09-248-796A-15968
Sequence 15968, Application US/09248796A


```
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15968
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (112)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknc
US-09-248-796A-15968

Query Match          62.2%; Score 46; DB 4; Length 439;
Best Local Similarity 57.1%; Pred. No. 3.6;
Matches      8; Conservative      4; Mismatches      2; Indels      0; Gaps      0;

Qy      1 SKUSGSLNSEPN 14
       |:|||||:|:|
Db      351 SPMSMGAGINWTP 364

RESULT 12
US-09-418-710-72
; Sequence 72, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418,710
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 1969
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-710-72

Query Match          58.1%; Score 43; DB 4; Length 1969;
Best Local Similarity 75.0%; Pred. No. 75;
Matches      9; Conservative      1; Mismatches      2; Indels      0; Gaps      0;

Qy      4 SMGSGNLSEPN 15
       |:|||||:|:|
Db      1454 SLGSGGLSEGN 1465

RESULT 13
US-09-839-479-71
; Sequence 71, Application US/09839479
; Patent No. 6727222
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042002
; CURRENT APPLICATION NUMBER: US/09/839,479
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 09/418,710
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
```

```
; CURRENT APPLICATION NUMBER: US/09/839,479
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 09/418,710
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 1969
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-839-479-71

Query Match          58.1%; Score 43; DB 4; Length 1969;
Best Local Similarity 75.0%; Pred. No. 75;
Matches      9; Conservative      1; Mismatches      2; Indels      0; Gaps      0;

Qy      4 SMGSGNLSEPN 15
       |:|||||:|:|
Db      1454 SLGSGGLSEGN 1465

RESULT 14
US-09-418-710-21
; Sequence 21, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418,710
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1972
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-710-21

Query Match          58.1%; Score 43; DB 4; Length 1972;
Best Local Similarity 75.0%; Pred. No. 75;
Matches      9; Conservative      1; Mismatches      2; Indels      0; Gaps      0;

Qy      4 SMGSGNLSEPN 15
       |:|||||:|:|
Db      1457 SLGSGGLSEGN 1468

RESULT 15
US-09-839-479-21
; Sequence 21, Application US/09839479
; Patent No. 6727222
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042002
; CURRENT APPLICATION NUMBER: US/09/839,479
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 09/418,710
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
```

```

; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 21
; LENGTH: 1972
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-839-479-21

```

```

Query Match      58.1%; Score 43; DB 4; Length 1972;
Best Local Similarity 75.0%; Pred. No. 75;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      4 SMGGLNLSEPN 15
      |:|||||
DB      1457 SLGGGLGLSRGN 1468

```

Search completed: November 1, 2005, 12:57:31
 Job time : 23.0588 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:54:52 ; Search time 75.8824 Seconds

(without alignments)

82.636 Million cell updates/sec

Title: US-10-612-162A-3

Perfect score: 74

Sequence: 1 SKLMSGGLNLSERN 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 1865214

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep:*

2: /cgn2_6/prodata/1/pubppaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/prodata/1/pubppaa/US06_NEW_PUB.pep:*

4: /cgn2_6/prodata/1/pubppaa/US06_PUBCOMB.pep:*

5: /cgn2_6/prodata/1/pubppaa/US07_NEW_PUB.pep:*

6: /cgn2_6/prodata/1/pubppaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/prodata/1/pubppaa/US08_NEW_PUB.pep:*

8: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*

9: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*

10: /cgn2_6/prodata/1/pubppaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/prodata/1/pubppaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/prodata/1/pubppaa/US09C_NEW_PUB.pep:*

13: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep:*

14: /cgn2_6/prodata/1/pubppaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/prodata/1/pubppaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/prodata/1/pubppaa/US10D_PUBCOMB.pep:*

17: /cgn2_6/prodata/1/pubppaa/US10E_PUBCOMB.pep:*

18: /cgn2_6/prodata/1/pubppaa/US10F_NEW_PUB.pep:*

19: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

20: /cgn2_6/prodata/1/pubppaa/US11_NEW_PUB.pep:*

21: /cgn2_6/prodata/1/pubppaa/US60_NEW_PUB.pep:*

22: /cgn2_6/prodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	15	US-10-612-162-3	Sequence 3, Appl1
2	60	81.1	42	US-10-378-094-15	Sequence 15, Appl1
3	60	81.1	42	US-10-384-060-36	Sequence 36, Appl1
4	60	81.1	328	US-09-891-126-5	Sequence 5, Appl1
5	60	81.1	328	US-10-266-745-5	Sequence 5, Appl1
6	60	81.1	679	US-10-378-094-3	Sequence 3, Appl1
7	60	81.1	679	US-10-384-060-3	Sequence 3, Appl1
8	60	81.1	679	US-10-231-494-3	Sequence 3, Appl1
9	60	81.1	679	US-10-429-482-4	Sequence 4, Appl1
10	60	81.1	679	US-10-429-497-4	Sequence 4, Appl1
11	60	81.1	679	US-10-429-515-4	Sequence 4, Appl1

ALIGNMENTS

12	60	81.1	679	16	US-10-429-598-4	Sequence 4, Appl1
13	60	81.1	679	16	US-10-429-635-4	Sequence 4, Appl1
14	60	81.1	679	16	US-10-429-653-4	Sequence 4, Appl1
15	60	81.1	679	16	US-10-429-659-4	Sequence 4, Appl1
16	60	81.1	679	16	US-10-429-661-4	Sequence 4, Appl1
17	60	81.1	679	16	US-10-429-664-4	Sequence 4, Appl1
18	60	81.1	679	16	US-10-429-665-4	Sequence 4, Appl1
19	60	81.1	679	16	US-10-429-665-4	Sequence 4, Appl1
20	60	81.1	679	16	US-10-429-654-4	Sequence 4, Appl1
21	60	81.1	698	10	US-09-935-642-6	Sequence 6, Appl1
22	60	81.1	698	15	US-10-378-094-2	Sequence 2, Appl1
23	60	81.1	698	15	US-10-384-060-2	Sequence 2, Appl1
24	60	81.1	698	15	US-10-231-494-2	Sequence 2, Appl1
25	60	81.1	698	15	US-10-383-201-10	Sequence 10, Appl1
26	60	81.1	698	15	US-10-383-201-14	Sequence 14, Appl1
27	60	81.1	698	17	US-10-887-711-2	Sequence 2, Appl1
28	60	81.1	698	18	US-10-513-523-3	Sequence 3, Appl1
29	60	81.1	1074	9	US-09-753-385-2	Sequence 2, Appl1
30	60	81.1	1410	9	US-09-753-385-4	Sequence 4, Appl1
31	60	81.1	1418	16	US-10-473-127-804	Sequence 804, App
32	57	77.0	1410	16	US-10-473-127-805	Sequence 805, App
33	55	74.3	15	16	US-10-769-514-10	Sequence 10, Appl1
34	55	74.3	15	16	US-10-769-514-42	Sequence 42, Appl1
35	55	74.3	15	17	US-10-801-990-180	Sequence 180, App
36	55	74.3	15	17	US-10-801-990-184	Sequence 184, App
37	55	74.3	26	17	US-10-801-990-14	Sequence 14, Appl1
38	47	63.5	340	16	US-10-437-963-110132	Sequence 110132, A
39	43	58.1	91	9	US-09-864-761-36754	Sequence 36754, A
40	43	58.1	1969	9	US-09-839-479-71	Sequence 71, Appl1
41	43	58.1	1969	15	US-10-376-537-72	Sequence 72, Appl1
42	43	58.1	1969	15	US-10-702-148-71	Sequence 71, Appl1
43	43	58.1	1972	9	US-09-839-479-21	Sequence 21, Appl1
44	43	58.1	1972	15	US-10-376-537-21	Sequence 21, Appl1
45	43	58.1	1972	15	US-10-702-148-21	Sequence 21, Appl1

RESULT 1

US-10-612-162-3

Sequence 3, Appl1 Application US/10612162

Publication No. US2004001415A1

GENERAL INFORMATION:

APPLICANT: Dade Behring Marburg GmbH

TITLE OF INVENTION: Carbohydrate deficient transferrin (CDT)-specific antibodies, their preparation and use

FILE REFERENCE: 2002/B001

CURRENT APPLICATION NUMBER: US/10/612,162

CURRENT FILING DATE: 2003-07-03

PRIOR APPLICATION NUMBER: 10230550.1

PRIOR FILING DATE: 2002-07-05

PRIOR APPLICATION NUMBER: 03011334.4

PRIOR FILING DATE: 2003-05-19

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3

LENGTH: 15

TYPE: PRT

ORGANISM: Homo sapiens

US-10-612-162-3

Query Match 100.0%; Score 74; DB 15; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.1e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLMSGGLNLSERN 15

Db 1 SKLMSGGLNLSERN 15

RESULT 2

US-10-378-094-15

```
/ Sequence 15, Application US/10378094
/ Publication No. US20030221201A1
/ GENERAL INFORMATION:
/ APPLICANT: PRIOR, Christopher P.
/ APPLICANT: LAI, Char-Huei
/ APPLICANT: SADEGH, Homayoun
/ APPLICANT: TURNER, Andrew
/ TITLE OF INVENTION: MODIFIED TRANSFERRIN FUSION PROTEINS
/ FILE REFERENCE: 54710-5001-01-US
/ CURRENT APPLICATION NUMBER: US/10/378,094
/ CURRENT FILING DATE: 2003-03-04
/ PRIOR APPLICATION NUMBER: US 10/221,494
/ PRIOR FILING DATE: 2002-08-30
/ PRIOR APPLICATION NUMBER: US 60/334,059
/ PRIOR FILING DATE: 2001-11-30
/ PRIOR APPLICATION NUMBER: US 60/315,745
/ PRIOR FILING DATE: 2001-08-30
/ NUMBER OF SEQ ID NOS: 66
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 15
/ LENGTH: 42
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ OTHER INFORMATION: C1 subdomain of transferrin
US-10-378-094-15
```

```
Query Match      81.1%; Score 60; DB 15; Length 42;
Best Local Similarity 85.7%; Pred. No. 0.0032;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 KLSMSGSLNLEPN 15
      || ||||| |||
Db      25 KLCMSGSLNLCBN 38
```

```
RESULT 3
US-10-384-060-36
/ Sequence 36, Application US/10384060
/ Publication No. US20030226155A1
/ GENERAL INFORMATION:
/ APPLICANT: SADEGH, Homayoun
/ APPLICANT: PRIOR, Christopher P.
/ APPLICANT: TURNER, Andrew
/ TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
/ FILE REFERENCE: 54710-5004-US
/ CURRENT APPLICATION NUMBER: US/10/384,060
/ CURRENT FILING DATE: 2003-03-10
/ PRIOR APPLICATION NUMBER: US 10/221,494
/ PRIOR FILING DATE: 2002-08-30
/ PRIOR APPLICATION NUMBER: US 60/334,059
/ PRIOR FILING DATE: 2001-11-30
/ PRIOR APPLICATION NUMBER: US 60/315,745
/ PRIOR FILING DATE: 2001-08-30
/ PRIOR APPLICATION NUMBER: US 60/406,977
/ PRIOR FILING DATE: 2002-08-30
/ NUMBER OF SEQ ID NOS: 80
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 36
/ LENGTH: 42
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: C1 domain of human Tf
US-10-384-060-36
```

```
Query Match      81.1%; Score 60; DB 15; Length 42;
Best Local Similarity 85.7%; Pred. No. 0.0032;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 KLSMSGSLNLEPN 15
      || ||||| |||
```

```
Db      25 KLCMSGSLNLCBN 38

RESULT 4
US-09-891-126-5
/ Sequence 5, Application US/09891126
/ Patent No. US20020072596A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruden et al.
/ TITLE OF INVENTION: Transferrin Polynucleotides, Polypeptides, and Antibodies
/ FILE REFERENCE: PT035PI
/ CURRENT APPLICATION NUMBER: US/09/891,126
/ CURRENT FILING DATE: 2001-06-26
/ PRIOR APPLICATION NUMBER: PCT/US00/34769
/ PRIOR FILING DATE: 2000-12-21
/ PRIOR APPLICATION NUMBER: 60/171,595
/ PRIOR FILING DATE: 1999-12-23
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 328
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-891-126-5
```

```
Query Match      81.1%; Score 60; DB 9; Length 328;
Best Local Similarity 85.7%; Pred. No. 0.032;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 KLSMSGSLNLEPN 15
      || ||||| |||
Db      179 KLCMSGSLNLCBN 192
```

```
RESULT 5
US-10-266-745-5
/ Sequence 5, Application US/10266745
/ Publication No. US20030149256A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruden et al.
/ TITLE OF INVENTION: Transferrin Polynucleotides, Polypeptides, and Antibodies
/ FILE REFERENCE: PT035PI
/ CURRENT APPLICATION NUMBER: US/10/266,745
/ CURRENT FILING DATE: 2002-10-09
/ PRIOR APPLICATION NUMBER: US/09/891,126
/ PRIOR FILING DATE: 2001-06-26
/ PRIOR APPLICATION NUMBER: PCT/US00/34769
/ PRIOR FILING DATE: 2000-12-21
/ PRIOR APPLICATION NUMBER: 60/171,595
/ PRIOR FILING DATE: 1999-12-23
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 328
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-266-745-5
```

```
Query Match      81.1%; Score 60; DB 14; Length 328;
Best Local Similarity 85.7%; Pred. No. 0.032;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 KLSMSGSLNLEPN 15
      || ||||| |||
Db      179 KLCMSGSLNLCBN 192
```

```
RESULT 6
US-10-378-094-3
/ Sequence 3, Application US/10378094
/ Publication No. US20030221201A1
/ GENERAL INFORMATION:
/ APPLICANT: PRIOR, Christopher P.
```

```

; APPLICANT: LAI, Char-Huei
; APPLICANT: SADEGH, Homayoun
; TITLE OF INVENTION: MODIFIED TRANSFERRIN FUSION PROTEINS
; FILE REFERENCE: 54710-5001-01-US
; CURRENT APPLICATION NUMBER: US/10/378,094
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR FILING DATE: 2001-11-30
; PRIOR FILING DATE: 2001-11-30
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Mature Transferrin Protein
; US-10-378-094-3
```

```

Query Match      81.1%; Score 60; DB 15; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.071;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      2 KLSMGSGLNSEPN 15
Db      496 KLCMGSGNLNCEPN 509
```

```

RESULT 7
; US-10-384-060-3
; Sequence 3, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGH, Homayoun
; APPLICANT: PRIOR, Christopher P.
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Mature Transferrin Protein
; US-10-384-060-3
```

```

Query Match      81.1%; Score 60; DB 15; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.071;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      2 KLSMGSGLNSEPN 15
Db      496 KLCMGSGNLNCEPN 509
```

```

RESULT 8
; US-10-231-494-3
; Sequence 3, Application US/10231494
; Publication No. US20040023334A1
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
; FILE REFERENCE: 54710-5001-US
; CURRENT APPLICATION NUMBER: US/10/231,494
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Mature transferrin protein
; US-10-231-494-3
```

```

Query Match      81.1%; Score 60; DB 15; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.071;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      2 KLSMGSGLNSEPN 15
Db      496 KLCMGSGNLNCEPN 509
```

```

RESULT 9
; US-10-429-482-4
; Sequence 4, Application US/10429482
; Publication No. US20040219097A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For The Diagnosis, Imaging and Treatment Of T
; FILE REFERENCE: 2537,000001
; CURRENT APPLICATION NUMBER: US/10/429,482
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-429-482-4
```

```

Query Match      81.1%; Score 60; DB 15; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.071;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      2 KLSMGSGLNSEPN 15
Db      496 KLCMGSGNLNCEPN 509
```

```

RESULT 10
; US-10-429-497-4
; Sequence 4, Application US/10429497
; Publication No. US20040219098A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For The Treatment of Tumors
; FILE REFERENCE: 2537,000006
; CURRENT APPLICATION NUMBER: US/10/429,497
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
```

```
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-497-4

Query Match      81.1%; Score 60; DB 16; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.071;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 KLSMSGSLNISEPN 15
      || ||||| |||
Db      496 KLCMSGSLNICEPN 509

RESULT 11
US-10-429-515-4
; Sequence 4, Application US/10429515
; Publication No. US20040219099A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Method For The Treatment Of Tumors
; FILE REFERENCE: 2537.000005
; CURRENT APPLICATION NUMBER: US/10/429,515
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-515-4

Query Match      81.1%; Score 60; DB 16; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.071;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 KLSMSGSLNISEPN 15
      || ||||| |||
Db      496 KLCMSGSLNICEPN 509

RESULT 12
US-10-429-598-4
; Sequence 4, Application US/10429598
; Publication No. US20040219100A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For The Treatment of Tumors
; FILE REFERENCE: 2537.000003
; CURRENT APPLICATION NUMBER: US/10/429,598
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-598-4

Query Match      81.1%; Score 60; DB 16; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.071;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 KLSMSGSLNISEPN 15
      || ||||| |||
Db      496 KLCMSGSLNICEPN 509

RESULT 13
US-10-429-635-4
; Sequence 4, Application US/10429635
; Publication No. US20040219101A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For Treatment Of Tumors
; FILE REFERENCE: 2537.000007
; CURRENT APPLICATION NUMBER: US/10/429,635
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-635-4

Query Match      81.1%; Score 60; DB 16; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.071;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 KLSMSGSLNISEPN 15
      || ||||| |||
Db      496 KLCMSGSLNICEPN 509

RESULT 14
US-10-429-653-4
; Sequence 4, Application US/10429653
; Publication No. US20040219102A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Compositions For Drug Delivery
; FILE REFERENCE: 2537.000009
; CURRENT APPLICATION NUMBER: US/10/429,653
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-653-4

Query Match      81.1%; Score 60; DB 16; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.071;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 KLSMSGSLNISEPN 15
      || ||||| |||
Db      496 KLCMSGSLNICEPN 509

RESULT 15
US-10-429-659-4
; Sequence 4, Application US/10429659
; Publication No. US20040219103A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Method Useful For The Diagnosis, Imaging and Treatment Of Tumor
; FILE REFERENCE: 2537.000004
; CURRENT APPLICATION NUMBER: US/10/429,659
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-659-4

Query Match      81.1%; Score 60; DB 16; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.071;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 KLSMSGSLNISEPN 15
      || ||||| |||
```

Tue Nov 1 17:05:15 2005

us-10-612-162a-3.rapb

Page 5

Db 496 KLCMGSGLNICEPN 509

Search completed: November 1, 2005, 13:26:07
Job time : 76.8824 secB

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:35:39 ; Search time 15.2206 Seconds
(without alignments)
94.822 Million cell updates/sec

Title: US-10-612-162A-3

Perfect score: 74

Sequence: 1 SKXSMGSLNLSFPN 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	81.1	698	1	TFHUP
2	41	55.4	148	2	C65068
3	41	55.4	163	2	C91092
4	41	55.4	163	2	G85937
5	40	54.1	382	2	T13474
6	40	54.1	384	2	T13469
7	40	54.1	400	1	SAVLA
8	40	54.1	400	2	S35528
9	40	54.1	445	2	S43492
10	40	54.1	448	2	D71852
11	40	54.1	448	2	H64663
12	40	54.1	516	2	T27845
13	39	52.7	338	2	C89991
14	39	52.7	400	1	UQ1575
15	39	52.7	400	1	SAVLKS
16	39	52.7	400	1	SAVLVD
17	39	52.7	494	2	T02523
18	39	52.7	545	2	JC2500
19	39	52.7	610	2	A96701
20	39	52.7	915	2	S24577
21	39	52.7	1268	2	AB0204
22	39	52.7	3828	2	T13857
23	38	51.4	289	2	T48108
24	38	51.4	293	2	T40702
25	38	51.4	311	2	T42088
26	38	51.4	316	2	T49376
27	38	51.4	317	1	S67781
28	38	51.4	322	2	S43453
29	38	51.4	465	2	G90961

30	38	51.4	465	2	G85809	flagellar capping
31	38	51.4	468	2	A64956	flagellar hook-ax
32	38	51.4	768	2	AH1085	hypothetical prote
33	38	51.4	769	1	WZBE54	gene 54 protein -
34	38	51.4	1021	2	T05901	hypothetical prote
35	38	51.4	2212	2	A41098	calcium channel pr
36	37.5	50.7	431	2	F95236	prg system, ITC co
37	37.5	50.7	431	2	H98100	hypothetical prote
38	37	50.0	106	2	T20860	hypothetical prote
39	37	50.0	124	2	B27632	T-cell receptor al
40	37	50.0	152	2	F71973	hypothetical prote
41	37	50.0	282	2	S31463	probable integrase
42	37	50.0	325	2	T35318	probable dehydroge
43	37	50.0	335	2	C95118	hypothetical prote
44	37	50.0	335	2	A97988	hypothetical prote
45	37	50.0	344	1	RWRTC2	T-cell surface gly

ALIGNMENTS

RESULT 1
TFHUP
transferrin precursor (validated) - human
N;Alternate names: siderophilin
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1982 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A20981; A92417; A94044; A23090; A23739; I51959; I63133; I54011; I68160; A0
R;Yang, F.; Lum, J.B.; McGill, J.R.; Moore, C.M.; Naylor, S.L.; van Bregt, P.H.; Balducci,
Proc. Natl. Acad. Sci. U.S.A. 81, 2752-2756, 1984
A;Title: Human transferrin: cDNA characterization and chromosomal localization.
A;Reference number: A20981; PMID:84194084; PMID:6585826
A;Content: variant C
A;Accession: A20981
A;Molecule type: mRNA
A;Residues: 1-698 <YAN>
A;Cross-references: UNIPROT:P02787; EMBL:M12530; NID:G339452; PIDN:AAA61140.1; PID:G339
R;MacGillivray, R.T.A.; Mendez, E.; Shewale, J.G.; Sinha, S.K.; Linbeck-Zins, J.; Brew
J. Biol. Chem. 258, 3543-3553, 1983
A;Title: The primary structure of human serum transferrin. The structures of seven cyan
A;Reference number: A92417; PMID:83160878; PMID:6833213
A;Accession: A92417
A;Molecule type: protein
A;Residues: 20-263, 'E', 265-328, 'N', 330-379, 'SD', 382-435, 'D', 437-557, 'T', 559-560, 'P', 562
A;Note: the sequence shown is the predominant electrophoretic genetic variant (C or TfC)
R;Park, I.; Schaeffer, B.; Sidoli, A.; Baralle, F.E.; Cohen, G.N.; Zakin, M.M.
Proc. Natl. Acad. Sci. U.S.A. 82, 3149-3153, 1985
A;Title: Organization of the human transferrin gene: direct evidence that it originated
A;Reference number: A94044; PMID:85216459; PMID:3858812
A;Accession: A94044
A;Molecule type: DNA
A;Residues: 73-263, 'E', 265-328, 'N', 330-562 <PAR>
A;Cross-references: EMBL:M1361
R;Adrian, G.S.; Korinek, B.W.; Bowman, B.H.; Yang, F.
Gene 49, 167-175, 1986
A;Title: The human transferrin gene: 5' region contains conserved sequences which match
A;Reference number: A23090; PMID:87192006; PMID:3106157
A;Accession: A23090
A;Molecule type: DNA
A;Residues: 1-72, 291-300 <ADR>
A;Cross-references: EMBL:M15673
R;Udan, G.; Frain, M.; Park, I.; Beemond, C.; Maessen, G.; Trepac, J.S.; Zakin, M.M.; K
Biochem. Biophys. Res. Commun. 119, 273-281, 1984
A;Title: Molecular cloning and sequence analysis of cDNA for human transferrin.
A;Reference number: A32739; PMID:84153910; PMID:6322780
A;Accession: A32739
A;Molecule type: mRNA
A;Residues: 422-690, 'G', 692-698 <UZA>
A;Cross-references: EMBL:M12525; NID:G339468; PIDN:AAA61142.1; PID:G339469
R;MacGillivray, R.T.A.; Mendez, E.; Sinha, S.K.; Sutton, M.R.; Linbeck-Zins, J.; Brew,
Proc. Natl. Acad. Sci. U.S.A. 79, 2504-2508, 1982

A>Title: The complete amino acid sequence of human serum transferrin.
A:Reference number: A93911; MUID:8222166; PMID:6553407
A:Contents: annotation; disulfide bonds
R:Herberberger, C.L.; Larson, O.L.; Arnold, B.; Roestek, P.R.
Ann. N. Y. Acad. Sci. 646, 140-154, 1991
A>Title: A cloned gene for human transferrin.
A:Reference number: I51959; MUID:9221399; PMID:1809186
A:Accession: I51959
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-698 <RES>
A:Cross-references: GB:S95936; NID:G248647; PIDN:AA622049.1; PID:G248648
R:Duguid, J.R.; Bohmont, C.W.; Liu, N.G.; Tourtellotte, W.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 7260-7264, 1989
A>Title: Changes in brain gene expression shared by scrapie and Alzheimer disease.
A:Reference number: I48174; MUID:89386721; PMID:2780570
A:Accession: I63133
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 636-696 <RE2>
A:Cross-references: GB:M26641; NID:G339988; PIDN:AA61233.1; PID:G339989
R:Schaeffer, E.; Lucero, M.A.; Jeltch, J.M.; Py, M.C.; Levin, M.J.; Chandon, P.; Cohen, Gene 56, 109-116, 1987
A>Title: Complete structure of the human transferrin gene. Comparison with analogous chi
A:Reference number: I54011; MUID:88056305; PMID:3678832
A:Accession: I54011
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-72 <RE3>
A:Cross-references: GB:M17611; NID:G339480; PIDN:AA61147.1; PID:G339485
A:Accession: I68160
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 564-698 <RE4>
A:Cross-references: GB:M1614; NID:G339483; PIDN:AA61148.1; PID:G339486
C:Comment: Each of the two repetitive domains binds a ferric ion and a bicarbonate anion
C:Genetic8:
A:Gene: GDB:TF
A:Cross-references: GDB:120432; OMIM:190000
A:Map position: 3q21-3q21
A:Introns: 15/1; 72/3; 119/1; 166/1; 212/2; 231/1; 290/3; 350/1; 401/3; 433/1; 444/1; 49
C:Function:
A:Description: binds iron for delivery into cells
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; glycoprotein; iron transport; metal binding; plasma
F:1-19/Domain: signal sequence #status predicted <Sig>
F:20-698/Product: transferrin #status experimental <MAT>
F:20-350/Domain: transferrin repeat homology <TRH2>
F:356-686/Domain: transferrin repeat homology <TRH2>
F:28-67,38-58,137-213,156-350,177-193,180-196,190-198,246-260,358-615,364-396,374-387,42
F:432,630/Binding site: carbohydrate (Aasn) (covalent) #status experimental
Query Match 81.1%; Score 60; DB 1; Length 698;
Best Local Similarity 85.7%; Pred. No. 0.0081;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 KLSMGSGLNLSEPN 15
DB 515 KLCMSGLNLCEPN 528
RESULT 2
C65068
hypothetical protein b2850 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
A:Accession: C65068
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A>Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: C65068

A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-148 <BLAT>
A:Cross-references: UNIPROT:Q46786; GB:AE000369; GB:U00096; NID:G2367168; PIDN:AACT5889
A:Experimental source: strain K-12, substrain MG1655
C:Superfamily: Escherichia coli hypothetical protein b2850
Query Match 55.4%; Score 41; DB 2; Length 148;
Best Local Similarity 66.7%; Pred. No. 4.8;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 KLSMGSGLNLSE 13
DB 35 KITMGSGLNYIE 46
RESULT 3
C91092
hypothetical protein EC93707 [imported] - Escherichia coli (strain O157:H7, substrain RI
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: C91092
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gatawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:1128796
A:Accession: C91092
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-163 <HAY>
A:Cross-references: UNIPROT:Q8X6H8; GB:BA000007; PIDN:BA937130.1; PID:G13363179; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetic8:
A:Gene: EC93707
C:Superfamily: Escherichia coli hypothetical protein b2850
Query Match 55.4%; Score 41; DB 2; Length 163;
Best Local Similarity 66.7%; Pred. No. 5.4;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 KLSMGSGLNLSE 13
DB 35 KITMGSGLNYIE 46
RESULT 4
G85937
hypothetical protein Z4171 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: G85937
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Gnaner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Llm, A.; Dialalata, E.; Potamoultis, K.; Apodaca,
Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: G85937
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-163 <STO>
A:Cross-references: UNIPROT:Q8X6H8; GB:AE005174; NID:G12517343; PIDN:AA657963.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetic8:
A:Gene: Z4171
C:Superfamily: Escherichia coli hypothetical protein b2850
Query Match 55.4%; Score 41; DB 2; Length 163;
Best Local Similarity 66.7%; Pred. No. 5.4;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 KLSMGSGLNLSE 13
DB 35 KITMGSGLNYIE 46

```

Db          35 KITWGSGLNTYIE 46

RESULT 5
T13474
large surface antigen - hepatitis B virus (isolate 29Y11HCC)
N:Alternate names: envelope protein, HBs antigen
C:Contains: major surface antigen; middle surface antigen
C:Species: hepatitis B virus, HBV
A:Variety: isolate 29Y11HCC
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T13474
R:Takahashi, K.; Akahane, Y.; Hino, K.; Ohta, Y.; Mishiro, S.
Arch. Virol. 143, 2313-2326, 1998
A:Title: Hepatitis B virus genomic sequence in the circulation of hepatocellular carcinoma
A:Reference number: Z17684; MUID:99129050; PMID:9930189
A:Accession: T13474
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Cross-references: UNIPROT:Q9YZS2; EMBL:AB014368; NID:G3582381; PIDN:BA432936.1; PID:G3582381
A:Experimental source: Japanese patient with hepatocellular carcinoma isolate 29Y11HCC
C:Genetics:
A:Gene: S
A:Introns: 123/2
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: glycoprotein; surface antigen

Query Match 54.1%; Score 40; DB 2; Length 384;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy          1 SKLWGSGLNTSEPN 15
      ||| |||||
Db          6 SKPRGSGMTNLSVNP 20

RESULT 6
T13469
large surface antigen - hepatitis B virus (isolate 09D09HCC)
N:Alternate names: envelope protein
C:Contains: major surface antigen; middle surface antigen
C:Species: hepatitis B virus, HBV
A:Variety: isolate 09D09HCC
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T13469
R:Takahashi, K.; Akahane, Y.; Hino, K.; Ohta, Y.; Mishiro, S.
Arch. Virol. 143, 2313-2326, 1998
A:Title: Hepatitis B virus genomic sequence in the circulation of hepatocellular carcinoma
A:Reference number: Z17684; MUID:99129050; PMID:9930189
A:Accession: T13469
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-384 <TK>
A:Cross-references: UNIPROT:Q9YZU2; EMBL:AB014368; NID:G3551304; PIDN:BA432864.1; PID:G3551304
A:Experimental source: Japanese patient with hepatocellular carcinoma isolate 09D09HCC
C:Genetics:
A:Gene: S
A:Introns: 123/2
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: glycoprotein; surface antigen

Query Match 54.1%; Score 40; DB 2; Length 384;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy          1 SKLWGSGLNTSEPN 15
      ||| |||||
Db          6 SKPRGSGMTNLSVNP 20

```

Large surface antigen - hepatitis B virus (subtype adr)
N:Contains: major surface antigen; middle surface antigen
C:Species: hepatitis B virus, HBV
C:Idate: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
A:Accession: A037053; S04569; JQ2107; PQ0608
R:Onto, Y.; Onda, H.; Saadada, R.; Igarashi, K.; Sugino, Y.; Nishioaka, K.
Nucleic Acids Res. 11, 1747-1757, 1983
A>Title: The complete nucleotide sequences of the cloned hepatitis B virus DNA; subtype
A:Reference number: A93460; MUID:63168919; PMID:6300776
A:Accession: A03705
A:Molecule type: DNA
A:Residues: 1-400 <ONO>
A:Cross-references: UNIPROT:P03140; GB:V00867
R:Rhoo, H.M.; Kim, K.; Hyun, S.W.; Kim, Y.S.
Nucleic Acids Res. 17, 2124, 1989
A>Title: The nucleotide sequence and reading frames of a mutant hepatitis B virus subtype
A:Reference number: S04568; MUID:63183619; PMID:2928116
A:Accession: S04569
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-50, 'R', 52-66, 'Y', 69-129, 'V', 131-142, 'P', 144-164, 'S', 166-176, 'S', 178-338,
R:Norder, H.; Courouce, A.M.; Magnus, L.O.
J. Gen. Virol. 73, 3141-3145, 1992
A>Title: Molecular basis of hepatitis B virus serotype variations within the four major
A:Reference number: JQ2044; MUID:93329382; PMID:8356122
A:Accession: JQ2107
A:Molecule type: DNA
A:Residues: 175-400 <NOR>
A:Experimental source: genogroup C, subtype adr, strain pBRHadr4
R:Norder, H.; Courouce, A.M.; Magnus, L.O.
J. Gen. Virol. 73, 3141-3145, 1992
A>Title: Molecular basis of hepatitis B virus serotype variations within the four major
A:Reference number: PQ0453; MUID:93107848; PMID:1469353
A:Accession: PQ0608
A:Molecule type: DNA
A:Residues: 275-354 <NO2>
A:Experimental source: subtype adrq+, Bau
C:Genetics:
A:Gene: pre-S1/pre-S2/S
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: glycoprotein; surface antigen
F:120-400/Product: middle surface antigen (gene pre-S2/S) #status predicted <NSA>
F:175-400/Product: major surface antigen (gene S) #status predicted <MSA>
F:115,123,177/Binding site: carbohydrate (Asn) #status predicted

Query Match 54.1%; Score 40; DB 1; Length 400;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 SKTSMGSGQLNSEPN 15
|| || || || ||
Db 6 SKPRQGWTNLNVN 20

RESULT 8
S35528
N:Alternate names: hepatitis B virus (subtype adr)
N:Alternate names: envelope protein; HBs antigen
N:Contains: surface antigen pre-S1 (large envelope protein); surface antigen pre-S2 (mLcag)
C:Species: hepatitis B virus, HBV
A:Variety: subtype adr
C:Idate: 09-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
A:Accession: S35528
R:Mukaike, M.; Kunazawa, T.; Hoshi, A.; Kawaguchi, R.; Hikiji, K.
Nucleic Acids Res. 20, 6105, 1992
A>Title: The complete nucleotide sequence of hepatitis B virus, subtype adr (SRADR) and
A:Reference number: S35527; MUID:93096607; PMID:1461746
A:Accession: S35528
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-400 <MUK>
A:Cross-references: UNIPROT:Q81108; EMBL:D12980; NID:g221500; PTDN:BAA02359.1; PID:g2215

```

A:Experimental source: subtype adr
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
C:Genetics:
A:Gene: S
A:Insertions: 165/2
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: surface antigen
F:1-400/Product: surface antigen pre-S1 (large envelope protein) #status predicted <PS1>
F:1-119/Domin: pre-S1 domain #status predicted <PRE1>
F:1120-400/Product: surface antigen pre-S2 (middle envelope protein) #status predicted <PS2>
F:1120-174/Domin: pre-S2 domain #status predicted <PRE2>
F:1175-400/Product: surface antigen S (small envelope protein) #status predicted <PSD>

Query Match          54.1% Score 40; DB 2; Length 400;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 SKLMSGSLNLEPN 15
    ||| ||| ||| |||
Db 6 SKPRQMGNTNLSVPN 20

RESULT 9
surface antigen - hepatitis B virus (subtype adr)
N:Alternate names: Hbs antigen
N:Contents: surface antigen pre-S1 (large envelope protein); surface antigen pre-S2 (mid
C:Species: hepatitis B virus, HBV
A:Variety: subtype adr
C:Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S43492; P06001; P06002
R:Loncarevic, I.F.; Zentgraf, H.; Schroeder, C.H.
Nucleic Acid Res. 18, 4940, 1990
A:Title: Sequence of a replication competent hepatitis B virus genome with a prex open r
A:Reference number: S12598; MUID:90370503; PMID:2395664
A:Accession: S43492
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-445 <LON>
A:Cross-references: UNIPROT:Q67953; EMBL:X52939; NID:g457780; PIDN:CAA37114.1; PID:g4577
A:Experimental source: subtype adr
R:Mims, L.T.; Solomon, L.R.; Ebert, J.W.; Field, H.
Biochem. Biophys. Res. Commun. 195, 186-191, 1993
A:Title: Unique Pres sequence in a gibbon-derived hepatitis B virus variant.
A:Reference number: P06001; MUID:93371402; PMID:8363598
A:Accession: P06001
A:Molecule type: protein
A:Residues: 57-95 <MIM>
A:Accession: P06002
A:Molecule type: protein
A:Residues: 165-196 <M12>
C:Genetics:
A:Gene: S
A:Insertions: 210/3
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: surface antigen
F:1-445/Product: surface antigen pre-S1 (large envelope protein) #status predicted <PS1>
F:1-164/Domin: pre-S1 domain #status predicted <PRE1>
F:165-445/Product: surface antigen pre-S2 (middle envelope protein) #status predicted <PS2>
F:165-219/Domin: pre-S2 domain #status predicted <PRE2>
F:220-445/Product: surface antigen S (small envelope protein) #status predicted <PSD>

Query Match          54.1% Score 40; DB 2; Length 445;
Best Local Similarity 60.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 SKLMSGSLNLEPN 15
    ||| ||| ||| |||
Db 51 SKPRQMGNTNLSVPN 65

RESULT 10
D71852

```

```

probable signal recognition particle protein - Helicobacter pylori (strain J99)
A:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: D71852
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Dolg, P.C.; Smith, D.R.;
; Ivers, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, O.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: D71852
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-448 <ARN>
A:Cross-references: UNIPROT:Q9ZK62; GB:AE001535; GB:AE001439; NID:g4155664; PIDN:AA00665
A:Experimental source: strain J99
C:Genetics:
A:Gene: fth
C:Superfamily: signal recognition particle 54k protein

Query Match          54.1% Score 40; DB 2; Length 448;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 2 KLSMSGSLNLEPN 15
    ::::|::|::|::|
Db 394 RIALGSLVSEIN 407

RESULT 11
signal recognition particle protein - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: H64663
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliq, H.G.; Glodek, A.; McKen
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watney, L.
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: H64663
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-448 <TOM>
A:Cross-references: UNIPROT:P56005; GB:AE000621; GB:AE000511; NID:g2314301; PIDN:AA00819
C:Superfamily: signal recognition particle 54k protein

Query Match          54.1% Score 40; DB 2; Length 448;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 2 KLSMSGSLNLEPN 15
    ::::|::|::|::|
Db 394 RIALGSLVSEIN 407

RESULT 12
hypothetical protein ZK402.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27845
R:Favella, T.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid ZK402.
A:Reference number: Z20429
A:Accession: T27845
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-516 <FAV>
A:Cross-references: UNIPROT:Q23477; EMBL:U40956; PIDN:AAAB1756.1; CESP:ZK402.5

```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:34:09 ; Search time 73.4559 Seconds
(without alignments)
104.569 Million cell updates/sec

Title: US-10-612-162A-3

Perfect score: 74

Sequence: 1 SKLMSGSLSEPN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UnIProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	81.1	698	1	TRFE_HUMAN
2	47	63.5	400	2	O9B9E2
3	47	63.5	521	2	O943K6
4	46	62.2	823	2	O8J2T2
5	43	58.1	368	2	O7PD10
6	43	58.1	796	2	O8NC87
7	43	58.1	1972	1	BA2B_HUMAN
8	42	56.8	307	2	O6FMK0
9	42	56.8	428	2	O8GP40
10	42	56.8	528	2	O8J289
11	42	56.8	528	2	O6CKZ8
12	42	56.8	867	2	O8U379
13	42	56.8	3358	2	O8INP9
14	42	56.8	3726	2	O9VPL1
15	41	55.4	148	1	YGER_ECOLI
16	41	55.4	148	2	O9D019
17	41	55.4	163	2	O8X6H8
18	41	55.4	174	2	O8V4P7
19	41	55.4	174	2	O8V4Q0
20	41	55.4	234	2	O647Z6
21	41	55.4	253	2	O6BCP0
22	41	55.4	400	2	O7TDQ3
23	41	55.4	400	2	O9Q3F5
24	41	55.4	645	2	O8K2Y0
25	41	55.4	1433	2	O8A043
26	40	54.1	92	2	O8OB33
27	40	54.1	97	2	O8OB32
28	40	54.1	119	2	O8U7I5
29	40	54.1	119	2	O8U7I9
30	40	54.1	119	2	O8U7J0
31	40	54.1	119	2	O91U85

32	40	54.1	119	2	O91U86	O91U86 hepatitis b
33	40	54.1	119	2	O91U87	O91U87 hepatitis b
34	40	54.1	119	2	O67867	O67867 hepatitis b
35	40	54.1	128	2	O91R75	O91R75 hepatitis b
36	40	54.1	135	2	O8G599	O8G599 oryza sativ
37	40	54.1	161	2	O91R76	O91R76 hepatitis b
38	40	54.1	174	2	O998U7	O998U7 hepatitis b
39	40	54.1	174	2	O998U8	O998U8 hepatitis b
40	40	54.1	204	2	O7THR6	O7THR6 hepatitis b
41	40	54.1	242	2	O80GT9	O80GT9 hepatitis b
42	40	54.1	242	2	O81128	O81128 hepatitis b
43	40	54.1	248	2	O86JC4	O86JC4 dicystosel
44	40	54.1	321	2	O90CF1	O90CF1 hepatitis b
45	40	54.1	325	2	O8P121	O8P121 streptococc

ALIGNMENTS

RESULT 1
TRFE_HUMAN STANDARD; PRT; 698 AA.
ID P02787; C43890; O9NOB8; O9UHV0;
AC P02787; C43890; O9NOB8; O9UHV0;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metab
DE binding globulin) (PRO1400).
GN Name=TF;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS TF*B2; TF*CHI AND TF*DI.
RX MEDLINE=84194084; PubMed=6585826;
RA Yang F., Lum J.B., McGill J.R., Moore C.M., Naylor S.L.,
RA van Bragt P.H., Baldwin W.D., Bowman B.H.,
RT "Human transferrin: cDNA characterization and chromosomal
RT localization".
RL Proc. Natl. Acad. Sci. U.S.A. 81:2752-2756(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88056305; PubMed=3678832; DOI=10.1016/0378-1119(87)90163-6;
RA Schaefer E., Lucero M.A., Jeltsch J.-M., Py M.-C., Levin M.U.,
RA Chamoun P., Cohen G.N., Zakim M.M.;
RT "Complete structure of the human transferrin gene. Comparison with
RT analogous chicken gene and human pseudogene".
RL Gene 56:109-116(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RC MEDLINE=92231399; PubMed=1809186;
RA Herberberger C.L., Larson J.L., Arnold B., Roestek P.R. Jr.,
RA Williams P., Dehoff B., Dunn P., O'Neal K.L., Rieman M.W., Tice P.A.;
RT "A cloned gene for human transferrin".
RL Ann. N. Y. Acad. Sci. 646:140-154(1991).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT ATRANSFERRINEMIA PRO-477.
RX MEDLINE=20563920; PubMed=1110675;
RA Beutler E., Gelbart T., Lee P.L., Trevino R., Fernandez M.A.,
RA Patranks V.F.;
RT "Molecular characterization of a case of atransferrinemia".
RL Blood 96:4071-4074(2000).
RN [5]
RP SEQUENCE FROM N.A.
RX Rieder M.J., Carrington D.P., da Ponte S.H., Haastings N.C.,
RA Abearn M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q.,
RA Nickerson D.A.;
RT "SeattlesNPB. NHLBI HUG6682 program for genomic applications, UM-
RT FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBD databases.
RN [6]

RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22288957; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Struhsberg R.L., Feltingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg K.H., Buelow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.J.,
RA Raha S.S., Locuallano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKean P.J., McEternan K.U., Malek U.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[17]
RP SEQUENCE OF 99-698 FROM N.A.
RC TISSUE=Fetal liver;
RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M.,
RA He F.;
RT "Functional prediction of the coding sequences of 33 new genes deduced
RT by analysis of cDNA clones from human fetal liver";
Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
[18]
RP SEQUENCE OF 422-698 FROM N.A.
RX MEDLINE=84153910; PubMed=6322780;
RX Uzan G., Frain M., Park I., Beemond C., Maessen G., Trepac J.S.,
RA Zakin M.M., Kahn A.;
RT "Molecular cloning and sequence analysis of cDNA for human
RT transferrin";
Biochem. Biophys. Res. Commun. 119:272-281(1984).
[19]
RP SEQUENCE OF 20-698.
RX MEDLINE=83160878; PubMed=6833213;
RA McGilivray R.T.A., Mendez E., Shevale J.G., Sinha S.K.,
RA Linbeck-Zins J., Brew K.;
RT "The primary structure of human serum transferrin. The structures of
RT seven cyanogen bromide fragments and the assembly of the complete
RT structure";
J. Biol. Chem. 258:3543-3553(1983).
[110]
RP SEQUENCE OF 73-698 FROM N.A.
RX MEDLINE=85216459; PubMed=3858812;
RA Park I., Schaeffer E., Sidoli A., Baralle F.E., Cohen G.N.,
RA Zakin M.M.;
RT "Organization of the human transferrin gene: direct evidence that it
RT originated by gene duplication";
Proc. Natl. Acad. Sci. U.S.A. 82:3149-3153(1985).
[111]
RP SEQUENCE OF 1-14 FROM N.A.
RX MEDLINE=87066744; PubMed=3786138;
RA Lucero M.A., Schaeffer E., Cohen G.N., Zakin M.M.;
RT "The 5' region of the human transferrin gene: structure and potential
RT regulatory sites";
Nucleic Acids Res. 14:8692-8692(1986).
[112]
RP SEQUENCE OF 1-72 AND 291-300 FROM N.A.
RX MEDLINE=87192006; PubMed=3106157; DOI=10.1016/0378-1119(86)90277-5;
RA Adrian G.S., Korinek B.W., Bowman B.H., Yang F.;
RT "The human transferrin gene: 5' region contains conserved sequences
RT which match the control elements regulated by heavy metals,
RT glucocorticoids and acute phase reaction";
Gene 49:167-175(1986).
[113]
RP SEQUENCE OF 45-72 FROM N.A.

RX MEDLINE=20392111; PubMed=10931525;
RX DOI=10.1002/1097-4547(20000815)61:4<388::AID-JNR53.0.CO;2-Q;
RA de Arriba Zepa G.A., Saleh M.-C., Fernandez P.M., Guillou F.,
RA Espinosa de los Monteros A., de Vellos J., Zakin M.M., Baron B.;
RT "Alternative splicing prevents transferrin secretion during
RT differentiation of a human oligodendrocyte cell line";
J. Neurosci. Res. 61:388-395(2000).
[114]
RP SEQUENCE OF 564-624 FROM N.A., AND VARIANT TF*G2.
RC TISSUE=Brain;
RX MEDLINE=97418135; PubMed=9272172;
RA Namakata K., Oyama F., Imagawa M., Itara Y.;
RT "Human transferrin (TF): a single mutation at codon 570 determines TF
RT C1 or TF C2 variant";
Hum. Genet. 100:457-458(1997).
[115]
RP SEQUENCE OF 564-624 FROM N.A.
RA Tsuchida S., Ikemoto S., Kajii E.;
RT Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
[116]
RP SEQUENCE OF 636-696 FROM N.A.
RX MEDLINE=89386721; PubMed=2780570;
RA Duguid J.R., Bohmont C.W., Liu N.G., Tourtelotte W.W.;
RT "Changes in brain gene expression shared by scrapie and Alzheimer
RT disease";
Proc. Natl. Acad. Sci. U.S.A. 86:7260-7264(1989).
[117]
RP SEQUENCE OF 263-266; 454-458; 531-538 AND 569-595.
RC TISSUE=Heart;
RX MEDLINE=96007936; PubMed=7498159;
RA Kovalyov L.I., Shishkin S.S., Efimochkin A.S., Kovalyova M.A.,
RA Ershova E.S., Egorov T.A., Musalyamov A.K.;
RT "The major protein expression profile and two-dimensional protein
RT database of human heart";
Electrophoresis 16:1160-1169(1995).
[118]
RP DISULFIDE BONDS.
RX MEDLINE=82222166; PubMed=6953407;
RA McGilivray R.T.A., Mendez E., Sinha S.K., Sutton M.R.,
RA Linbeck-Zins J., Brew K.;
RT "The complete amino acid sequence of human serum transferrin";
Proc. Natl. Acad. Sci. U.S.A. 79:2504-2508(1982).
[119]
RP MUTAGENESIS.
RX MEDLINE=92031536; PubMed=1932003;
RA Woodworth R.C., Mason A.B., Funk W.D., McGilivray R.T.A.;
RT "Expression and initial characterization of five site-directed mutants
RT of the N-terminal half-molecule of human transferrin";
Biochemistry 30:10824-10829(1991).
[120]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 22-350.
RX MEDLINE=98272655; PubMed=9609685; DOI=10.1021/b1980355j; Baker H.,
RA McGilivray R.T.A., Moore S.A., Chen J., Anderson B.F.,
RA Luo Y., Bewley M.C., Smith C.A., Murphy M.E.P., Wang Y., Mason A.B.,
RA Woodworth R.C., Brayer G.D., Baker E.N.;
RT "Two high-resolution crystal structures of the recombinant N-lobe of
RT human transferrin reveal a structural change implicated in iron
RT release";
Biochemistry 37:7919-7928(1998).
[121]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-350.
RX MEDLINE=98434369; PubMed=9760232; DOI=10.1021/b19812064j; Baker H.,
RA Jeffrey P.D., Bewley M.C., McGilivray R.T.A., Mason A.B.,
RA Woodworth R.C., Baker E.N.;
RT "Ligand-induced conformational change in transferrins: crystal
RT structure of the open form of the N-terminal half-molecule of human
RT transferrin";
Biochemistry 37:13978-13986(1998).
[122]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 23-352.
RX MEDLINE=99155227; PubMed=10029548; DOI=10.1021/b19824543j; Baker H.,
RA Bewley M.C., Tam B.M., Grewal J., He S., Shewry S., Murphy M.E.P.,
RA Mason A.B., Woodworth R.C., Baker E.N., McGilivray R.T.A.;

RT "X-ray crystallography and mass spectroscopy reveal that the N-lobe of human transferrin expressed in *Pichia pastoris* is folded correctly but

Query Match 81.4%; Score 60; DB 1; Length 698;
 Best Local Similarity 85.7%; Pred. No. 0.059;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMGSGLNLEPN 15
 DB 515 KLCMSGGLNLEPN 528

RESULT 2
 Q9E952 PRELIMINARY; PRT; 400 AA.
 ID Q9E952;
 AC Q9E952;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Large surface antigen.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirine.
 NC NCBITaxid=10407;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20528423; PubMed=11074474;
 RX DOI=10.1002/1096-9071(200012)62:4<456::AID-JMV10-3.CO;2-3;
 RA Suganchi F., Mizokami M., Orito E., Ohno T., Kato H., Maki M.,
 RA Suzuki H., Ojika K., Ueda R.;
 RT "Hepatitis B virus infection among residents of a nursing home for the
 RT elderly: seroepidemiological study and molecular evolutionary
 RT analysis.";
 RT J. Med. Virol. 62:456-462(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Suganchi F.;
 RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL:AB042246; BAB17298.1; -.
 DR PIR:JQ2094; JQ2094.
 DR PIR:JQ2095; JQ2095.
 DR PIR:JQ2096; JQ2096.
 DR PIR:JQ2097; JQ2097.
 DR PIR:JQ2098; JQ2098.
 DR PIR:JQ2099; JQ2099.
 DR PIR:JQ2100; JQ2100.
 DR PIR:JQ2101; JQ2101.
 DR PIR:JQ2102; JQ2102.
 DR PIR:JQ2106; JQ2106.
 DR PIR:JQ2108; JQ2108.
 DR PIR:JQ2109; JQ2109.
 DR PIR:JQ2111; JQ2111.
 DR PIR:JQ2112; JQ2112.
 DR PIR:JQ2116; JQ2116.
 DR GO:GO:0016032; P:Viral life cycle; IEA.
 DR InterPro:IPR000349; Hepvir_surtag.
 DR Pfam:PF00695; VMSA; 1.
 KW Antigen.
 SQ SEQUENCE 400 AA; 43655 MW; 3B22DF329A8266C6 CRC64;

Query Match 63.5%; Score 47; DB 2; Length 400;
 Best Local Similarity 66.7%; Pred. No. 7.6;
 Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KLSMGSGLNLEPN 15
 DB 6 SKLRGSGTLNLSVPN 20

RESULT 3
 Q943K6 PRELIMINARY; PRT; 521 AA.
 ID Q943K6;
 AC Q943K6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Putative SLT1 protein (ion homeostasis related protein)
 DE (Sodium/lithium tolerance protein).
 GN Name=P0031D11.29; Synonyms=P0408C03.13;
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Enarthrodidae; Oryzaceae; Oryza.
 NC NCBITaxid=3947;
 OX [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=12447438; DOI=10.1038/nature01184;
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
 RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
 RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayaishi M.,
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
 RA Hijiabita S., Honda M., Ichikawa Y., Iidoma A., Iijima M., Ikeda M.,
 RA Ikono M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
 RA Katsawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
 RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
 RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
 RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
 RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
 RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
 RA Yano M., Jiang J., Gojobori T.;
 RT "The genome sequence and structure of rice chromosome 1.";
 RL Nature 420:312-316(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Antoine W., Stewart J.M., de los Reyes B.G.;
 RT "Evolution of SLT gene family: a new subclass of plant-specific heat
 RT shock proteins.";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Antoine W., Stewart J.M., de los Reyes B.G.;
 RT "Posttranslational modification of the rice SLT proteins is required
 RT for chaperone activity under stress conditions.";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL:AP003231; BAB67895.1; -.
 DR EMBL:AP003241; BAB93215.1; -.
 DR EMBL:AF672599; AAT81168.1; -.
 DR Gramene:Q943K6; -.
 DR InterPro:IPR008978; HSP20_chap.
 DR InterPro:IPR000834; Peptidase M14.
 DR PROSITE:PS00133; CARBOXYPEPT_ZN_2; UNKNOWN 1.
 DR PROSITE:PS00133; CARBOXYPEPT_ZN_2; UNKNOWN 1.
 SQ SEQUENCE 521 AA; 58300 MW; 4CA7F68BB35F570 CRC64;

Query Match 63.5%; Score 47; DB 2; Length 521;
 Best Local Similarity 71.4%; Pred. No. 10;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KLSMGSGLNLEPN 15
 DB 303 KLSMGSGLNLEPN 316

RESULT 4
 O8J2T2 PRELIMINARY; PRT; 823 AA.
 ID O8J2T2;
 AC O8J2T2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE G-protein coupled receptor.
 GN Name=cagPR1;
 OS Candida albicans (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 NC NCBITaxid=5476;
 OX [1]

```

RP SEQUENCE FROM N.A.
RX PubMed=15302825;
RA Miwa T., Takagi Y., Shinozaki M., Yun C.W., Schell W.A., Perfect J.R.,
RA Kumagai H., Tamaki H.;
RT "Gpr1, a putative G-protein-coupled receptor, regulates morphogenesis
RT and hypha formation in the pathogenic fungus Candida albicans.";
RL Eukaryotic Cell 3:919-931(2004).
DR EMBL, AB084519; BAC22916.1; -.
DR GO, GO:0004872; P:receptor activity; IEA.
DR InterPro, IPR002048; EF-hand.
DR PROSITE, PS00018; EF_HAND; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 823 AA; 92340 MW; 4B3A61EBDD6E709 CRC64;

Query Match
Best Local Similarity 57.1%; Score 46; DB 2; Length 823;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SKLMSGGLNISEPN 14
Db 656 SPMSGAGINWTEP 669

RESULT 5
Q7PD10 PRELIMINARY; PRT; 368 AA.
AC Q7PD10;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE ENSANG00000015427 (ENSANGP0000006590) (Fragment).
GN Name=ENSANG00000012938; Synonyms=ENSANG00000049922;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxId=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
FT EMBL; AAA01008192; EAA03293.2; -.
FT NON_TER 1 368
FT NON_TER 368 368
SQ SEQUENCE 368 AA; 40792 MW; 8D3D3663C0A29CF CRC64;

Query Match
Best Local Similarity 58.1%; Score 43; DB 2; Length 368;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 LSMGGLNISEPN 15
Db 147 ISLGLGNADPN 159

RESULT 6
Q8NC87 PRELIMINARY; PRT; 796 AA.
AC Q8NC87;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ90414.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,

```

```

RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Maeshio Y., Oho T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Nishimura K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK074895; BAC11274.1; -.
DR HSSP; Q9UG0.1P62.
DR GO, GO:0003577; P:DNA binding; IEA.
DR GO, GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro, IPR01011; FIVE_PHD_Znf.
DR InterPro, IPR01965; Znf_PHD.
DR Pfam; PF00628; PHD; 1.
DR SMART; SM00249; PHD; 1.
DR PROSITE; PS0016; ZF_PHD_2; 1.
FT NON_TER 796 796
SQ SEQUENCE 796 AA; 88462 MW; 2EDB8BCAF9720C1E CRC64;

Query Match
Best Local Similarity 58.1%; Score 43; DB 2; Length 796;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 SMGGLNISEPN 15
Db 416 SLGSLGISEGN 427

RESULT 7
BA2B HUMAN STANDARD; PRT; 1972 AA.
AC Q9UJF8; Q96EAL; Q96SQ8; Q9P252; Q9Y4N8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Bromodomain adjacent to zinc finger domain 2B (hMALP4).
GN Name=BA2B2; Synonyms=KIAA1476;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Testis;
RA Nagase T., Kikuno R., Ishikawa K.-I., Hirosewa M., Ohara O.;
RX MEDLINE=20130112; PubMed=10662543; DOI=10.1006/geno.1999.6071;
RA Jones M.H., Hamana N., Nezu J., Shimane M.;
RT "A novel family of bromodomain genes.";
RL Genomics 63:40-45(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RA Ohara O., Nagase T., Kikuno R.;
RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 753-1972 FROM N.A.
RA MEDLINE=20277482; PubMed=10819331;
RX Nagase T., Kikuno R., Ishikawa K.-I., Hirosewa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XVII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 7:143-150(2000).
RN [4]
RP SEQUENCE OF 1-776 FROM N.A. (ISOFORM 1).
RC TISSUE=Melanoma;
RA Ansoerge W., Winkner U., Mewes H.-W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 1-799 FROM N.A. (ISOFORM 2).
RC TISSUE=Skeletal muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffner C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

```

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrincci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Vallion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield J.S.N., Krzywiński M.I., Skalska A., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [6]
 RN SEQUENCE OF 427-1215 FROM N.A. (ISOFORM 3).
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Ohtsuki T., Sugiyama T., Irie R.,
 RA Makamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohtsuka M., Nishitani T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
 RA Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
 RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
 RA Omura Y., Abe K., Kamihara K., Katsuma N., Sato K., Tanikawa M.,
 RA Yamazaki M., Ninomiya K., Iwihashi T., Yamashita H., Murakawa K.,
 RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y.,
 RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Houchi T.,
 RA Kusano Y., Kanohori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
 RA Nomura Y., Togiyasu K., Komai F., Hara R., Takeuchi K., Arita M.,
 RA Imose N., Mueselsho K., Yuki H., Oshima A., Sasaki N., Aoseuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakeda H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kishigaki A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiro M., Ohnishi Y.,
 RA Kawabata A., Hikiyama T., Kobayashi N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togaishi T., Oyama H., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Saito T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Maeno Y., Yamashita R.,
 RA Nakai K., Iada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs";
 RT Nat. Genet. 36:40-45(2004).
 RN [7]
 RP SEQUENCE OF 1524-1972 FROM N.A.
 RC TISSUE=Testis;
 RA Pousetka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.,
 RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ database.
 CC -1- FUNCTION: May play a role in transcriptional regulation
 CC interacting with ISW1.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing, Named isoforms=3;
 CC Comment=Experimental confirmation may be lacking for some
 CC isoforms;
 CC Name=1;
 CC IsoId=Q9UIF8-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9UIF8-2; Sequence=VSP_000553;
 CC Name=3;
 CC IsoId=Q9UIF8-3; Sequence=VSP_000554;
 CC Note=Inferred from Ref.5;
 CC Note=Inferred from Ref.4;
 CC -1- TISSUE SPECIFICITY: Expressed at varying levels in several
 CC tissues, whereas a smaller transcript was expressed specifically
 CC in testis.
 CC -1- SIMILARITY: Belongs to the WAL family.
 CC -1- SIMILARITY: Contains 1 bromodomain.
 CC -1- SIMILARITY: Contains 1 DDT domain.

CC -1- SIMILARITY: Contains 1 methyl-CpG-binding (MBD) domain.
 CC -1- SIMILARITY: Contains 1 PHD-type zinc finger.
 CC -1- CAUTION: Ref.5 sequence differs from that shown due to a
 CC frameshift in position 731.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AB032255; BAA89212.1; -;
 CC EMBL; AB040909; BAA96000.2; ALT INIT.
 CC EMBL; AL834381; CAD39044.1; ALT INIT.
 CC EMBL; BC012576; AAH12576.1; ALT FRAME.
 CC EMBL; AK027612; BAB55231.1; ALT INIT.
 CC EMBL; AL080173; CB45759.1; -;
 CC F1R; T12495; T12495.
 CC HSSP; Q9UIG0; I162.
 CC GENEW; HGNC:963; BAZ2B.
 CC MIM; 605683; -;
 CC InterPro: IPR001487; Bromodomain.
 CC InterPro: IPR004032; DDT.
 CC InterPro: IPR001739; Methyl-CpG bind.
 CC InterPro: IPR001965; ZnF_PHD.
 CC Pfam; PF00439; Bromodomain; 1.
 CC Pfam; PF02791; DDT; 1.
 CC Pfam; PF01429; MBD; 1.
 CC Pfam; PF00628; PHD; 1.
 CC PRINTS; PR00503; BROMODOMAIN.
 CC PROSITE; PS00653; BROMODOMAIN_1; FALSE_NEG.
 CC PROSITE; PS50014; BROMODOMAIN_2; 1.
 CC PROSITE; PS50827; DDT; 1.
 CC PROSITE; PS50982; MBD; 1.
 CC PROSITE; PS01359; ZF_PHD_1; FALSE_NEG.
 CC PROSITE; PS50016; ZF_PHD_2; 1.
 CC KX Alternative splicing; Bromodomain; Coiled coil; DNA-binding;
 CC KW Nuclear protein; Transcription regulation; zinc-finger.
 CC FT DOMAIN 543 614
 CC FT DOMAIN 891 956
 CC FT ZN FING 1735 1765
 CC FT DOMAIN 1881 1951
 CC FT DOMAIN 45 69
 CC FT DOMAIN 73 79
 CC FT DOMAIN 399 470
 CC FT DOMAIN 641 672
 CC FT DOMAIN 687 865
 CC FT DOMAIN 706 875
 CC FT DOMAIN 1100 1143
 CC FT DOMAIN 1138 1179
 CC FT VARSPPLIC 437 534
 CC FT
 CC FT VARSPPLIC 593 626
 CC FT
 CC FT CONFLICT 137 137
 CC FT CONFLICT 226 226
 CC FT CONFLICT 627 627
 CC FT CONFLICT 722 722
 CC FT CONFLICT 790 799
 CC FT CONFLICT 1128 1128
 CC FT CONFLICT 1183 1183
 CC FT CONFLICT 1195 1195
 CC FT CONFLICT 1453 1453
 CC FT CONFLICT 1838 1838
 CC SO SEQUENCE 1972 AA; 220709 MW; D4F105C927B91569 CRC64;
 CC -----
 CC Query Match 58.1%; Score 43; DB 1; Length 1972;
 CC Best Local Similarity 75.0%;
 CC Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 SWGSGINLSEPN 15

DB 1457 SLGSGGLSEGN 1468

RESULT 8

Q6FMKO: PRELIMINARY; PRT; 307 AA.
 ID Q6FMKO: PRELIMINARY; PRT; 307 AA.
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Similar to sp|Q04013 Saccharomyces cerevisiae YMR241w.
 GN ORFNames=CAGL0K07436g;
 OS Candida glabrata CBS138.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Microsporici Saccharomycetales; Candida.
 OC NCBI_TaxID=284593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS138;
 RC Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marc C., Neuvéglise C., Talla E.,
 RA Goffard N., Frangoul L., Aigle M., Anthonard V., Babour A., Barde V.,
 RA Baray S., Blanchin S., Beckerich J.M., Beyne E., Bleyaesten C.,
 RA Bolgerme A., Boyer J., Catolico L., Confantoleri F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lebur I., Ma L., Muller H.,
 RA Nicod J.M., Nikolaki M., Otae S., Oster-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zentgraf-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudon B., Scarpelli C., Galliard C., Weisenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 CC -1 SIMILARITY: Belongs to the mitochondrial carrier family.
 DR EMBL: CR380957; CAG61507.1; -;
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0005488; F:binding; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR001993; Mitoch carrier.
 DR Pfam: PF00153; Mitoc carr; 2.
 DR PROSITE: PS50920; SOLCAR; 2.
 KW Transmembrane; Transport.
 SQ SEQUENCE 307 AA; 33587 MW; 1A5859ADDBA74C47 CRC64;

Query Match

Best Local Similarity 56.8%; Score 42; DB 2; Length 307;
 Pred. No. 47;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SKLWSGSLNSE 13
 DB 13 SNILGAGLISB 25

RESULT 9

Q8GPA0: PRELIMINARY; PRT; 428 AA.
 ID Q8GPA0: PRELIMINARY; PRT; 428 AA.
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Epaillo.
 GN Name=epaillo;
 OS Streptococcus thermophilus.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 GN NCBI_TaxID=1308;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rallu F., Ehrlich D.S., Renault P.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF454501; AAN63800.1; -;
 SQ SEQUENCE 428 AA; 50454 MW; D2PB3E0EDD466547 CRC64;

Query Match 56.8%; Score 42; DB 2; Length 428;
 Best Local Similarity 69.2%; Pred. No. 68;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 KLSWGSGLNSEP 14
 DB 20 KKSWMGYNLKEP 32

RESULT 10

Q8J289: PRELIMINARY; PRT; 528 AA.
 ID Q8J289: PRELIMINARY; PRT; 528 AA.
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE YGL104C.
 OS Kluyveromyces lactic (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetales; Kluyveromyces.
 OC NCBI_TaxID=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22307030; PubMed=12420142;
 RA Takcova M., Sklennar P., Gbeliska Y., Breunig K., Subik J.;
 RT "Isolation, heterologal cloning and sequencing of the RPL28 gene in
 RT Kluyveromyces lactic."
 RL Curr. Genet. 42:21-26(2002).
 CC -1 SIMILARITY: Integral membrane protein (By similarity).
 DR EMBL: AF493565; AAN65374.1; -;
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0005351; C:sugar porter activity; IEA.
 DR GO: GO:0005215; F:transporter activity; IEA.
 DR GO: GO:0006643; P:carbohydrate transport; IEA.
 DR InterPro: IPR007114; MFS.
 DR InterPro: IPR005828; Sub_transporter.
 DR InterPro: IPR003663; Sugar_transp.
 DR InterPro: IPR005829; Sug transporter.
 DR Pfam: PF00083; Sugar tr; 1.
 DR PRINTS: PR00171; SUGTRNSPORT.
 DR TIGRFAMs: TIGR00879; SP; 1.
 DR PROSITE: PS50850; MFS; 1.
 DR PROSITE: PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
 DR PROSITE: PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.
 KW Sugar transport; Transmembrane; Transport.
 SQ SEQUENCE 528 AA; 58196 MW; 140D68B8E3E26E732 CRC64;

Query Match

Best Local Similarity 56.8%; Score 42; DB 2; Length 528;
 Pred. No. 86;
 Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 SKLWSGSLNSEPN 15
 DB 288 SQMNGSNLNERPS 302

RESULT 11

Q6CKZ8: PRELIMINARY; PRT; 528 AA.
 ID Q6CKZ8: PRELIMINARY; PRT; 528 AA.
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Similarity.
 GN ORFNames=KLIA0F06853g;
 OS Kluyveromyces lactic NRRL Y-1140.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetales; Kluyveromyces.

OX NCBI_TaxId=284590;
RN SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RG Genolevures;
RA Goffard N., Sherman D., Fischer G., Durieux P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neveuglise C., Talla E.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleykasten C.,
RA Boistrame A., Boyer J., Cateoico L., Confantollet F., de Darvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nkolleli M., Ozras S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swenne D., Terafa F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Weyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpeilli C., Gaillardin C., Weissenbach J.,
RA Mancker P., Souclet J.L.;
RT "Genome evolution in yeasts."
RL Nature 430:35-44(2004).
RN SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the sugar transporter family.
DR EMBL: CB382126; CAG98099.1; -;
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005351; F:sugar porter activity; IEA.
DR GO: GO:0005215; F:transporter activity; IEA.
DR GO: GO:0006643; P:carbohydrate transport; IEA.
DR InterPro: IPR007114; MFS.
DR InterPro: IPR005828; Sub_transporter.
DR InterPro: IPR003663; Sugar_transp.
DR InterPro: IPR005829; Sug_transporter.
DR Pfam: PF00083; Sugar tr; 1.
DR PRINTS: PR00171; SUGTRANSPORT.
DR TIGRFAIR: TIGR00879; SP; 1.
DR PROSITE: PS50850; MFS; 1.
DR PROSITE: PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
DR PROSITE: PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.
KW Sugar transporter; Transmembrane; Transport.
SQ SEQUENCE 528 AA; 58196 MW; 14068B83E26E732 CRC64;
Query Match 56.8%; Score 42; DB 2; Length 528;
Best Local Similarity 46.7%; Pred. No. 86;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 1 SKLMSGSLNLEPN 15
DB 288 SQMNLGSNLEPN 302
RESULT 12
ID 08U379 PRELIMINARY; PRT; 867 AA.
AC 08U379;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ATP-dependent RNA helicase, putative.
GN OrderedLocNames=PF0592;
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxId=2261;
RN SEQUENCE FROM N.A.
RC STRAIN=Vci / DSM 3638 / ATCC 43587 / JCM 8422;
RC Weiss B.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE010181; AAL80716.1; -;
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO: GO:0003676; P:nucleic acid binding; IEA.
DR Pfam: PF00270; DEAD; 1.
DR Pfam: PF00271; Helicase_C; 1.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00490; HELIC; 1.
KW ATP-binding; Complete proteome; Helicase; Hydrolyase.
SQ SEQUENCE 867 AA; 101122 MW; 8F633D547552448B CRC64;
Query Match 56.8%; Score 42; DB 2; Length 867;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 SKLMSGSLNLEPN 15
DB 753 SKDGISGLHAIEN 767
RESULT 13
ID 08INF9 PRELIMINARY; PRT; 3358 AA.
AC 08INF9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG8651-PB (CG8651-PC).
GN Name=trix; ORFNames=CG8651;
OS Drosophila melanogaster (Fruit fly).
OC Diptera; Insecta; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,
RA Abril J.F., Agbayani A., An H.V., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brodeur P., Brotier P.,
RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Idegam C.,
RA Jalali M., Kalish F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Paclib J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wastaman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 13:53:15 ; Search time 161 Seconds
(without alignments)
36.034 Million cell updates/sec

Title: US-10-612-162a-3

Sequence: 1 SKLSMGSGNLSEPN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 632537

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	74	100.0	15	8	ADG46077	Adg46077 Human CDT
2	65	87.8	13	8	ADG46094	Adg46094 Human CDT
3	55	74.3	15	8	ADRI5909	Adri5909 Transferr
4	55	74.3	15	8	ADRI5970	Adri5970 Transferr
5	55	74.3	15	8	ADSI3393	Adsi3393 Human rbe
6	55	74.3	15	8	ADSI3389	Adsi3389 Human rbe
7	33	44.6	15	3	AAV70486	AAV70486 Synthesis
8	30	40.5	9	5	ABU08867	Abj08867 Hepatitis
9	30	40.5	9	5	ABU09159	Abj09159 Hepatitis
10	30	40.5	9	8	ADQ12374	Adq12374 Hepatitis
11	30	40.5	10	2	AAK38384	AAK38384 T-cell ep
12	30	40.5	10	2	AAK38384	AAK38384 T-cell ep
13	30	40.5	10	5	ABU07286	Abj07286 Hepatitis
14	30	40.5	10	5	ABU06082	Abj06082 Hepatitis
15	30	40.5	10	8	ADK37389	Adk37389 Hepatitis
16	30	40.5	10	8	ADK38506	Adk38506 Hepatitis
17	30	40.5	10	8	ADK38506	Adk38506 Hepatitis
18	30	40.5	14	2	AAV23365	AAV23365 CDR3 sequ
19	30	40.5	15	2	AAK52914	AAK52914 V-alpha c
20	30	40.5	15	2	AAK34866	AAK34866 Peptide f
21	30	40.5	15	2	AAK43544	AAK43544 Mycobacte
22	30	40.5	15	5	ABJ08961	Abj08961 Hepatitis
23	30	40.5	15	5	ABJ09253	Abj09253 Hepatitis
24	30	40.5	15	5	ADK39233	Adk39233 Hepatitis
25	30	40.5	15	8	ADK39233	Adk39233 Hepatitis

26	29	39.2	10	2	AAW21293	AAW21293 Hydroxyne
27	29	39.2	13	4	AAU02673	AAU02673 CDR regio
28	29	39.2	13	4	AAU03316	AAU03316 Fruit fly
29	29	39.2	13	6	ABJ36774	Abj36774 G protein
30	29	39.2	13	6	ABJ36773	Abj36773 G protein
31	29	39.2	13	7	ABW00016	Abw00016 Human G a
32	29	39.2	13	7	ABW00017	Abw00017 Human G a
33	29	39.2	13	7	ADL14646	Adel14646 DmgPCR bl
34	29	39.2	13	7	ADP45271	Adp45271 G alpha c
35	29	39.2	13	7	ADP45270	Adp45270 G alpha c
36	29	39.2	13	7	ADL83494	Adl83494 Drosophila
37	29	39.2	13	8	ADR03214	Adr03214 G-protein
38	29	39.2	15	4	AAK78238	AAK78238 Human hex
39	29	39.2	15	6	ABR31310	Abri31310 Human can
40	29	39.2	15	6	ABR31106	Abri31106 Human can
41	29	39.2	15	6	ABR30735	Abri30735 Human can
42	29	39.2	15	6	ABR30664	Abri30664 Human can
43	29	39.2	15	6	ABR31569	Abri31569 Human can
44	29	39.2	15	6	ABR30379	Abri30379 Human can
45	29	39.2	15	6	ABR30870	Abri30870 Human can

ALIGNMENTS

RESULT 1
ADG46077
ID ADG46077 standard; peptide; 15 AA.

AC ADG46077;

DT 25-MAR-2004 (first entry)

DE Human CDT peptide fragment #3.

KW antibody; carbohydrate-deficient transferrin; CDT;
non-glycosylated transferrin; alcoholism; alcoholic; diagnosis; human.

XX Homo sapiens.

XX EP1378521-A1.

XX 07-JUN-2004.

XX 19-MAY-2003; 2003EP-00011334.

XX 05-JUL-2002; 2002DE-01030550.

XX (DADE-) DABE BEHRING MAREBURG GMBH.

XX Althaus H;

XX WPI; 2004-073743/08.

PT New antibody specific for carbohydrate-deficient transferrin, useful for
diagnosis of alcoholism, can bind its target in solution, eliminating
need for immobilization.

PT Claim 4; SEQ ID NO 3; 21bp; German.

XX This invention describes a novel antibody that, in aqueous solution,
binds selectively to carbohydrate-deficient transferrin (CDT) without
having to bind CDT to a solid phase. The invention also describes an
antibody that binds selectively to CDT at regions containing the
sequences VVARSMGSGKDLIMELT, TTEDSIAXIMNGEADAMSLDGF, SKLSMGSGNLSEPN and
YEKYGEYVRAV (ADG46075-ADG46078) and an immunoassay for detecting CDT
using the antibodies of the invention. The antibodies of the invention
are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
antibodies are obtained by immunisation with non-glycosylated
transferrin, or a fragment, then generation of hybridomas by standard
fusion of spleen and myeloma cells. Hybridomas are then selected for
production of antibodies that specifically bind CDT from the aqueous
phase. The antibodies are useful for diagnosis of alcoholism, CDT, which

CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
 CC alcoholics. The antibodies allow direct detection of CDT in solution,
 CC eliminating the need for immobilizing it on a solid phase (as required
 CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
 CC fragments used in the method of the invention.

CC Sequence 15 AA;

Query Match 100.0%; Score 74; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3,3e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SKLSMGSGLNLSPPN 15
 |||||
 1 SKLSMGSGLNLSPPN 15

Db

RESULT 2
 ADG46094
 ID ADG46094 standard; peptide; 13 AA.
 XX
 AC ADG46094;

XX 25-MAR-2004 (first entry)

XX Human CDT peptide fragment #20.

DE antibody; carbohydrate-deficient transferrin; CDT;
 XX non-glycosylated transferrin; alcoholism; diagnosis; human.

OS Homo sapiens.

XX EP1378521-A1.

XX 07-JAN-2004.

XX 19-MAY-2003; 2003EP-00011334.

XX 05-JUL-2002; 2002DE-01030550.

XX (DADE-) DADE BEHRING MARBURG GMBH.

XX Althaus H;

XX WPI; 2004-073743/08.

XX New antibody specific for carbohydrate-deficient transferrin, useful for
 PT diagnosis of alcoholism, can bind its target in solution, eliminating
 PT need for immobilization.

XX Example 7; Page 15; 21pp; German.

CC This invention describes a novel antibody that, in aqueous solution,
 CC binds selectively to carbohydrate-deficient transferrin (CDT) without
 CC having to bind CDT to a solid phase. The invention also describes an
 CC antibody that binds selectively to CDT at regions containing the
 CC sequences VVAASMGSGKEDLWEEL, TTEDSIAKRMNGEADAMSIDGGF, SKLSMGSGLNLSPPN and
 CC VERKIGEEYKAV (ADG46075-ADG46078) and an immunoassay for detecting CDT
 CC using the antibodies of the invention. The antibodies of the invention
 CC are monoclonal, specifically from hybridomas DSM ACC2540, or 2541. The
 CC antibodies are obtained by immunisation with non-glycosylated
 CC transferrin, or a fragment, then generation of hybridomas by standard
 CC fusion of spleen and myeloma cells. Hybridomas are then selected for
 CC production of antibodies that specifically bind CDT from the aqueous
 CC phase. The antibodies are useful for diagnosis of alcoholism, CDT, which
 CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
 CC alcoholics. The antibodies allow direct detection of CDT in solution,
 CC eliminating the need for immobilizing it on a solid phase (as required
 CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
 CC fragments used in the method of the invention.

XX Sequence 13 AA;

Query Match 87.8%; Score 65; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 LSMGSGLNLSPPN 15
 |||||
 1 LSMGSGLNLSPPN 13

Db

RESULT 3
 ADRI5909
 ID ADRI5909 standard; peptide; 15 AA.
 XX
 AC ADRI5909;

XX 04-NOV-2004 (first entry)

XX Transferrin peptide fragment #67.

XX glycosylation; proteolytic enzyme; proteolysis; detection; transferrin.

OS Synthetic.

XX WO2004070389-A1.

XX 19-AUG-2004.

XX 06-FEB-2004; 2004WO-GB000480.

XX 06-FEB-2003; 2003GB-00002740.

XX (AXIS-) AXIS-SHIELD ASA.

XX Rye PD;

XX WPI; 2004-625547/60.

XX Assay for differentiating protein isoforms to determine their
 PT concentrations in sample e.g. blood, involves contacting the sample with
 PT proteolytic enzyme to produce peptide fragment by proteolysis followed by
 PT detecting.

XX Disclosure; Page 15; 30pp; English.

XX The present invention describes an assay for a protein having at least
 CC two isoforms with different glycosylation patterns. The assay involves
 CC contacting a sample containing the protein with a proteolytic enzyme,
 CC followed by detecting the content or relative content of at least one
 CC peptide fragment produced by proteolysis. Also described is a kit for the
 CC assay method comprising the proteolytic enzyme and a substrate bound
 CC specific binding partner (S1) for at least 2 of the isoforms of the
 CC proteins. The method can be used for assaying isoforms of proteins
 CC according to their glycosylation pattern to determine their concentration
 CC or relative concentration in the sample or material (e.g. blood). The
 CC method avoids use of antibodies for distinguishing between glycosylated
 CC isoforms of the proteins. The present sequence represents a transferrin
 CC peptide fragment which is used in the exemplification of the present
 CC invention.

XX Sequence 15 AA;

Query Match 74.3%; Score 55; DB 8; Length 15;
 Best Local Similarity 84.6%; Pred. No. 0.0087;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 LSMGSGLNLSPPN 15
 |||||
 1 LCMGSGLNLSPPN 13

Db

RESULT 4
 ADRI5970
 ID ADRI5970 standard; peptide; 15 AA.

```

XX AC ADR15970;
XX
XX DT 04-NOV-2004 (first entry)
XX
XX DE Transferrin peptide fragment #128.
XX
XX KM glycosylation; proteolytic enzyme; proteolysis; detection; transferrin.
XX
XX OS Synthetic.
XX
XX PN WO2004070389-A1.
XX
XX PD 19-AUG-2004.
XX
XX PF 06-FEB-2004; 2004WO-GB000480.
XX
XX PR 06-FEB-2003; 2003GB-00002740.
XX
XX PA (AXIS-) AXIS-SHIELD ASA.
XX
XX PI Rye PD;
XX
XX DR WPI; 2004-625547/60.
XX
XX PT Assay for differentiating protein isoforms to determine their
XX concentrations in sample e.g. blood, involves contacting the sample with
XX proteolytic enzyme to produce peptide fragment by proteolysis followed by
XX detecting.
XX
XX PS Disclosure; Page 17; 30pp; English.
XX
XX CC The present invention describes an assay for a protein having at least
XX two isoforms with different glycosylation patterns. The assay involves
XX contacting a sample containing the protein with a proteolytic enzyme,
XX followed by detecting the content or relative content of at least one
XX peptide fragment produced by proteolysis. Also described is a kit for the
XX assay method comprising the proteolytic enzyme and a substrate bound
XX specific binding partner (S1) for at least 2 of the isoforms of the
XX proteins. The method can be used for assaying isoforms of proteins
XX according to their glycosylation pattern to determine their concentration
XX or relative concentration in the sample or material (e.g. blood). The
XX method avoids use of antibodies for distinguishing between glycosylated
XX isoforms of the proteins. The present sequence represents a transferrin
XX peptide fragment which is used in the exemplification of the present
XX invention.
XX
XX SQ Sequence 15 AA;
XX
XX Query Match 74.3%; Score 55; DB 8; Length 15;
XX Best Local Similarity 84.6%; Pred. No. 0.0087;
XX Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 3 LSWGSGLNISEPN 15
XX | | | | | | | | | |
XX Db 1 LCMGSGLNICEPN 13
XX
XX RESULT 5
XX ADS13393
XX ID ADS13393 standard; peptide; 15 AA.
XX
XX AC ADS13393;
XX
XX DT 16-DEC-2004 (first entry)
XX
XX DE Human rheumatoid arthritis marker peptide - SEQ ID 184.
XX
XX KM rheumatoid arthritis; marker; antiinflammatory; antiarthritic.
XX
XX OS Homo sapiens.
XX
XX PN WO2004082617-A2.

```

```

XX PD 30-SEP-2004.
XX
XX PF 15-MAR-2004; 2004WO-US007880.
XX
XX PR 14-MAR-2003; 2003US-0455037P.
XX
XX PA (SURR-) SURROMED INC.
XX
XX PI Kantor AB, Becker CH, Schulman H;
XX
XX DR WPI; 2004-690929/67.
XX
XX PT New isolated marker for rheumatoid arthritis, useful in preparing a
XX composition for diagnosing or treating rheumatoid arthritis.
XX
XX PS Claim 1; SEQ ID NO 184; 184pp; English.
XX
XX CC The invention relates to a novel isolated marker for rheumatoid arthritis
XX selected from one of many (around 400) markers defined in the
XX specification. Rheumatoid arthritis is a chronic inflammatory disorder of
XX the small joints which is estimated to affect 2.1 million people in the
XX United States alone. Current approaches to treat the disease include the
XX use of non-steroidal antiinflammatory drugs (NSAIDs), which may reduce
XX pain, swelling and inflammation, and disease-modifying anti-rheumatic
XX drugs (DMARDs), which act to slow the progression of the disease and
XX avoid further joint injury. These drugs are associated with a number of
XX serious side effects and the search for improved therapeutics is a
XX subject of active research. The marker of the invention demonstrates
XX antiarthritic activity and may be useful in preparing a composition for
XX diagnosing or treating rheumatoid arthritis. The current sequence is that
XX of a human rheumatoid arthritis marker peptide of the invention.
XX
XX SQ Sequence 15 AA;
XX
XX Query Match 74.3%; Score 55; DB 8; Length 15;
XX Best Local Similarity 84.6%; Pred. No. 0.0087;
XX Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 3 LSWGSGLNISEPN 15
XX | | | | | | | | | |
XX Db 1 LCMGSGLNICEPN 13
XX
XX RESULT 6
XX ADS13389
XX ID ADS13389 standard; peptide; 15 AA.
XX
XX AC ADS13389;
XX
XX DT 16-DEC-2004 (first entry)
XX
XX DE Human rheumatoid arthritis marker peptide - SEQ ID 180.
XX
XX KM rheumatoid arthritis; marker; antiinflammatory; antiarthritic.
XX
XX OS Homo sapiens.
XX
XX PN WO2004082617-A2.
XX
XX PD 30-SEP-2004.
XX
XX PF 15-MAR-2004; 2004WO-US007880.
XX
XX PR 14-MAR-2003; 2003US-0455037P.
XX
XX PA (SURR-) SURROMED INC.
XX
XX PI Kantor AB, Becker CH, Schulman H;
XX
XX DR WPI; 2004-690929/67.
XX
XX PT New isolated marker for rheumatoid arthritis, useful in preparing a

```

PT composition for diagnosing or treating rheumatoid arthritis.
XX
PS Claim 1; SEQ ID NO 180; 184bp; English.
XX
CC The invention relates to a novel isolated marker for rheumatoid arthritis
CC selected from one of many (around 400) markers defined in the
CC specification. Rheumatoid arthritis is a chronic inflammatory disorder of
CC the small joints which is estimated to affect 2.1 million people in the
CC United States alone. Current approaches to treat the disease include the
CC use of non-steroidal antiinflammatory drugs (NSAIDs), which may reduce
CC pain, swelling and inflammation, and disease-modifying anti-rheumatic
CC drugs (DMARDs), which act to slow the progression of the disease and
CC avoid further joint injury. These drugs are associated with a number of
CC serious side effects and the search for improved therapeutics is a
CC subject of active research. The marker of the invention demonstrates
CC antiarthritis activity and may be useful in preparing a composition for
CC diagnosing or treating rheumatoid arthritis. The current sequence is that
CC of a human rheumatoid arthritis marker peptide of the invention.
XX
SQ Sequence 15 AA;

Query Match 74.3%; Score 55; DB 8; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.0087;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 LSMGSLNLEPN 15
| | | | | | | | | | | | | | | | |
DB 1 LCMGSLNLEPN 13

RESULT 7
AAV70486
ID AAV70486 standard; protein; 15 AA.
AC AAV70486;
XX
DT 04-JUL-2000 (first entry)
XX
DE Synthesised peptide-1 from human prothrombin kringle-2 protein.
XX
KM Human prothrombin kringle-2; prothrombin; kringle domain; cancer therapy;
KM anti-endothelial cell proliferation; anti-tumour; angiogenesis; cancer;
KM skin; laryngeal; uterine; colon; lung; bone marrow; cytostatic;
KM anti-angiogenic.
XX
OS Homo sapiens.
XX
FN WO200014209-A1.
XX
PD 16-MAR-2000.
XX
PF 07-SEP-1999; 99WO-KR000525.
XX
PR 07-SEP-1998; 98KR-00036786.
XX
PA (KIMS/) KIM S. S.
PA (GENO-) GENOTECH CORP.
XX
PI Rhim TY, Park CS, Kim EK;
XX
DR WPI; 2000-256965/22.
XX
PT Human prothrombin kringle-1 and kringle-2 polypeptides that inhibit
PT angiogenesis, useful for treating cancer.
XX
PS Example 7; Page 19; 43bp; English.
XX
CC The present sequence is a synthesised peptide of human prothrombin
CC kringle-2 protein which is derived from human plasma prothrombin.
CC Peptides were synthesised having amino acid sequences in order from N-
CC terminal sequence of prothrombin kringle-2 by overlapping 2-5 amino acids
CC of both N-terminal and C-terminal of peptides. These peptides were
CC purified by high performance liquid chromatography (HPLC). Kringle

CC domains from prothrombin have anti-endothelial cell proliferation and
CC anti-tumour activities. These inhibit angiogenesis which is involved in
CC tumour growth. They are also useful for the treatment of cancer, e.g.
CC skin, laryngeal, uterine, colon, lung and bone marrow cancer. The human
CC prothrombin kringle-2 significantly suppresses tumour growth in vivo
XX
SQ Sequence 15 AA;

Query Match 44.6%; Score 33; DB 3; Length 15;
Best Local Similarity 63.6%; Pred. No. 78;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 4 SMGSLNLEPN 14
| | | | | | | | | | | | | | | | |
DB 1 SEGSSVNLSP 11

RESULT 8
ABJ08867
ID ABJ08867 standard; peptide; 9 AA.
XX
AC ABJ08867;
XX
DT 14-NOV-2002 (first entry)
XX
DE Hepatitis B virus epitope #3085.
XX
KM Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
KM virucide; hepatotropic; antiinflammatory.
XX
OS Hepatitis B virus.
XX
PN WO200219986-A1.
XX
PD 14-MAR-2002.
XX
PF 08-SEP-2000; 2000WO-US024802.
XX
PR 08-SEP-2000; 2000WO-US024802.
XX
PA (EPI-M-) EPI-MUNE INC.
PA (SETT/) SETTLE A.
XX
PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
PI Cells B, Kubo RT, Grey HM, Chesnut RW;
XX
DR WPI; 2002-643192/69.
XX
PT Vaccine composition for treating or preventing hepatitis B virus (HBV)
PT infection, and/or for stimulating an immune response to HBV, comprises a
PT HBV peptide epitope.
XX
PS Disclosure; Page 178; 228bp; English.
XX
CC The present invention relates to a composition comprising at least one
CC hepatitis B virus epitope. This can be used in the production of a
CC vaccine for use in preventing or treating hepatitis B virus infection.
CC The present sequence is a peptide described in the exemplification of the
CC invention
XX
SQ Sequence 9 AA;

Query Match 40.5%; Score 30; DB 5; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 8 GLNLSEPN 15
| | | | | | | | | | | | | | | | |
DB 2 GTNLSEPN 9

RESULT 9
ABJ09159

ID ABJ09159 standard; peptide; 9 AA.
XX
AC ABJ09159;
XX
DT 14-NOV-2002 (first entry)
XX
DE Hepatitis B virus epitope #3377.
XX
KM Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
KW virulence; hepatocytic; antiinflammatory.
XX
OS Hepatitis B virus.
XX
PN MO200219986-A1.
XX
PD 14-MAR-2002.
XX
PF 08-SEP-2000; 2000MO-US024802.
XX
PR 08-SEP-2000; 2000MO-US024802.
XX
PA (EPLM-) EPLMUNE INC.
XX
PI (SETT/) SETT A.
XX
PI Sette A, Sidney J, Southwood S, Vitello MA, Livingstone BD;
PI Cells E, Kubo RT, Grey HM, Chesnut RW;
XX
DR WPI; 2002-643192/69.
XX
PT Vaccine composition for treating or preventing hepatitis B virus (HBV)
PT infection, and/or for stimulating an immune response to HBV, comprises a
PT HBV peptide epitope.
XX
PS Disclosure; Page 181; 228pp; English.
XX
CC The present invention relates to a composition comprising at least one
CC hepatitis B virus epitope. This can be used in the production of a
CC vaccine for use in preventing or treating hepatitis B virus infection.
CC The present sequence is a peptide described in the exemplification of the
CC invention
XX
SQ Sequence 9 AA;
XX
Query Match 40.5%; Score 30; DB 5; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 GUNLSEPN 15
| | | | |
| | | | |
Db 2 GTNLSTVFN 9
XX
RESULT 10
ADQ12374
ID ADQ12374 standard; peptide; 9 AA.
XX
AC ADQ12374;
XX
DT 07-OCT-2004 (first entry)
XX
DE Hepatitis B virus MHC class I restricted T-cell stimulating peptide 173.
XX
KM HBV, MHC class I restricted T-cell stimulating peptide; surface peptide;
KW core peptide; polymerase peptide; immunogenic composition; vaccine;
KW cytotoxic T-lymphocyte response; CTL response.
XX
OS Hepatitis B virus.
XX
PN MO2004058807-A2.
XX
PD 15-JUL-2004.
XX
PF 09-DEC-2003; 2003MO-EP013948.
XX

XX
PR 24-DEC-2002; 2002EP-00447276.
XX
PA (ALGO-) ALGONOMICS NV.
XX
PI Lasters I, Desmet J, Stegmann T, Castelein B;
XX
DR WPI; 2004-525861/50.
XX
PT New peptide comprising a major histocompatibility complex class I
PT restricted T-cell stimulating epitope of the hepatitis B virus (HBV)
PT surface, core and/or polymerase polypeptide, for preparation of an HBV
PT immunogenic composition.
XX
PS Example 7; SEQ ID NO 173; 108pp; English.
XX
CC The invention comprises major histocompatibility complex (MHC) class I
CC restricted T-cell stimulating epitopes of the hepatitis B virus (HBV)
CC surface, core and polymerase proteins. The peptides of the invention are
CC useful for generating an HBV immunogenic composition (e.g. vaccine) that
CC induces a cytotoxic T-lymphocyte (CTL) response. The present amino acid
CC sequence represents an MHC class I restricted T-cell stimulating HBV
CC peptide of the invention.
XX
SQ Sequence 9 AA;
XX
Query Match 40.5%; Score 30; DB 8; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 GUNLSEPN 15
| | | | |
| | | | |
Db 2 GTNLSTVFN 9
XX
RESULT 11
ADQ12375
ID ADQ12375 standard; peptide; 9 AA.
XX
AC ADQ12375;
XX
DT 07-OCT-2004 (first entry)
XX
DE Hepatitis B virus MHC class I restricted T-cell stimulating peptide 174.
XX
KM HBV, MHC class I restricted T-cell stimulating peptide; surface peptide;
KW core peptide; polymerase peptide; immunogenic composition; vaccine;
KW cytotoxic T-lymphocyte response; CTL response.
XX
OS Hepatitis B virus.
XX
PN MO2004058807-A2.
XX
PD 15-JUL-2004.
XX
PF 09-DEC-2003; 2003MO-EP013948.
XX
PR 24-DEC-2002; 2002EP-00447276.
XX
PA (ALGO-) ALGONOMICS NV.
XX
PI Lasters I, Desmet J, Stegmann T, Castelein B;
XX
DR WPI; 2004-525861/50.
XX
PT New peptide comprising a major histocompatibility complex class I
PT restricted T-cell stimulating epitope of the hepatitis B virus (HBV)
PT surface, core and/or polymerase polypeptide, for preparation of an HBV
PT immunogenic composition.
XX
PS Example 7; SEQ ID NO 174; 108pp; English.
XX
CC The invention comprises major histocompatibility complex (MHC) class I

CC restricted T-cell stimulating epitopes of the hepatitis B virus (HBV)
CC surface, core and polymerase proteins. The peptides of the invention are
CC useful for generating an HBV immunogenic composition (e.g. vaccine) that
CC induces a cytotoxic T-lymphocyte (CTL) response. The present amino acid
CC sequence represents an MHC class I restricted T-cell stimulating HBV
CC peptide of the invention.

XX Sequence 9 AA;

Query Match 40.5%; Score 30; DB 8; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 8 GINLSEPN 15
DB 1 GTNLSPVN 8

RESULT 12

AA38384
ID AA38384 standard; peptide; 10 AA.

AC AA38384;

DT 25-MAR-2003 (revised)

DT 21-OCT-1993 (first entry)

XX T-cell epitope from HBsAg/p43 pre-S(1).

XX Hybrid; immunogen; T-cell; epitope; antigen; HIV; cyclic;

KM principal neutralising determinant; CPND; hepatitis-B pre-S(1); antibody;

XX immunity.

XX Synthetic.

XX EP547689-A2.

XX 23-JUN-1993.

XX 10-DEC-1992; 92EP-00203855.

XX 18-DEC-1991; 91US-00811041.

XX (MERI) MERCK & CO INC.

XX Hannah J, Tolman RL;

XX WPI; 1993-198695/25.

XX Hybrid immunogens for treatment or prevention of HIV - comprise cyclic

XX HIV principal neutralising determinant and T cell stimulatory epitope of

XX hepatitis B.

XX Claim 3, Page 23; 24pp; English.

XX A hybrid immunogen comprises a T-cell stimulatory epitope from HBsAg/p43

XX pre-S(1) (AA38384) and a cyclic HIV principal neutralising determinant,

XX CPND (AA38384). The two components may be linked via an intervening

XX sequence of 1-4 amino acids which may include a maker amino acid. The

XX hybrid immunogen is used to induce anti-HIV PND, anti-HIV or HIV-

XX neutralising immune response. (Updated on 25-MAR-2003 to correct PN

XX field.)

XX Sequence 10 AA;

XX Query Match 40.5%; Score 30; DB 2; Length 10;

XX Best Local Similarity 75.0%; Pred. No. 1.7e+02;

XX Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 13
AB06595
ID AB06595 standard; peptide; 10 AA.

XX AB06595;

XX 14-NOV-2002 (first entry)

XX Hepatitis B virus epitope #813.

XX Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;

KM virucide; hepatotropic; antiinflammatory.

XX Hepatitis B virus.

XX WO200219986-A1.

XX 14-MAR-2002.

XX 08-SEP-2000; 2000WO-US024802.

XX 08-SEP-2000; 2000WO-US024802.

XX (EPIM-) EPIMUNE INC.

XX (SETT/) SETTE A.

PI Sette A, Sidney J, Southwood S, Vitello MA, Livingstone BD;

PI Cells E, Kudo RT, Grey HM, Chesnut RM;

XX WPI; 2002-643192/69.

XX Vaccine composition for treating or preventing hepatitis B virus (HBV)

XX infection, and/or for stimulating an immune response to HBV, comprises a

XX HBV peptide epitope.

XX Disclosure; Page 128; 228pp; English.

XX The present invention relates to a composition comprising at least one

XX hepatitis B virus epitope. This can be used in the production of a

XX vaccine for use in preventing or treating hepatitis B virus infection.

XX The present sequence is a peptide described in the exemplification of the

XX invention

XX Sequence 10 AA;

Query Match 40.5%; Score 30; DB 5; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 8 GINLSEPN 15
DB 1 GTNLSPVN 8

RESULT 14
AB07286
ID AB07286 standard; peptide; 10 AA.

XX AB07286;

XX 14-NOV-2002 (first entry)

XX Hepatitis B virus epitope #1504.

XX Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;

KM virucide; hepatotropic; antiinflammatory.

XX Hepatitis B virus.

XX WO200219986-A1.

XX 14-MAR-2002.

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: November 1, 2005, 14:06:05 ; Search time 42 seconds
(without alignments)
26,660 Million cell updates/sec

Title: US-10-612-162a-3

Perfect score: 74

Sequence: 1 SKLSMSGSLSEPN 15

Scoring table: BLOSUM62

Searched: Gapop 10.0 ; Gapext 0.5

Total number of hits satisfying chosen parameters: 164526

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/1aa/5A COMB.pep:*

2: /cgn2_6/prodata/1/1aa/5B COMB.pep:*

3: /cgn2_6/prodata/1/1aa/6A COMB.pep:*

4: /cgn2_6/prodata/1/1aa/6B COMB.pep:*

5: /cgn2_6/prodata/1/1aa/PCTUS COMB.pep:*

6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	30	40.5	10	4	US-09-239-043D-257	Sequence 257, App
2	30	40.5	10	4	US-09-239-043D-743	Sequence 743, App
3	30	40.5	10	4	US-09-239-043D-1374	Sequence 1374, App
4	30	40.5	15	4	US-09-239-043D-2101	Sequence 2101, App
5	29	39.2	13	4	US-09-489-156-22	Sequence 22, App
6	29	39.2	13	4	US-09-489-156-23	Sequence 23, App
7	29	39.2	13	4	US-09-693-746-124	Sequence 124, App
8	28	37.8	10	1	US-08-462-949-11	Sequence 11, App
9	28	37.8	10	1	US-08-023-764B-11	Sequence 11, App
10	27	36.5	13	4	US-08-200-900A-23	Sequence 23, App
11	27	36.5	13	4	US-09-489-156-25	Sequence 25, App
12	27	36.5	13	4	US-08-794-042-23	Sequence 23, App
13	27	36.5	13	5	PCT-US94-00616-23	Sequence 23, App
14	27	36.5	15	4	US-09-255-501-96	Sequence 96, App
15	27	36.5	15	4	US-09-255-501-97	Sequence 97, App
16	27	36.5	15	4	US-09-060-872A-96	Sequence 96, App
17	27	36.5	15	4	US-09-060-872A-97	Sequence 97, App
18	27	36.5	15	4	US-09-500-135C-96	Sequence 96, App
19	27	36.5	15	4	US-09-500-135C-97	Sequence 97, App
20	26	35.1	10	5	PCT-US94-01234-39	Sequence 39, App
21	26	35.1	11	4	US-09-239-043D-44	Sequence 44, App
22	26	35.1	11	4	US-09-239-043D-796	Sequence 796, App
23	26	35.1	12	3	US-09-239-043D-1585	Sequence 1585, App
24	26	35.1	12	3	US-09-248-588-113	Sequence 113, App
25	26	35.1	12	3	US-09-261-368-35	Sequence 35, App
26	26	35.1	12	4	US-09-106-568B-66	Sequence 66, App
27	26	35.1	12	4	US-09-106-568B-82	Sequence 82, App

28	26	35.1	12	4	US-10-114-176-35	Sequence 35, App
29	26	35.1	12	6	5178861-10	Patent No. 5178861
30	26	35.1	12	6	5178861-10	Patent No. 5178861
31	26	35.1	15	2	US-08-572-951-6	Sequence 6, App
32	26	35.1	15	2	US-08-572-951-23	Sequence 23, App
33	26	35.1	15	4	US-09-255-501-98	Sequence 98, App
34	26	35.1	15	4	US-09-239-043D-2113	Sequence 2113, App
35	26	35.1	15	4	US-09-239-043D-2120	Sequence 2120, App
36	26	35.1	15	4	US-09-060-872A-98	Sequence 98, App
37	26	35.1	15	4	US-09-500-135C-98	Sequence 98, App
38	25	33.8	8	4	US-09-239-043D-298	Sequence 298, App
39	25	33.8	8	4	US-09-239-043D-372	Sequence 372, App
40	25	33.8	8	4	US-09-239-043D-795	Sequence 795, App
41	25	33.8	8	4	US-09-239-043D-897	Sequence 897, App
42	25	33.8	8	4	US-10-152-158-8	Sequence 8, App
43	25	33.8	9	4	US-09-239-043D-1221	Sequence 1221, App
44	25	33.8	10	1	US-08-462-949-23	Sequence 23, App
45	25	33.8	10	1	US-08-023-764B-23	Sequence 23, App

ALIGNMENTS

RESULT 1
US-09-239-043D-257
Sequence 257, Application US/09239043D
Patent No. 6689363
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Vitellio, Maria A.
APPLICANT: Livingston, Brian D.
APPLICANT: Celis, Esben
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Cheenut, Robert
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
FILE OF INVENTION: Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.006007
CURRENT FILING DATE: 1999-01-27
CURRENT FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/978,291
PRIOR FILING DATE: 1997-11-25
PRIOR APPLICATION NUMBER: US 08/820,360
PRIOR FILING DATE: 1997-03-12
PRIOR APPLICATION NUMBER: US 60/013,363
PRIOR FILING DATE: 1996-03-13
PRIOR APPLICATION NUMBER: US 08/461,603
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
PRIOR APPLICATION NUMBER: US 08/344,824
PRIOR FILING DATE: 1994-11-23
PRIOR APPLICATION NUMBER: US 08/278,634
PRIOR FILING DATE: 1994-07-21
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/197,484
PRIOR FILING DATE: 1994-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2579
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 257
LENGTH: 10
TYPE: PRT
ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-257
Query Match 40.5%; Score 30; DB 4; Length 10;

Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 8 GLNISEPN 15
| | | | |
Db 1 GTNLSVFN 8

RESULT 2

US-09-239-043D-743
; Sequence 743, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.006007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 743
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus

US-09-239-043D-743

Query Match 40.5%; Score 30; DB 4; Length 10;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 8 GLNISEPN 15
| | | | |
Db 1 GTNLSVFN 8

RESULT 3

US-09-239-043D-1374
; Sequence 1374, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John

; APPLICANT: Southwood, Scott
; APPLICANT: Vitello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: EpiImmune Inc.

; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.006007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1374
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus

US-09-239-043D-1374

Query Match 40.5%; Score 30; DB 4; Length 10;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 8 GLNISEPN 15
| | | | |
Db 1 GTNLSVFN 8

RESULT 4

US-09-239-043D-2101
; Sequence 2101, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.006007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10

PRIOR APPLICATION NUMBER: US 08/978,291
PRIOR FILING DATE: 1997-11-25
PRIOR APPLICATION NUMBER: US 08/820,360
PRIOR FILING DATE: 1997-03-12
PRIOR APPLICATION NUMBER: US 60/013,363
PRIOR FILING DATE: 1996-03-13
PRIOR APPLICATION NUMBER: US 08/461,603
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
PRIOR APPLICATION NUMBER: US 08/344,824
PRIOR FILING DATE: 1994-11-23
PRIOR APPLICATION NUMBER: US 08/278,634
PRIOR FILING DATE: 1994-07-21
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/197,484
PRIOR FILING DATE: 1994-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2879
SOFTWARE: PaeSeq for Windows Version 4.0
SEQ ID NO 2101
LENGTH: 15
TYPE: PRT
ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-2101

Query Match 40.5%; Score 30; DB 4; Length 15;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 GNLSEPN 15
DB 1 GTNLSPVN 8

RESULT 5
US-09-489-156-22
Sequence 22, Application US/09489156
Patent No. 6559128
GENERAL INFORMATION:
APPLICANT: HAMM, Heidi
APPLICANT: GILCHRIST, Annette
TITLE OF INVENTION: INHIBITORS OF G PROTEIN-MEDIATED SIGNALING, METHODS OF MAKING THE
FILE REFERENCE: 0290-29 (NU 99037)
CURRENT APPLICATION NUMBER: US/09/489,156
CURRENT FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: G alpha 11 peptide
US-09-489-156-22

Query Match 39.2%; Score 29; DB 4; Length 13;
Best Local Similarity 63.6%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 MGSGLNSEPN 15
DB 1 MGLQLNLKEYN 11

RESULT 6
US-09-489-156-23
Sequence 23, Application US/09489156
Patent No. 6559128
GENERAL INFORMATION:
APPLICANT: HAMM, Heidi

APPLICANT: GILCHRIST, Annette
TITLE OF INVENTION: INHIBITORS OF G PROTEIN-MEDIATED SIGNALING, METHODS OF MAKING THE
FILE REFERENCE: 0290-29 (NU 99037)
CURRENT APPLICATION NUMBER: US/09/489,156
CURRENT FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: G alpha q peptide
US-09-489-156-23

Query Match 39.2%; Score 29; DB 4; Length 13;
Best Local Similarity 63.6%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 MGSGLNSEPN 15
DB 1 MGLQLNLKEYN 11

RESULT 7
US-09-693-746-124
Sequence 124, Application US/09693746
Patent No. 6835546
GENERAL INFORMATION:
APPLICANT: Lowery, David E.
APPLICANT: Smith, Valdin G.
APPLICANT: Kubiak, Teresa M.
APPLICANT: Larsen, Martha J.
TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
FILE REFERENCE: 6297,1CD
CURRENT APPLICATION NUMBER: US/09/693,746
CURRENT FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/425,676
PRIOR FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 168
SOFTWARE: PatentIn version 3.1
SEQ ID NO 124
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: No. 6835546e1 Sequence
US-09-693-746-124

Query Match 39.2%; Score 29; DB 4; Length 13;
Best Local Similarity 55.6%; Pred. No. 72;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 SGLINSEPN 15
DB 1 SDIGISEPN 9

RESULT 8
US-08-462-949-11
Sequence 11, Application US/08462949
Patent No. 5606022
GENERAL INFORMATION:
APPLICANT: Rasmussen, Beth Ann
TITLE OF INVENTION: Cloning and Identification of a Two
TITLE OF INVENTION: Component Signal Transducing Regulatory System from
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby P.C.
STREET: 805 Third Avenue

CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,949
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/023,764
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph R.
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/1B024-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 201-753-6237
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-462-949-11

Query Match 37.8%; Score 28; DB 1; Length 10;
Best Local Similarity 85.7%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GSGGLTSL 12
Db 2 GSGGLTSL 8

RESULT 9
US-08-023-764B-11
Sequence 11, Application US/08023764B
Patent No. 5679540
GENERAL INFORMATION:
APPLICANT: Rasmussen, Beth Ann
TITLE OF INVENTION: Cloning and Identification of a Two
TITLE OF INVENTION: Component Signal Transducing Regulatory System from
TITLE OF INVENTION: Bacterioides Fragilis
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSER: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/023,764B
FILING DATE: 26-FEB-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,658-00

TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 831-3246
TELEFAX: (201) 831-3305
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-023-764B-11

Query Match 37.8%; Score 28; DB 1; Length 10;
Best Local Similarity 85.7%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GSGGLTSL 12
Db 2 GSGGLTSL 8

RESULT 10
US-08-200-900A-23
Sequence 23, Application US/08200900A
Patent No. 5665566
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc. - Legal Affairs
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/200,900A
FILING DATE: 23-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Melnert, Maureen C.
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: GI 5201-FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170 X8574
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-200-900A-23

Query Match 36.5%; Score 27; DB 1; Length 13;
Best Local Similarity 55.6%; Pred. No. 1-7e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 GSGGLTSL 14
Db 5 GYGLGIRP 13

RESULT 11

US-09-489-156-25
; Sequence 25, Application US/09489156
; Patent No. 6559128
; GENERAL INFORMATION:
; APPLICANT: HAMM, Heidi
; APPLICANT: GILCHRIST, Annette
; TITLE OF INVENTION: INHIBITORS OF G PROTEIN-MEDIATED SIGNALING, METHODS OF MAKING THE
; FILE REFERENCE: 0290-29 (NU 99037)
; CURRENT APPLICATION NUMBER: US/09/489,156
; CURRENT FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 25
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: G alpha 14 peptide
US-09-489-156-25

Query Match 36.5%; Score 27; DB 4; Length 13;
Best Local Similarity 63.6%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 MSGNLSEPN 15
DB 1 MGLQNLNREFN 11

RESULT 12

US-08-794-042-23
; Sequence 23, Application US/08794042
; Patent No. 6746859

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE

; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genetics Institute, Inc. - Legal Affairs

; STREET: 87 CambridgePark Drive

; CITY: Cambridge

; STATE: MA

; COUNTRY: USA

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/794,042

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/200,900

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Weinert, Maureen C.

; REGISTRATION NUMBER: 31,544

; REFERENCE/DOCKET NUMBER: GI 5201-FWC

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 876-1170 X8574

; TELEFAX: (617) 876-5851

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-794-042-23

Query Match 36.5%; Score 27; DB 4; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 GSGNLSEPN 14
DB 5 GYGGLGIRP 13

RESULT 13

PCT-US94-00616-23

; Sequence 23, Application PC/TUS9400616

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE

; NUMBER OF SEQUENCES: 33

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/00616

; FILING DATE:

; CLASSIFICATION:

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US94-00616-23

Query Match 36.5%; Score 27; DB 5; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 GSGNLSEPN 14
DB 5 GYGGLGIRP 13

RESULT 14

US-09-255-501-96

; Sequence 96, Application US/09255501

; Patent No. 6596525

; GENERAL INFORMATION:

; APPLICANT: Batell, David

; APPLICANT: Harding, Fiona

; TITLE OF INVENTION: MUTANT PROTEINS HAVING LOWER ALLERGENIC RESPONSE IN

; TITLE OF INVENTION: HUMANS AND METHODS FOR CONSTRUCTING, IDENTIFYING AND

; FILE REFERENCE: GCS27

; CURRENT APPLICATION NUMBER: US/09/255,501

; CURRENT FILING DATE: 1999-02-23

; NUMBER OF SEQ ID NOS: 211

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO: 96

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-255-501-96

Query Match 36.5%; Score 27; DB 4; Length 15;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SKLSMSG 8
DB 5 ASLSLMSG 12

RESULT 15

US-09-255-501-97
; Sequence 97, Application US/09255501
; Patent No. 6596525
; GENERAL INFORMATION:
; APPLICANT: Esteil, David
; APPLICANT: Harding, Fiona
; TITLE OF INVENTION: MUTANT PROTEINS HAVING LOWER ALLERGENIC RESPONSE IN
; TITLE OF INVENTION: HUMANS AND METHODS FOR CONSTRUCTING, IDENTIFYING AND
; TITLE OF INVENTION: PRODUCING SUCH PROTEINS
; FILE REFERENCE: GC527
; CURRENT APPLICATION NUMBER: US/09/255,501
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-255-501-97

Query Match 36.5%; Score 27; DB 4; Length 15;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SKLSMSG 8
: ||: ||
Db 2 ASLSLGS 9

Search completed: November 1, 2005, 14:21:31
Job time : 47 sec


```
; Sequence 10, Application US/10769514
; Publication No. US20040258695A1
; GENERAL INFORMATION:
; APPLICANT: Schryvers, Anthony
; TITLE OF INVENTION: Transferrin Binding Peptides and Uses Thereof
; FILE REFERENCE: 028722-001
; CURRENT APPLICATION NUMBER: US/10/769,514
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/444,113
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-514-10
```

```
Query Match          74.3%; Score 55; DB 16; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.0082;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      3 LMSGGLNLSEPN 15
        |||||
Db       1 LCMGSGNLCEPN 13
```

```
RESULT 3
US-10-769-514-42
; Sequence 42, Application US/10769514
; Publication No. US20040258695A1
; GENERAL INFORMATION:
; APPLICANT: Schryvers, Anthony
; TITLE OF INVENTION: Transferrin Binding Peptides and Uses Thereof
; FILE REFERENCE: 028722-001
; CURRENT APPLICATION NUMBER: US/10/769,514
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/444,113
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TdpB-binding peptides
US-10-769-514-42
```

```
Query Match          74.3%; Score 55; DB 16; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.0082;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      3 LMSGGLNLSEPN 15
        |||||
Db       1 LCMGSGNLCEPN 13
```

```
RESULT 4
US-10-801-990-180
; Sequence 180, Application US/10801990
; Publication No. US20050048574A1
; GENERAL INFORMATION:
; APPLICANT: Kantor, Aaron B.
; APPLICANT: Schulman, Howard
; APPLICANT: Becker, Christopher
; TITLE OF INVENTION: BIOMARKERS FOR RHEUMATOID ARTHRITIS
; FILE REFERENCE: SURR.121
; CURRENT APPLICATION NUMBER: US/10/801,990
; PRIOR FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US 60/455,037
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NUMBER OF SEQ ID NOS: 395
```

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 180
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-801-990-180
```

```
Query Match          74.3%; Score 55; DB 17; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.0082;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      3 LMSGGLNLSEPN 15
        |||||
Db       1 LCMGSGNLCEPN 13
```

```
RESULT 5
US-10-801-990-184
; Sequence 184, Application US/10801990
; Publication No. US20050048574A1
; GENERAL INFORMATION:
; APPLICANT: Kantor, Aaron B.
; APPLICANT: Schulman, Howard
; APPLICANT: Becker, Christopher
; TITLE OF INVENTION: BIOMARKERS FOR RHEUMATOID ARTHRITIS
; FILE REFERENCE: SURR.121
; CURRENT APPLICATION NUMBER: US/10/801,990
; PRIOR FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US 60/455,037
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 184
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-801-990-184
```

```
Query Match          74.3%; Score 55; DB 17; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.0082;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      3 LMSGGLNLSEPN 15
        |||||
Db       1 LCMGSGNLCEPN 13
```

```
RESULT 6
US-10-059-271-37
; Sequence 37, Application US/10059271
; Publication No. US20030082208A1
; GENERAL INFORMATION:
; APPLICANT: REPPE, HEINRICH
; APPLICANT: BUDDÉ, ECKHARD
; APPLICANT: NICOLAUS, STEFAN
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-059-271-37
```


Query Match 44.6%; Score 33; DB 14; Length 14;
Best Local Similarity 41.7%; Pred. No. 70;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 4 SMGGLNLEPN 15
:|:|:|:|
DB 1 AVGIGINCIRPN 12

RESULT 7
US-10-992-351-3
; Sequence 3, Application US/10992351
; Publication No. US2005013562A1
; GENERAL INFORMATION:
; APPLICANT: Dade Behring Marburg GmbH
; TITLE OF INVENTION: Antibodies directed against prothrombin fragment F1+2, the prepar
; FILE REFERENCE: 05552.1454
; CURRENT APPLICATION NUMBER: US/10/992,351
; CURRENT FILING DATE: 2004-11-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent version 3.1
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-992-351-3

Query Match 41.9%; Score 31; DB 17; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSGGLNLEPN 14
:|:|:|:|
DB 1 GSSVNLSP 9

RESULT 8
US-10-654-601-257
; Sequence 257, Application US/10654601
; Publication No. US20050063983A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitellio, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esleben
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Cheenut, Robert
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/10/654,601
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/239,043
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23

; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FaetsSQ for Windows Version 4.0
; SEQ ID NO 257
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-10-654-601-257

Query Match 40.5%; Score 30; DB 17; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 GNLNLEPN 15
:|:|:|:|
DB 1 GNLNLEPN 8

RESULT 9
US-10-654-601-743
; Sequence 743, Application US/10654601
; Publication No. US20050063983A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitellio, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esleben
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Cheenut, Robert
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/10/654,601
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/239,043
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FaetsSQ for Windows Version 4.0
; SEQ ID NO 743
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-10-654-601-743

Query Match 40.5%; Score 30; DB 17; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;

```
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 GINLSEPN 15
Db 1 GTNLSVFN 8

RESULT 10
US-10-654-601-1374
; Sequence 1374, Application US/10654601
; Publication No. US20050063983A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/10/654,601
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1374
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-10-654-601-1374

Query Match 40.5%; Score 30; DB 17; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 GINLSEPN 15
Db 1 GTNLSVFN 8

RESULT 11
US-10-654-601-2101
; Sequence 2101, Application US/10654601
; Publication No. US20050063983A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
```

```
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT FILING DATE: US/10/654,601
; PRIOR APPLICATION NUMBER: US/09/239,043
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2101
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-10-654-601-2101

Query Match 40.5%; Score 30; DB 17; Length 15;
Best Local Similarity 75.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 GINLSEPN 15
Db 1 GTNLSVFN 8

RESULT 12
US-10-930-300-93
; Sequence 93, Application US/10930300
; Publication No. US20050014138A1
; GENERAL INFORMATION:
; APPLICANT: Rath, Matthias
; TITLE OF INVENTION: METHOD OF PRODUCING VACCINES FROM PROTEIN SIGNAL
; OLIGOPEPTIDES
; NUMBER OF SEQUENCES: 360
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: INHOUSE IP MANAGEMENT
; STREET: 280 Colorado Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk, 3.50 inch, 1.44MB Storage
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: MS WORD 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/930,300
```

```
/
/ FILING DATE: 30-Aug-2004
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/182,248
/ FILING DATE: 14-JAN-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: ALI KAMAREI
/ REGISTRATION NUMBER: 37000
/ REFERENCE/DOCKET NUMBER: 10262-10US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-322-7371
/ TELEFAX: 650-322-7389
/ INFORMATION FOR SEQ ID NO: 93:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 93:
US-10-930-300-93
```

```
Query Match          39.2%; Score 29; DB 17; Length 10;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 6 GSGGLNS 12
DB 4 GSGGLNS 10
```

```
RESULT 13
US-09-852-910-114
/ Sequence 114, Application US/09852910
/ Publication No. US20030096297A1
/ GENERAL INFORMATION:
/ APPLICANT: Hamm, Heidi
/ APPLICANT: Gilchrist, Annette
/ TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor
/ FILE REFERENCE: 2661-101
/ CURRENT APPLICATION NUMBER: US/09/852,910
/ CURRENT FILING DATE: 2001-09-18
/ PRIOR APPLICATION NUMBER: US 60/275,472
/ PRIOR FILING DATE: 2001-03-14
/ NUMBER OF SEQ ID NOS: 271
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 114
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(13)
/ OTHER INFORMATION: G alpha q minigene peptide
US-09-852-910-114
```

```
Query Match          39.2%; Score 29; DB 10; Length 13;
Best Local Similarity 63.6%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 5 MSGGLNLSEPN 15
DB 1 MGLQLNLKEYN 11
```

```
RESULT 14
US-09-852-910-115
/ Sequence 115, Application US/09852910
/ Publication No. US20030096297A1
/ GENERAL INFORMATION:
/ APPLICANT: Hamm, Heidi
/ APPLICANT: Gilchrist, Annette
/ TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor
/ FILE REFERENCE: 2661-101
```

```
/
/ CURRENT APPLICATION NUMBER: US/09/852,910
/ CURRENT FILING DATE: 2001-09-18
/ PRIOR APPLICATION NUMBER: US 60/275,472
/ PRIOR FILING DATE: 2001-03-14
/ NUMBER OF SEQ ID NOS: 271
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 115
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(13)
/ OTHER INFORMATION: G alpha q** minigene peptide
US-09-852-910-115
```

```
Query Match          39.2%; Score 29; DB 10; Length 13;
Best Local Similarity 63.6%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 5 MSGGLNLSEPN 15
DB 1 MGLQLNLKEYN 11
```

```
RESULT 15
US-10-283-423-124
/ Sequence 124, Application US/10283423
/ Publication No. US2003016223A1
/ GENERAL INFORMATION:
/ APPLICANT: Lowery, David E.
/ APPLICANT: Smith, Valdin G.
/ APPLICANT: Kubiak, Teresa M.
/ APPLICANT: Larsen, Martha J.
/ TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Metho
/ FILE REFERENCE: PHRM0002-102
/ Application Project
/ -----
/ CURRENT APPLICATION NUMBER: US/10/283,423
/ CURRENT FILING DATE: 2002-10-30
/ Earlier Applications
/ -----
/ PRIOR APPLICATION NUMBER: PriorAppNumber : 09/693,746
/ PRIOR FILING DATE: PriorFilingDate : 2000-10-20
/ PRIOR APPLICATION NUMBER: PriorAppNumber : 09/425,676
/ PRIOR FILING DATE: PriorFilingDate : 1999-10-22
/ NUMBER OF SEQ ID NOS: 187
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 124
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: No. US2003016223A1el Sequence
US-10-283-423-124
```

```
Query Match          39.2%; Score 29; DB 14; Length 13;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 7 SGLNLSEPN 15
DB 1 SDIGISEPN 9
```

```
Search completed: November 1, 2005, 14:26:03
Job time : 171 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 14:01:36 ; Search time 39 Seconds
(without alignments)
37.006 Million cell updates/sec

Title: US-10-612-162a-3

Perfect score: 74
Sequence: 1 SKLSMGSGUNLSEPN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	32.4	13	2 E47630	Ig kappa chain J r
2	23	31.1	10	2 PT0289	Ig heavy chain CRD
3	23	31.1	14	2 PH0801	T-cell receptor al
4	21	28.4	9	2 A44873	caldesmon - rabbit
5	21	28.4	12	2 D20907	Ig kappa-1 chain J
6	21	28.4	13	2 H33932	Ig kappa chain J r
7	21	28.4	15	2 S21238	hydrogen sulfite re
8	21	28.4	15	2 C36198	T-cell receptor be
9	21	28.4	15	2 A36315	recycling receptor
10	21	28.4	15	2 PH1455	T-cell receptor al
11	20	27.0	10	2 H60589	sperm-activating p
12	20	27.0	10	2 A37933	Ig lambda chain J
13	20	27.0	13	2 B25448	Ig kappa chain J r
14	20	27.0	13	2 D47630	Ig kappa chain J r
15	20	27.0	15	2 S49409	H+-transporting tw
16	20	27.0	15	2 A56049	urinary tract ston
17	20	27.0	12	2 PT0319	Ig heavy chain CRD
18	19	25.7	12	2 PH1183	T-cell receptor al
19	19	25.7	12	2 S25830	dimethylamine mo
20	19	25.7	13	2 PH0445	urotensin II - lau
21	19	25.7	14	2 PH0795	T-cell receptor al
22	19	25.7	15	2 S25527	T-cell receptor al
23	19	25.7	15	2 S43634	cytochrome-c oxida
24	19	25.7	15	2 PH0775	T-cell receptor al
25	18	24.3	5	2 D44823	synaptoosomal-asso
26	18	24.3	7	2 PT0579	T-cell receptor be
27	18	24.3	9	2 S70345	amine oxidase (cop
28	18	24.3	9	2 A47364	placental lactogen
29	18	24.3	10	2 A47364	placental lactogen

30	18	24.3	10	2 E60787	sperm-activating p
31	18	24.3	10	2 C60588	sperm-activating p
32	18	24.3	10	2 E60527	Ig kappa chain J r
33	18	24.3	12	2 A20907	Ig kappa chain J r
34	18	24.3	12	2 F20907	Ig kappa-2 chain J
35	18	24.3	12	2 E58502	43.2K bile stone p
36	18	24.3	13	2 PH0783	T-cell receptor al
37	18	24.3	13	2 S03879	6-phosphofructokin
38	18	24.3	14	2 B29743	translation initia
39	18	24.3	14	2 PH0776	T-cell receptor al
40	18	24.3	14	2 B56819	PS I complex subun
41	18	24.3	15	2 PH0784	T-cell receptor al
42	18	24.3	15	2 PH0751	T-cell receptor be
43	18	24.3	15	2 S05699	insulin-like grow
44	18	24.3	15	2 G24417	interphotoreceptor
45	17	23.0	6	2 A44916	mosquito cidal toxi

ALIGNMENTS

RESULT 1
E47630
Ig kappa chain J region J4 - southeastern Australian rat
C/Species: Rattus norvegicus villosissimus (southeastern Australian rat)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 05-Nov-1999
C/Accession: E47630
R/Gutman, G.A.; Beeta, R.M.; Frank, M.B.; Baverstock, P.R.
Immunogenetics 26, 14-20, 1987
A/Title: Duplication of J-kappa genes within genus Rattus.
A/Reference number: A47630; MUID:87278355; PMID:3111993
A/Accession: E47630
A/Status: preliminary; not compared with conceptual translation
A/Residues: 1-13 <GUT>
A/Molecule type: DNA
A/References: GB:M17319; NID:G204788; PIDN:AAA41401.1; PID:G204793
C/Keywords: heterotrimer; immunoglobulin

Query Match
Best Local Similarity 32.4%; Score 24; DB 2; Length 13;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 ISMSGUNL 11
DB 1 LTFSGSTKL 9

RESULT 2
PT0289
Ig heavy chain CRD3 region (clone 4-109) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PT0289
R/Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J

A/Reference number: PT0222; MUID:91108337; PMID:1899102
A/Accession: PT0289
A/Molecule type: DNA
A/Residues: 1-10 <YAM>
A/Experimental source: B lymphocyte
C/Keywords: heterotrimer; immunoglobulin

Query Match
Best Local Similarity 31.1%; Score 23; DB 2; Length 10;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 ISMSG 8
DB 5 ISMSG 10

RESULT 3

PH0801
T-cell receptor alpha chain (J5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0801
R:Caanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-T
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; PMID:92078846; PMID:1636010
A:Accession: PH0801
A:Molecule type: mRNA
A:Residues: 1-14 <CDS>
A:Cross-references: EMBL:X60909
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 31.1%; Score 23; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 SKLSWG 6
Db 9 SKLSFG 14

RESULT 4
A44873
caldesmon - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A44873
R:Ikabe, M.; Hornick, T.
Arch. Biochem. Biophys. 288, 538-542, 1991
A:Title: Determination of the phosphorylation sites of smooth muscle caldesmon by protei
A:Reference number: A44873; PMID:91378498; PMID:1896046
A:Accession: A44873
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <IKE>
A:Cross-references: UNIPROT:Q9TRW2
A:Experimental source: skeletal myosin
A:Note: Sequence extracted from NCBI Backbone (NCBI:63199)
C:Superfamily: caldesmon

Query Match 28.4%; Score 21; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 6 GSGNLSE 13
Db 1 GSSLKIEE 8

RESULT 5
D20907
I9 kappa-1 chain J4 segment (b95 allele) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 05-Nov-1999
C:Accession: D20907; D53275
R:Emorine, L.; Max, E.E.
Nucleic Acids Res. 11, 8877-8890, 1983
A:Title: Structural analysis of a rabbit immunoglobulin kappa2 J-C locus reveals multipl
A:Reference number: A20907; PMID:84169523; PMID:6324107
A:Accession: D20907
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-12 <EMO>
A:Cross-references: GB:X00231; NID:G1577; PIDN:CAA25049.1; PID:e8275; PID:g1364234
R:Avadl, H.; Marche, P.N.; Cazenave, P.A.
Immunogenetics 34, 201-207, 1991
A:Title: Evolution of the rabbit immunoglobulin kappa chain genes.
A:Reference number: A53275; PMID:91372868; PMID:1909995

A:Accession: D53275
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-12 <ATA>
A:Note: Sequence extracted from NCBI backbone (NCBI:56069, NCBI:56166)
C:Comment: This J4 segment may not be functional because of a short space between the 7
C:Keywords: heterotrimer; immunoglobulin

Query Match 28.4%; Score 21; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 3 LSMGSG 8
Db 1 LTFGSG 6

RESULT 6
H33932
I9 kappa chain J region (D23) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C:Accession: H33932
R:Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
A:Title: Two murine natural polyclonal antibodies are encoded by nonmutated germ-1
A:Reference number: A33932; PMID:69282823; PMID:2499887
A:Accession: H33932
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-13 <BAC>
A:Cross-references: UNIPROT:Q8K1F2; UNIPROT:Q8R028
C:Keywords: heterotrimer; immunoglobulin

Query Match 28.4%; Score 21; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.5e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 3 LSMGGLNL 11
Db 1 LTRGAGTKL 9

RESULT 7
S21238
hydrogenulfite reductase (BC 1.8.99.3) beta chain - Desulfovibrio vulgaris (fragment)
N:Alternate names: bsulfite reductase; desulfotetradin; desulfotribidin; desulfovibridin;
C:Species: Desulfovibrio vulgaris
C:Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C:Accession: S21238
R:Pierik, A.J.; Duyvis, M.G.; van Helyvoort, J.M.L.M.; Wolbert, R.B.G.; Hagen, W.R.
Eur. J. Biochem. 205, 111-115, 1992
A:Title: The third subunit of desulfovibridin-type dissimilatory sulfite reductases.
A:Reference number: S21197; PMID:92209491; PMID:1555572
A:Accession: S21238
A:Molecule type: protein
A:Residues: 1-15 <PIE>
A:Experimental source: strain Hildenborough
C:Genetics:
A:Gene: dsyB
C:Complex: heterohexamer: two alpha, two beta and two gamma chains
C:Function:
A:Description: catalyzes the six-electron reduction of sulfite to sulfide
A:Pathway: the terminal oxidase in the sulfate-reduction pathway
C:Keywords: heterohexamer; oxidoreductase

Query Match 28.4%; Score 21; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 5 MGSGNLSE 14
Db 3 ISSGVNPKP 12

RESULT 8

C36198
T-cell receptor beta chain J region - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 28-Mar-1991 #sequence_rev1sion 28-Mar-1991 #text_change 21-Jul-2000
C:Accession: C36198
R:Joolker, L.W.; Carlson, L.M.; Lee, K.; Lahti, J.; McCormack, W.T.; Leiden, J.M.; Chen
Proc. Natl. Acad. Sci. U.S.A. 87, 7856-7860, 1990
A:Title: Evolutionary conservation of antigen recognition: the chicken T-cell receptor B
A:Reference number: A36198; PMID:91045896; PMID:2236002
A:Accession: C36198
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-15 <TTO>
A:Cross-references: EMBL:M37799; NID:9212737; PIDN:AAA62754.1; PID:9555475
C:Keywords: T-cell receptor

Query Match

Best Local Similarity 28.4%; Score 21; DB 2; Length 15;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 LSMGSGTLLS 12
| | | | |
DB 4 LNRGQCTRLT 13

RESULT 9

A36315
recycling receptor p180 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 25-Jan-1991 #sequence_rev1sion 25-Jan-1991 #text_change 30-Sep-1993
C:Accession: A36315
R:Baake, C.M.; van der Geer, P.; Hunter, T.; Trowbridge, I.S.
Mol. Cell. Biol. 10, 2606-2618, 1990
A:Title: p180, a novel recycling transmembrane glycoprotein with restricted cell type ex
A:Reference number: A36315; PMID:90288946; PMID:2188094
A:Accession: A36315
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <ISA>

Query Match

Best Local Similarity 28.4%; Score 21; DB 2; Length 15;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 LSEPN 15
| | | | |
DB 7 LPEPN 11

RESULT 10

PH1455
T-cell receptor alpha chain (clone A24/PEF4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 10-Mar-1994 #sequence_rev1sion 10-Mar-1994 #text_change 15-Mar-2004
C:Accession: PH1455
R:Casanova, J.L.; Martinou, F.; Gournier, H.; Barra, C.; Panetier, C.; Regnault, A.; Ko
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatib
A:Reference number: PH1430; PMID:93171821; PMID:8436911
A:Accession: PH1455
A:Molecule type: mRNA
A:Residues: 1-15 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Keywords: receptor; T-cell

Query Match 28.4%; Score 21; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.8e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LSMGSGT 9

DB 3 LSMGSGT 9
| | | | |

RESULT 11

F60589
sperm-activating peptide (Asn-3, Ser-5 SAP-I) - Echinosmetra mathaei (type A)
C:Species: Echinosmetra mathaei
C:Date: 17-Apr-1993 #sequence_rev1sion 17-Apr-1993 #text_change 16-Aug-2004
C:Accession: F60589
R:Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamagu
Comp. Biochem. Physiol. B 94, 739-751, 1989
A:Title: A halogenated amino acid-containing sperm activating peptide and its related p
otus nudus, Echinosmetra mathaei and Heterocentrotus mamillatus.
A:Reference number: A60527
A:Accession: F60589
A:Molecule type: protein
A:Residues: 1-10 <YOS>
A:Cross-references: UNIPROT:Q7MAC5

Query Match

Best Local Similarity 27.0%; Score 20; DB 2; Length 10;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 GNTLS 12
| | | | |
DB 1 GFTLS 5

RESULT 12

H60588
sperm-activating peptide (Thr-2,5, Leu-3, Pro-4, Ser-7,10 SAP-I) - slate-pencil urchin
C:Species: Heterocentrotus mamillatus
C:Date: 17-Apr-1993 #sequence_rev1sion 17-Apr-1993 #text_change 16-Aug-2004
C:Accession: H60588
R:Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamagu
Comp. Biochem. Physiol. B 94, 739-751, 1989
A:Title: A halogenated amino acid-containing sperm activating peptide and its related p
otus nudus, Echinosmetra mathaei and Heterocentrotus mamillatus.
A:Reference number: A60527
A:Accession: H60588
A:Molecule type: protein
A:Residues: 1-10 <YOS>
A:Cross-references: UNIPROT:Q7MAC8

Query Match

Best Local Similarity 27.0%; Score 20; DB 2; Length 10;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 LSMGSGT 10
| | | | |
DB 3 LPTGSGT 10

RESULT 13

A37933
Ig lambda chain J region - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 26-Jul-1991 #sequence_rev1sion 26-Jul-1991 #text_change 05-Nov-1999
C:Accession: A37933
R:Reynaud, C.A.; Mackay, C.R.; Mueller, R.G.; Wells, J.C.
Cell 64, 995-1005, 1991
A:Title: Somatic generation of diversity in a mammalian primary lymphoid organ: the shee
A:Reference number: A37933; PMID:91160063; PMID:1900459
A:Accession: A37933
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-12 <REV>
A:Cross-references: GB:M60440; NID:9165946; PIDN:AAA1550.1; PID:9552425
C:Keywords: heterotrimer; immunoglobulin

Query Match 27.0%; Score 20; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 6 GSGGLNLS 12
|||
|:

Db 4 GSGTRLT 10

RESULT 14

B25448 Ig kappa chain, 69 allotype, J-K1.1 segment - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999

C:Accession: B25448

R:Akimenko, M.A.; Mariame, B.; Rougeon, F.

Proc. Natl. Acad. Sci. U.S.A. 83, 5180-5183, 1986

A:Title: Evolution of the immunoglobulin kappa light chain locus in the rabbit: evidence

A:Reference number: A94110; MUID:86259753; PMID:3088570

A:Accession: B25448

A:Molecule type: DNA

A:Residues: 1-13 <AKT>

A:Cross-references: GB:M14067; GB:M14062; GB:M14063; GB:M14064; GB:M14065; GB:M14066; NT

C:Keywords: heterotetramer; immunoglobulin

Query Match 27.0%; Score 20; DB 2; Length 13;

Best Local Similarity 37.5%; Pred. No. 2.3e+03;

Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 4 SMGSGGLN 11
:|:|:|:

Db 2 AFGAGTNV 9

RESULT 15

D47630

Ig kappa chain J region J3 - southeastern Australian rat

C:Species: Rattus sordidus villosissimus (southeastern Australian rat)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 05-Nov-1999

C:Accession: D47630

R:Gutman, G.A.; Beeta, R.M.; Frank, M.B.; Bayerstock, P.R.

Immunogenetics 26, 14-20, 1987

A:Title: Duplication of J-kappa genes within genus Rattus.

A:Reference number: A47630; MUID:87278355; PMID:3111993

A:Accession: D47630

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-13 <GUT>

A:Cross-references: GB:M17319; NID:9204788; PIDN:AAA41400.1; PID:9204792

C:Keywords: heterotetramer; immunoglobulin

Query Match 27.0%; Score 20; DB 2; Length 13;

Best Local Similarity 50.0%; Pred. No. 2.3e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 4 SMGSGGLN 11
:|:|:|:

Db 2 TFGSCTKL 9

Search completed: November 1, 2005, 14:12:30
Job time : 41 sec

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 13:52:29 ; Search time 172 Seconds
(without alignments)
44.658 Million cell updates/sec

Title: US-10-612-162a-3
Perfect score: 74
Sequence: 1 SKLMSGSGUNLSEPN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 6622

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	39.2	13	1	P43173 ascaris suu
2	26	35.1	11	2	Q80B26 hepatitis b
3	24	32.4	13	1	P82064 limodysac
4	24	32.4	14	2	Q8JUG5 asbha goss
5	23	31.1	8	2	P83531 lactobacill
6	22	29.7	10	1	P80699 bacillus su
7	22	29.7	11	2	Q77913 oreochromis
8	22	29.7	13	2	Q6R272 lactococcus
9	22	29.7	14	2	Q73591 gallus gall
10	21	28.4	9	2	Q9TRW2 oryctolagus
11	21	28.4	14	2	Q7SAV2 neurospora
12	21	28.4	14	2	Q9QVM9 rattus sp.
13	21	28.4	15	2	Q65177 mesembryant
14	21	28.4	10	1	DY82 LIMDU
15	20	27.0	10	2	Q7M4B8 heterocent
16	20	27.0	11	2	Q7M4C5 echinometra
17	20	27.0	11	2	Q16217 homo sapien
18	20	27.0	11	2	Q7RH33 plasmodium
19	20	27.0	11	2	Q6LA95 rattus norv
20	20	27.0	11	2	Q9Z1H5 mus musculu
21	20	27.0	13	2	Q7BD41 streptococ
22	20	27.0	14	2	Q7SD23 neurospora
23	20	27.0	15	2	F1BA_SYNCA
24	20	27.0	15	2	Q7S362 neurospora
25	20	27.0	15	2	Q9UC83 homo sapien
26	20	27.0	15	2	Q9TWB6 tritaneustes
27	20	27.0	15	2	Q798U8 streptococ
28	20	27.0	15	2	Q843J2 simian viru
29	19.5	26.4	13	2	Q13377 homo sapien
30	19.5	26.4	15	1	GTER_PSEUD
31	19	25.7	8	1	P41872 pseudomonas

32	19	25.7	8	2	Q83349 murine hepa
33	19	25.7	9	2	Q7BE72 rattus norv
34	19	25.7	10	2	Q9UJ48 homo sapien
35	19	25.7	12	2	Q7M2Q0 macaca fasc
36	19	25.7	14	1	TEMB_RANLU
37	19	25.7	14	2	Q50845 rana luteiv
38	19	25.7	14	2	Q50845 methanococ
39	19	25.7	14	2	Q9S179 homo sapien
40	19	25.7	14	2	P82326 pium sacti
41	19	25.7	14	2	Q61864 mus musculu
42	19	25.7	15	2	Q86WB2 homo sapien
43	19	25.7	15	2	Q9WTA3 amorophophal
44	18.5	25.0	15	2	Q8USK4 human immun
45	18	24.3	8	1	DY81 LIMIN
					P82079 limodysac

ALIGNMENTS

RESULT 1	FARB_ASCSU	STANDARD;	PRT;	13 AA.
AC	P43173;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	FMRFamide-like neuropeptide Af11.			
DB	Ascaris suum (Pig roundworm) (Ascaris lumbricoidea).			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;			
OC	Ascarididae; Ascaris.			
OX	NCBI_TaxID=6253;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=95380362; PubMed=7651904; DOI=10.1016/0196-9781(94)00211-N;			
RA	Cowden C., Stretton A.O.W.;			
RT	*Eight novel FMRFamide-like neuropeptides isolated from the nematode			
RT	Ascaris suum.*;			
RL	Peptides 16:491-500(1995).			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.			
KW	Amidation; Direct protein sequencing; Neuropeptide.			
FT	MOD RES 13 13 Phenylalanine amide.			
SQ	SEQUENCE 13 AA; 1495 MM; 9CAEC650D6886B05 CRC64;			
Query Match 39.2%; Score 29; DB 1; Length 13;				
Best Local Similarity 55.6%; Pred. No. 3.2e+02;				
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;				
QY	7 SGLNLSSEPN 15			
DB	1 SDIGISEPN 9			
RESULT 2				
ID	Q80B26;	PRELIMINARY;	PRT;	11 AA.
AC	Q80B26;			
DT	01-JUN-2003 (TREMBLrel. 24, Created)			
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)			
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
DE	Pre-S1 protein (Fragment).			
OS	Hepatitis B virus.			
OC	Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.			
OX	NCBI_TaxID=10407;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95011308; PubMed=7926515;			
RA	Chen C.H., Chen P.J., Chu J.S., Yeh K.H., Lai M.Y., Chen D.S.;			
RT	"RiboSving cholestatic hepatitis in a hepatitis B surface antigen			
RT	carrier after renal transplantation.";			
RL	Gastroenterology 107:1514-1518(1994).			
DR	EMBL; S74182; AAP21092.1; -			

FT NON TER 11 11
SQ SEQUENCE 11 AA; 1161 MW; 1535A06CA1B5B724 CRC64;
Query Match 35.1%; Score 26; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 9.4e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
OY 5 MSGSGLNSEP 14
DB 1 MGNLSTSNP 10
RESULT 3
ID FLET LIMFT STANDARD; PRT; 13 AA.
AC P82064;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fletcherin.
OS Limnodynastes fletcheri (Barking marsh frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Limnodynastidae; Limnodynastes.
OX NCBI_TaxID=39403;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion.
RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structure of the dynastins from
RL Limnodynastes salmiani and fletcheri from Limnodynastes fletcheri";
RL Aust. J. Chem. 46:1235-1244(1993).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Secreted by the skin dorsal glands.
CC -1- MASS SPECTROMETRY: MW=1197; METHOD=PIB; RANGE=4-13; NOTE=Ref.1.
KW Direct protein sequencing.
SQ SEQUENCE 13 AA; 1197 MW; 56B5B1FAEA7C723 CRC64;
Query Match 32.4%; Score 24; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 2.6e+03;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 SKLSMSGSL 9
DB 5 SKLVSGIGL 13
RESULT 4
ID O8JIG5 PRELIMINARY; PRT; 14 AA.
AC O8JIG5;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE YLR191 (Fragment).
GN Name=YLR191;
OS Asbaya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A.
RA Alberti-Segui C., Dietrich F., Philippen P.;
RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF378569; AAN8136.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1205 MW; 36967F5A00467868 CRC64;
Query Match 32.4%; Score 24; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 4 SMGSGLNISE 13

DB 1 SAGSGTGPSE 10
RESULT 5
ID P83531 PRELIMINARY; PRT; 8 AA.
AC P83531;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Unknown protein from 2D-page (fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 20451;
RX PubMed=12112860;
DOI=10.1002/1615-9861(200206)2:6<765::AID-PROT765>3.0.CO;2-V;
RA Draws O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
RT "High pressure effects, step-wise altered protein expression in
RL Lactobacillus sanfranciscensis".
RL Proteomics 2:765-774(2002).
CC -1- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
CC protein is: 15 kDa.
FT NON TER 1
FT NON TER 8
SQ SEQUENCE 8 AA; 677 MW; C835B87865B87735 CRC64;
Query Match 31.1%; Score 23; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.6e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 4 SMGSGLNIL 11
DB 1 SLGSGSL 8
RESULT 6
ID VEG6_BACSU STANDARD; PRT; 10 AA.
AC VEG6_BACSU;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Vegetative protein 6 (VEG6) (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE.
RC STRAIN=168 / 1558;
RX MEDLINE=97237728; PubMed=9084183;
RA Schmid R., Bernhardt J., Antelmann H., Voelker U., Mach H.,
RA Voelker A., Hecker M.;
RT "Identification of vegetative proteins for a two-dimensional protein
index of Bacillus subtilis".
RL Microbiology 143:991-998(1997).
CC -1- CAUTION: Could not be found in the genome of B.subtilis 168.
KW Direct protein sequencing.
FT NON TER 10
SQ SEQUENCE 10 AA; 973 MW; 8793A6B2C8772861 CRC64;
Query Match 29.7%; Score 22; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 4.6e+03;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
OY 5 MSGSGLNSE 13
DB 1 LGTGLGVDQ 9

```
RESULT 7
077913 PRELIMINARY; PRT; 11 AA.
AC 077913;
DT 01-NOV-1998 (TRENBLREL. 08, Created)
DT 01-NOV-1998 (TRENBLREL. 08, Last sequence update)
DE 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
OC MHC class II B locus 4 (Fragment).
OC Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=6128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid MHC
RT class II B loci."
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050024; AAC41363.1; -.
FT NON_TER 1 1
FT SEQUENCE 11 AA; 1181 MW; 723258737EASB72B CRC64;

Query Match 29.7%; Score 22; DB 2; Length 11;
Best Local Similarity 71.4%; Pred. No. 5.1e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SKLSMGS 7
DB 3 SELSCGS 9

RESULT 8
06R272 PRELIMINARY; PRT; 13 AA.
AC 06R272;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Arca (Fragment).
GN Name=arca;
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=AG1363;
RA PubMed=14762010; DOI=10.1128/JB.186.4.1147-1157.2004;
RA Larsen R., Bulst G., Kuipers O.P., Kok J.;
RT "ArgR and ArgC are both required for regulation of arginine metabolism
RT in Lactococcus lactis."
RL J. Bacteriol. 186:1147-1157(2004).
DR EMBL; AF518515; AAR9646.1; -.
FT NON_TER 13 13
FT SEQUENCE 13 AA; 1390 MW; 0F4287F1AC8D52C4 CRC64;

Query Match 29.7%; Score 22; DB 2; Length 13;
Best Local Similarity 37.5%; Pred. No. 6.2e+03;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 MSGSLNLS 12
DB 1 MANGINVN 8

RESULT 9
073591 PRELIMINARY; PRT; 14 AA.
ID 073591
```

```
AC 073591;
DT 01-AUG-1998 (TRENBLREL. 07, Created)
DT 01-AUG-1998 (TRENBLREL. 07, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE Hox C10 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phaethidae; Phaethinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=White Leghorn;
RX MEDLINE=98141813; PubMed=9473273; DOI=10.1006/abio.1997.2500;
RA Reale F.V. Jr., Mason K., Hunter A.W., Botwell M.;
RT "Multiplex display polymerase chain reaction amplifies and resolves
RT related sequences sharing a single moderately conserved domain."
RL Anal. Biochem. 256:158-168(1998).
DR EMBL; U34614; AAC36452.1; -.
FT NON_TER 1 1
FT SEQUENCE 14 AA; 1673 MW; 81258FC9E81FDA45 CRC64;

Query Match 29.7%; Score 22; DB 2; Length 14;
Best Local Similarity 25.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 KLSMSGSLNLS 13
DB 1 RLEISKSINLTD 12

RESULT 10
09TRW2 PRELIMINARY; PRT; 9 AA.
AC 09TRW2;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE CALDESNON=PHOSPHORYLATION site (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=91378498; PubMed=1898046;
RA Ikebe M., Hornick T.;
RT "Determination of the phosphorylation sites of smooth muscle caldesmon
RT by protein kinase C."
RL Arch. Biochem. Biophys. 288:538-542(1991).
DR PIR; A44873; A44873.
FT NON_TER 1 1
FT SEQUENCE 9 AA; 1018 MW; 8C901B10533735A5 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 GSGSLNLS 13
DB 1 GSSLKIEE 8

RESULT 11
07SAV2 PRELIMINARY; PRT; 14 AA.
ID 07SAV2;
AC 07SAV2;
DT 01-MAR-2004 (TRENBLREL. 26, Created)
DT 01-MAR-2004 (TRENBLREL. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Predicted protein.
```

GN Name=NCU05682.1;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCB1_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=0874A;
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
 RA Valte D., Fitzhugh W., Ma L.-U., Smirnov S., Purcell S., Reisman B.,
 RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
 RA Qui D., Ianakiev P., Pedersen D., Nelson M., Mashburne M.,
 RA Selitrenkoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
 RA Koche G.O., Jedd G., Mewes W., Straben C., Marcotte E., Greenberg D.,
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
 RA Kanal M., Kamysebellis M., Maucell E., Bielke C., Rudd S., Frisman D.,
 RA Kyrstofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
 RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
 RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
 RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
 RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.,
 RA "The Genome Sequence of the Filamentous Fungus Neurospora crassa.",
 RL Nature 0:0-0(2003).
 RT -! CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABX01000180; EAAJ3560.1; -
 SQ SEQUENCE 14 AA; 1354 MW; 90BC62C653BB8CBE CRC64;

Query Match 28.4%; Score 21; DB 2; Length 14;
 Best Local Similarity 44.4%; Pred. No. 1e+04;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 5 MGSGLINSE 13
 ||| : |||
 Db 1 MGLGVGCS D 9

RESULT 12
 O9QVM9 PRELIMINARY; PRT; 14 AA.
 AC O9QVM9;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Gila-derived nexin, GDN, protease nexin-1 (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCB1_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE=92207980; PubMed=1554734;
 RA Roveelli G., Stone S.R., Guidolin A., Sommer J., Monard D.,
 RT "Characterization of the heparin-binding site of gila-derived
 RT nexin/protease nexin-1.";
 RL Biochemistry 31:3542-3549(1992).
 FT NON_TER 1 1
 FT 14 14
 SQ SEQUENCE 14 AA; 1498 MW; 21ACE79A02590957 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 1e+04;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 10 NLSEPN 15
 ||| |||
 Db 3 NLSPN 8

RESULT 13
 065177

ID 065177 PRELIMINARY; PRT; 15 AA.
 AC 065177;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Turgor responsive protein homolog (Fragment).
 OS Mesembryanthemum crystallinum (Common ice plant).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Alnaceae; Mesembryanthemum.
 OX NCB1_TaxID=3544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Root;
 RA Michalowski C.B., Bohmert H.J.;
 RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF054444; AAC14178.1; -
 FT NON_TER 1 1
 SQ SEQUENCE 15 AA; 1607 MW; 4137ED0DF9B3FC21 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 15;
 Best Local Similarity 30.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 SKLSMGSGLN 10
 :|| : |||
 Db 4 NELPLAQGIN 13

RESULT 14
 DYS2 LIMDU STANDARD; PRT; 10 AA.
 ID DYS2 LIMDU
 AC P82080;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Dynastin 2.
 OS Limnodynastes dumerilii (Eastern banjo frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;
 OC Limnodynastidae; Limnodynastes.
 OX NCB1_TaxID=104065;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Tibial gland;
 RA Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structure of the dynastin from
 RT the banjo frogs Limnodynastes terrestris.";
 RT Limnodynastes terrestris.
 AU Aust. J. Chem. 46:833-842(1993).
 CC -! SUBCELLULAR LOCATION: Secreted.
 CC -! TISSUE SPECIFICITY: Skin.
 CC -! MASS SPECTROMETRY: MW=986; METHOD=FAB; RANGE=1-10; NOTE=Ref.1.
 KW Direct protein sequencing.
 SQ SEQUENCE 10 AA; 986 MW; 550FDC287735A5B7 CRC64;

Query Match 27.0%; Score 20; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 GLNL 11
 ||| |||
 Db 7 GLNL 10

RESULT 15
 ID Q7M4B8 PRELIMINARY; PRT; 10 AA.
 AC Q7M4B8;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Sperm-activating peptide (Thr-2,5, Leu-3, Pro-4, Ser-7,10 SAP-1).

OS Heterocentrotus mammillatus (Slate-pencil urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinometridae;
 OC Heterocentrotus.
 OK NCBI_TaxID=31180;
 RN [1]
 RP SEQUENCE.
 RA Yoshino K.I., Kajihara H., Nomura K., Takao T., Shimonishi Y.,
 Kurita M., Yamaguchi M., Suzuki N.;
 RT "A halogenated amino acid-containing sperm activating peptide and its
 RT related peptides isolated from the egg jelly of sea urchins,
 RT Tripleneutes gracillia, Pseudobolita maculata, Strongylocentrotus
 RT nudus, Echinometra mathaei and Heterocentrotus mammillatus.";
 RL Comp. Biochem. Physiol. 94:739-751(1989).
 DR PIR: H60588; H60588
 SQ SEQUENCE 10 AA; 875 MW; 59F15365B861B767 CRC64;

Query Match 27.0%; Score 20; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.1e+04;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 3 LSMGSGLN 10
 | |||:
 Db 3 LPTGSGVS 10

Search completed: November 1, 2005, 14:09:02
 Job time : 183 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

CM protein - protein search, using sw model

Run on: November 1, 2005, 12:28:13 ; Search time 74.3676 Seconds
(without alignment)
67.608 Million cell updates/sec

Title: US-10-612-162a-4

Perfect score: 68

Sequence: 1 YEKVLGEYVAV 13

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16dec04:*

1: geneseqp19808:*\n2: geneseqp19908:*\n3: geneseqp20008:*\n4: geneseqp20018:*\n5: geneseqp20028:*\n6: geneseqp20038:*\n7: geneseqp20038:*\n8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	100.0	13	ADG46078	Adg46078 Human CDT
2	68	100.0	49	ABP72836	Abp72836 Human tra
3	68	100.0	49	ADH89394	Adh89394 Human tra
4	68	100.0	49	ADK15882	Adk15882 Human tra
5	68	100.0	49	ADL70756	Adl70756 Human tra
6	68	100.0	137	ADF74798	Adf74798 Human NOV
7	68	100.0	328	AAH84371	Aah84371 Amino aci
8	68	100.0	539	AAU02980	Aau02980 Angiotens
9	68	100.0	575	ABR82321	Abre82321 Human met
10	68	100.0	609	ABM83782	Abm83782 Human dia
11	68	100.0	627	ABM83781	Abm83781 Human dia
12	68	100.0	628	ABM83779	Abm83779 Human dia
13	68	100.0	643	ABM83778	Abm83778 Human dia
14	68	100.0	645	ABM83783	Abm83783 Human dia
15	68	100.0	646	AAU02938	Aau02938 Angiotens
16	68	100.0	646	ABM83780	Abm83780 Human tra
17	68	100.0	679	ABP72820	Abp72820 Human tra
18	68	100.0	679	ADH89360	Adh89360 Human tra
19	68	100.0	679	ADK15869	Adk15869 Mature hu
20	68	100.0	679	ADL70732	Adl70732 Human tra
21	68	100.0	679	ADL24413	Adl24413 Human tra
22	68	100.0	696	AAH70394	Aah70394 Sequence
23	68	100.0	698	AAH12499	Aah12499 Human tra
24	68	100.0	698	AAH64492	Aah64492 Human tra
25	68	100.0	698	AAH54354	Aah54354 Serotrans

ALIGNMENTS

26	68	100.0	698	3	AAH50717	Aay50717 Human ser
27	68	100.0	698	6	ABP72819	Abp72819 Human tra
28	68	100.0	698	7	ADP45282	Adp45282 Human pro
29	68	100.0	698	7	ADF74796	Adf74796 Human NOV
30	68	100.0	698	7	ADF74800	Adf74800 Human NOV
31	68	100.0	698	8	ADH34559	Adh34559 Human tra
32	68	100.0	698	8	ADH89359	Adh89359 Human tra
33	68	100.0	698	8	ADK15868	Adk15868 Human tra
34	68	100.0	698	8	ADL70731	Adl70731 Human tra
35	68	100.0	698	8	ADL24412	Adl24412 Human tra
36	68	100.0	698	8	ADP21259	Adp21259 Human tra
37	68	100.0	1074	2	AAW07621	Aaw07621 LDLR/TF c
38	68	100.0	1410	2	AAW07622	Aaw07622 LDLR/TF c
39	68	100.0	1410	6	ABU04139	Abu04139 Human exp
40	68	100.0	1418	4	AAU32831	Aau32831 Novel hum
41	68	100.0	1418	6	ABU04138	Abu04138 Human exp
42	58	85.3	676	8	ADL70764	Adl70764 Rabbit tr
43	58	85.3	676	8	ADL24458	Adl24458 Rabbit tr
44	56	82.4	685	2	AAH11664	Aah11664 Partial p
45	56	82.4	685	2	AAH11663	Aah11663 Partial p

RESULT 1
ADG46078 standard; peptide; 13 AA.
ADG46078;
ADG46078; (first entry)
25-MAR-2004
Human CDT peptide fragment #4.
antibody; carbohydrate-deficient transferrin; CDT;
non-glycosylated transferrin; alcoholism; alcoholic; diagnosis; human.
Homo sapiens.
EP1378521-A1.
07-JAN-2004.
19-MAY-2003; 2003EP-00011334.
05-JUL-2002; 2002DE-01030550.
(DADE-) DADE BEHRING MARBURG GMBH.
Althaus H;
WPI; 2004-073743/08.
New antibody specific for carbohydrate-deficient transferrin; useful for diagnosis of alcoholism; can bind its target in solution, eliminating need for immobilization.
Claim 4; SEQ ID NO 4; 21bp; German.
This invention describes a novel antibody that, in aqueous solution, binds selectively to carbohydrate-deficient transferrin (CDT) without having to bind CDT to a solid phase. The invention also describes an antibody that binds selectively to CDT at regions containing the sequences VVARSMGSGKEDLIWELL, TTEDSIKIMNGEADAMSIDGCF, SKLSMGSLINSEPN and YEKVLGEYVAV (ADG46075-ADG46078) and an immunoassay for detecting CDT using the antibodies of the invention. The antibodies of the invention are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The antibodies are obtained by immunisation with non-glycosylated transferrin, or a fragment, then generation of hybridomas by standard fusion of spleen and myeloma cells. Hybridomas are then selected for production of antibodies that specifically bind CDT from the aqueous phase. The antibodies are useful for diagnosis of alcoholism, CDT, which

CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
 CC alcoholic. The antibodies allow direct detection of CDT in solution,
 CC eliminating the need for immobilising it on a solid phase (as required
 CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
 CC fragments used in the method of the invention.

XX Sequence 13 AA;

Query March 100.0%; Score 68; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00038;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGESEYKAV 13
 |||||
 Db 1 YEKYLGESEYKAV 13

RESULT 2
 ABP72836
 ID ABP72836 standard; peptide; 49 AA.

XX ABP72836;

DT 11-AUG-2003 (first entry)

XX Human transferrin peptide insertion region.

XX Transferrin; neuroprotective; cerebroprotective; vasotropic;
 KW antiparkinsonian; nootropic; anti-HIV; antileukemic; antiallergic;
 KW cytostatic; immunosuppressive; antithrombotic; cardiac;
 KW gynaecological; immunostimulant; antianemic; haemostatic;
 KW antinflammatory; dermatological; antibacterial; virucide; antiparasitic;
 KW fungicide; hepatotropic; antitubercular; antidiabetic; antipruritic;
 KW tranquilizer; vulnery; antidiabetic; nephroprotective; antipruritic;
 KW gastroenteric; gene therapy; transgenic animal.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 1..3 /note="Asn is N-glycosylated"

FT Misc-difference 15..16 /note="peptide insertion site"

XX MO2003020746-A1.

XX 13-MAR-2003.

XX 30-AUG-2002; 2002MO-US027637.

XX 30-AUG-2001; 2001US-0315745P.

XX 30-NOV-2001; 2001US-0334059P.

XX (BIOR-) BIOREXIS PHARM CORP.

XX Prior CP;

XX WPI; 2003-332916/31.

XX New fusion protein, useful in the diagnosis and treatment of diseases or
 PT disorders relating to the respiratory, cardiovascular and digestive
 PT systems, comprises a transferrin protein fused to a therapeutic protein.

XX Example 3; Page 249; 298pp; English.

XX The present sequence is a portion of the human transferrin (Tf) C domain,
 CC comprising amino acids 611-659 of the Tf sequence given in ABP72820. The
 CC invention relates to novel fusion proteins of Tf and a therapeutic
 CC protein or peptide. The therapeutic protein or peptide, e.g. an
 CC erythropoietin mimetic (see ABP72834), can be fused to the N- or C-
 CC terminus of Tf, or inserted into Tf especially between residues Glu-625
 CC and Thr-626 of the Tf N domain. Modified Tf fusion proteins of the
 CC invention can be used in the diagnosis, prognosis, prevention and/or

CC treatment of diseases and/or disorders of the endocrine, nervous, immune,
 CC respiratory, cardiovascular, reproductive and digestive systems, diseases
 CC and/or disorders relating to the blood or to cell proliferation,
 CC inflammatory conditions and infectious diseases, or to deliver a
 CC therapeutic agent to a cell or across the blood-brain barrier

XX Sequence 49 AA;

Query March 100.0%; Score 68; DB 6; Length 49;
 Best Local Similarity 100.0%; Pred. No. 0.0015;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGESEYKAV 13
 |||||
 Db 37 YEKYLGESEYKAV 49

RESULT 3
 ADH89394
 ID ADH89394 standard; protein; 49 AA.

XX ADH89394;

DT 15-APR-2004 (first entry)

XX Human transferrin protein domain SegID38.

XX fusion protein; transferrin protein; glycosylation;
 KW antibody variable region; cytostatic; antibacterial; virucide;
 KW antiparasitic; immunosuppressive; antidiabetic; gene therapy;
 KW septic shock; endotoxic shock; cachexia syndrome; bacterial infection;
 KW viral infection; parasitic infection; neoplasm; autoimmune disease;
 KW arthritis; graft rejection; human.

XX Homo sapiens.

XX US2003226155-A1.

XX 04-DEC-2003.

XX 10-MAR-2003; 2003US-00384060.

XX 30-AUG-2001; 2001US-0315745P.

XX 30-NOV-2001; 2001US-0334059P.

XX 30-AUG-2002; 2002US-0023149P.

XX 30-AUG-2002; 2002US-0406977P.

XX (BIOR-) BIOREXIS PHARM CORP.

XX Sadeghi H, Prior CP, Turner A;

XX WPI; 2004-022093/02.

XX New fusion protein comprising a transferrin protein exhibiting reduced
 PT glycosylation fused to at least one antibody variable region, useful for
 PT preparing a composition for treating e.g., septic shock, neoplasm or
 PT autoimmune disease.

XX Example 2; SEQ ID NO 38; 82pp; English.

XX This invention relates to a novel fusion protein which comprises a
 CC transferrin protein exhibiting reduced glycosylation fused to at least
 CC one antibody variable region. The invention may be useful for the
 CC development of compounds with cytostatic, antibacterial, virucide,
 CC antiparasitic, immunosuppressive or antidiabetic activity. In addition,
 CC the sequences disclosed may be useful for gene therapy. The fusion
 CC protein is useful for preparing a composition for treating a disease or
 CC disease symptom in a patient for example septic shock, endotoxic shock,
 CC cachexia syndrome associated with bacterial, viral or parasitic
 CC infections, neoplasm, autoimmune disease, arthritis or adverse effects
 CC associated with treatment for preventing graft rejection. The present
 CC sequence is that of a domain of the human transferrin protein which was
 CC used in the exemplification of the invention.


```
XX SQ Sequence 49 AA;
XX Query Match 100.0%; Score 68; DB 8; Length 49;
XX Best Local Similarity 100.0%; Pred. No. 0.0015;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEKYLGESEYVKAV 13
   |||||
   |||||
   |||||
DB 37 YEKYLGESEYVKAV 49

RESULT 4
ADK15882
ID ADK15882 standard; protein; 49 AA.
XX
XX ADK15882;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Human transferrin (Tf) protein fragment #4.
XX
XX KW fusion protein; transferrin; Tf; beta-interferon; beta-IFN;
XX KW glucagon-like peptide; GLP-1; erythropoietin mimetic peptide; EMP1;
XX KW T-20; soluble toxin receptor; epitope tagging; human.
XX
XX OS Homo sapiens.
XX
XX PN US2003221201-A1.
XX
XX PD 27-NOV-2003.
XX
XX PF 04-MAR-2003; 2003US-00378094.
XX
XX PR 30-AUG-2001; 2001US-0315745P.
XX PR 30-NOV-2001; 2001US-0334059P.
XX PR 30-AUG-2002; 2002US-00231494.
XX PR 30-AUG-2002; 2002US-0406977P.
XX
XX PA (BIOREXIS PHARM CORP.
XX
XX PI Prior CP, Lai C, Sadeghi H, Turner A;
XX
XX DR WPI, 2004-010899/01.
XX
XX PT New fusion protein comprising a modified transferrin (Tf) protein fused
XX to a therapeutic protein or peptide, useful for epitope tagging.
XX
XX PS Example 5; SEQ ID NO 16; 70pp; English.
XX
XX CC The invention comprises a fusion protein that contains a modified
XX transferrin (Tf) protein fused to a therapeutic protein/peptide (e.g.
XX beta-interferon - IFN, glucagon-like peptide - GLP-1, erythropoietin
XX mimetic peptide - EMP1, T-20 and soluble toxin receptor). The fusion
XX protein of the invention is useful for epitope tagging. The present amino
XX acid sequence represents a fragment of the human Tf protein.
XX
XX SQ Sequence 49 AA;
XX Query Match 100.0%; Score 68; DB 8; Length 49;
XX Best Local Similarity 100.0%; Pred. No. 0.0015;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEKYLGESEYVKAV 13
   |||||
   |||||
   |||||
DB 37 YEKYLGESEYVKAV 49

RESULT 5
ADL70756
ID ADL70756 standard; peptide; 49 AA.
XX
XX AC ADL70756;
```

```
XX DT 03-JUN-2004 (first entry)
XX
XX DE Human transferrin, Tf, insertion region SEQ ID 27.
XX
XX KW Immunosuppressive; Haemostatic; Anti-allergic; Antiasthmatic;
XX Dermatological; Anti-inflammatory; Antibacterial; Vasotropic;
XX Nephrotropic; Neuroprotective; Cytostatic; Cardioprotective; Vulnerary;
XX Antiparkinsonian; Nootropic; Cardiant; Antianaemic; Antithrombotic;
XX Thrombolytic; Anticoagulant; Gastrointestinal; Respiratory; transferrin;
XX Tf; transferrin fusion protein; Tf fusion protein; human.
XX
XX OS Homo sapiens.
XX
XX PN WO2004020588-A2.
XX
XX PD 11-MAR-2004.
XX
XX PF 28-AUG-2003; 2003WO-US026779.
XX
XX PR 30-AUG-2002; 2002US-0406977P.
XX PR 10-MAR-2003; 2003US-00384060.
XX PR 09-JUL-2003; 2003US-0485404P.
XX
XX PA (BIOREXIS PHARM CORP.
XX
XX PI Prior CP, Turner AJ, Sadeghi H;
XX
XX DR WPI, 2004-239175/22.
XX
XX PT Novel library containing several fusion proteins each of which comprises
XX first transferrin polypeptide fused to at least one second peptide,
XX useful for screening for transferrin fusion protein having the particular
XX activity.
XX
XX PS Example 3; SEQ ID NO 27; 243pp; English.
XX
XX CC The present invention relates to a library (1) of modified fusion
XX proteins of transferrin (Tf) and therapeutic proteins with increased
XX serum half-life or serum stability. Preferred fusion proteins include
XX those modified so that the Tf moiety exhibits no or reduced
XX glycosylation, iron binding and/or Tf receptor binding. The transferrin
XX fusion proteins are useful for treating, preventing or ameliorating
XX disorders or diseases of endocrine system, nervous system, immune system,
XX respiratory system, cardiovascular system, diseases and/or disorders
XX relating to cell proliferation, and/or diseases or disorders relating to
XX blood. The modified fusion proteins are useful in diagnosis, prognosis,
XX prevention and/or treatment of autoimmune disorders; diseases and
XX disorders of haematopoietic cells (e.g., leukaemia, neutropenia, anaemia
XX and thrombocytopenia); allergic reactions such as asthma, rhinitis and
XX anaphylaxis; IgE-mediated allergic reactions such as asthma, rhinitis and
XX eczema; inflammatory conditions e.g., inflammation associated with
XX infection (e.g., septic shock, sepsis), ischaemia-reperfusion injury,
XX nephritis, Crohn's disease, multiple sclerosis, respiratory disorders
XX (asthma and allergy), gastrointestinal disorders (inflammatory bowel
XX disease), cancers (e.g., gastric, ovarian, lung, bladder), CNS disorders
XX (multiple sclerosis, stroke, traumatic brain injury, neurodegenerative
XX disorders such as Parkinson's disease, Alzheimer's disease), etc. The
XX fusion protein is also useful as an adjuvant to enhance antibacterial or
XX antifungal immune responses, antiparasitic immune responses, etc. The
XX fusion protein is also useful for treating monoclonal gammopathy of
XX undetermined significance (MGUS), Waldenstrom's disease, plasmacytomas,
XX adult respiratory distress syndrome, for stimulating wound repair, for
XX preventing or treating infections of joints, bones, skin, etc. The fusion
XX protein is also useful for treating or preventing thrombosis, myocardial
XX infarction, cancers, thrombocytopenia, sickle cell anaemia,
XX glomerulonephritis, cardiac arrest, edema, pulmonary embolism,
XX atherosclerosis, etc. The present sequence is a DNA sequence for a
XX peptide fragment of Tf(611-659) illustrating an insertion site
XX (Glu625/Thr626) for producing the Tf fusion proteins.
XX
XX SQ Sequence 49 AA;
```

Query Match 100.0%; Score 68; DB 8; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEERYKAV 13
|||
37 YEKYLGEERYKAV 49

DB

RESULT 6
ADP74798
ID ADF74798 standard; protein; 137 AA.
XX
AC ADF74798;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human NOXV protein to treat human pathological conditions (SeqID 12).
XX
KW human; NOXV; metabolic disorder; diabetes; anorexia; cancer;
KW cardiovascular; infectious; neurodegenerative; immune;
KW haematopoietic disease; dyslipidaemia; anorectic; virucide; nootropic;
KW antiinflammatory; neuroprotective; antilipaeimic; anabolic; cardiatic;
KW neurogenesis; wound healing; angiogenesis; chromosome mapping;
KW tissue typing; preventive medicine; pharmacogenomic.
XX
XX Homo sapiens.
OS
PN WO2003076578-A2.
XX
PD 18-SEP-2003.
XX
PF 06-MAR-2003; 2003WO-US006794.
XX
PR 06-MAR-2002; 2002US-0361974P.
PR 08-MAR-2002; 2002US-00093463.
PR 08-MAR-2002; 2002WO-US007288.
PR 15-MAR-2002; 2002US-0365034P.
PR 19-MAR-2002; 2002US-0365477P.
PR 20-MAR-2002; 2002US-0365884P.
PR 20-MAR-2002; 2002US-0365984P.
PR 20-MAR-2002; 2002US-0365985P.
PR 22-MAR-2002; 2002US-0366928P.
PR 12-APR-2002; 2002US-0372018P.
PR 12-APR-2002; 2002US-0372022P.
PR 23-APR-2002; 2002US-0374682P.
PR 12-JUN-2002; 2002US-0388095P.
PR 14-JUN-2002; 2002US-0389143P.
PR 26-JUN-2002; 2002US-0391779P.
PR 15-AUG-2002; 2002US-0403743P.
PR 13-SEP-2002; 2002US-0410755P.
PR 23-SEP-2002; 2002US-0412957P.
PR 22-OCT-2002; 2002US-0420382P.
PR 05-MAR-2003; 2003US-00420382.
XX
XX (CURA-) CURAGEN CORP.
XX
PI Alesbrook JP, Anderson DM, Boldog FL, Burgess CE, Chaudhuri A;
PI Colman SD, Edinger SR, Eitenberg S, Gangoli EA, Gerlach VL;
PI Gorman U, Guo X, Kekuda R, Li U, MacLachlan T, Malynkar DM;
PI Mezes PS, Miller CE, Millet I, Padigaru M, Patuturajan M, Peyman J;
PI Qian X, Rasetelli L, Rieger DK, Smithson G, Spytek KA, Stone DJ;
PI Sukumaran S, Vernet CM, Voss EZ, Zhong M;
XX
XX WPI; 2003-697890/66.
DR
DR N-PSDB; ADF74797.
XX
XX
XX New isolated NOXV polypeptides and polynucleotides, useful for
XX preventing, diagnosing or treating NOXV-associated disorders, e.g.
XX osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
XX asthma, or infections.
PS Claim 1; SEQ ID NO 12; 282pp; English.

XX
CC This invention relates to a novel nucleic acid, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOXV proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The polypeptides, nucleic acid molecules and antibodies are useful in the
CC manufacture of a medicament for treating metabolic disorders, diabetes,
CC anorexia, cancer, cardiovascular, infectious, neurodegenerative, immune
CC and haematopoietic diseases as well as various dyslipidaemias.
CC Accordingly, these molecules have many activities including anorectic,
CC virucide, nootropic, antiinflammatory, neuroprotective, antilipaeimic,
CC anabolic and cardiatic. Furthermore, they are useful in screening assays
CC to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a human NOXV protein of the
CC invention.
XX
XX
SO Sequence 137 AA;

Query Match 100.0%; Score 68; DB 7; Length 137;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEERYKAV 13
|||
105 YEKYLGEERYKAV 117

DB

RESULT 7
AAB84371
ID AAB84371 standard; protein; 328 AA.
XX
AC AAB84371;
XX
DT 22-AUG-2001 (first entry)
XX
DE Amino acid sequence of a human transferrin.
XX
XX Human; transferrin; autoimmune disease; rheumatoid arthritis;
XX hyperproliferative disorder; neoplasm; cardiovascular disorder;
XX cardiac arrest; cerebrovascular disorder; cerebral ischemia;
XX angiogenesis; nervous system disorder; Alzheimer's disease; infection;
KW ocular disorder; corneal infection; wound healing;
KW epithelial cell proliferation; aging; organ transplant.
XX
XX Homo sapiens.
OS
PN WO200146254-A1.
XX
PD 28-JUN-2001.
XX
PF 21-DEC-2000; 2000WO-US034769.
XX
PR 23-DEC-1999; 99US-0171595P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Shi Y, Choi GH;
XX
XX WPI; 2001-381910/40.
DR
DR N-PSDB; AAB84371.
XX
XX
XX Isolated nucleic acid molecule encoding a human transferrin protein is
XX used in preventing, treating or ameliorating a medical condition.
PS Claim 11; Page 286-287; 290pp; English.
XX
XX The present sequence represents human transferrin polypeptide.

CC Transferrin polypeptides and polymucleotides are used to prevent, treat
CC or ameliorate a medical condition in e.g. humans, mice, rabbits, goats,
CC horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or
CC treated include autoimmune diseases e.g. Rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and
CC ocular disorders e.g. corneal infection. The polypeptides can also be
CC used to aid wound healing and epithelial cell proliferation, to prevent
CC skin aging due to sunburn, to maintain organs before transplantation, for
CC supporting cell culture of primary tissues, to regenerate tissues and in
CC chemotaxis. The polypeptides can also be used as a food additive or
CC preservative to increase or decrease storage capabilities

SQ Sequence 328 AA;

Query Match 100.0%; Score 68; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEERYKAV 13
|||||
DB 296 YEKYLGEERYKAV 308

RESULT 8

AAU02980

ID AAU02980 standard; protein; 539 AA.

AC AAU02980;

DT 12-SEP-2001 (first entry)

DE Angiotensin converting enzyme (ACEV) splice variant protein #80.

XX Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW platelet-derived endothelial cell growth factor; cardiovascular disease;
KW cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
KW vasodilative intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW myocardial infarction; coronary arterial thrombosis; renal disease;
KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW nonarctodictic pulmonary granulomatous disease; endothelial abnormality;
KW vascular disorder; asbestosis.

OS Homo sapiens.

PN WO200136632-A2.

PD 25-MAY-2001.

PF 17-NOV-2000; 2000WO-IL000766.

PR 17-NOV-1999; 99IL-00132978.

PR 10-DEC-1999; 99IL-00133455.

PA (COMP-) COMPUGEN LTD.

PI Levine Z, David A, Azar I, Khosravi R, Bernstein U;

DR WPI; 2001-336004/35.

DR N-PSDB; AAS06080.

PT Novel alternative splicing variants e.g. variant of angiotensin
PT converting enzyme (ACEV), useful in identifying candidate compounds
PT capable of binding to the variant and to detect anti-variant antibodies.

PS Claim 4; Fig 80; 519pp; English.

CC The sequence represents an angiotensin converting enzyme splice variant
CC (ACEV) polypeptide. The polypeptides of the invention include variants of

CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
CC inhibitor 1C, cellular tumour antigen P53, and vasodilative intestinal
CC polypeptide receptor 2. The polypeptides and their associated nucleic
CC acids are useful for identification of variant sequences and detection of
CC candidate compounds capable of binding the molecules. The sequences of
CC the invention can be used in the treatment and diagnosis of various
CC disorders including cardiovascular diseases such as arteriosclerosis,
CC myocardial infarction and coronary arterial thrombosis, renal diseases
CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
CC immune disorders such as immune complex nephritis, multiple sclerosis,
CC cancer, sarcoidosis, nonarctodictic pulmonary granulomatous diseases such
CC as asbestosis and vascular pathologies involving an endothelial
CC abnormality such as deep vein thrombosis

SQ Sequence 539 AA;

Query Match 100.0%; Score 68; DB 4; Length 539;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEERYKAV 13
|||||
DB 507 YEKYLGEERYKAV 519

RESULT 9

ABR82321

ID ABR82321 standard; protein; 575 AA.

AC ABR82321;

DT 06-NOV-2003 (first entry)

DE Human metalloprotein (MEPR) polypeptide (Id-7509328CD1).

XX MEPR; metalloprotein; anti-HIV; antiallergic; antiinflammatory; human;
KW antianemic; antiparkinsonian; nootropic; anticonvulsant; cytostatic;
KW antiatherosclerotic; antiaesthetic; immunosuppressive; antichytoid;
KW hepatotropic; dermatological; antidiabetic; nephrotoxic; antigout;
KW thymomastic; neuoprotective; osteopathic; antiarthritic; utropathic;
KW antiparasitic; antihelminthic; antiprosaritic; ophthalmological; virucide;
KW antitumoric; haemostatic; antibacterial; protozoacide; fungicide;
KW gene therapy; transgenic.

OS Homo sapiens.

PN WO200306089-A2.

PD 24-JUL-2003.

PF 14-JAN-2003; 2003WO-US001485.

PR 14-JAN-2002; 2002US-0348769P.

PR 18-JAN-2002; 2002US-0350701P.

PR 19-MAR-2002; 2002US-036059P.

PR 10-MAY-2002; 2002US-0379907P.

PA (INCY-) INCYTE GENOMICS INC.

PI Kable AE, Griffin UB, Gorrad AE, Becha SD, Richardson TW;

DR Emerling BW, Chlen D, Jin P, Chawla NK, Yue H, Khare R, Marquis JP;

DR Tang YT;

DR WPI; 2003-598523/56.

DR N-PSDB; ACP35812.

PT New human metalloproteins and polymucleotides, useful for diagnosing,
PT treating or preventing autoimmune or inflammatory disorders (e.g. AIDS,
PT allergy or anemia), multiple sclerosis, osteoarthritis, cancer or
PT hepatitis.

PS Claim 1; Page 146-148; 153pp; English.

XX The invention relates to novel human metalloproteins (MEPR) and encoding
CC polynucleotides. The human MEPR polypeptides, polynucleotides and
CC modulators are useful for diagnosing, treating or preventing disorders
CC associated with aberrant expression of MEPR, particularly cell
CC proliferative disorders (e.g. arteriosclerosis, atherosclerosis,
CC cirrhosis, hepatitis, paroxysmal nocturnal hemoglobinuria, polycythemia
CC vera, psoriasis, primary thrombocytopenia or cancer), developmental
CC disorders (e.g. renal tubular acidosis, anemia or mental retardation),
CC neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or
CC epilepsy), autoimmune/inflammatory disorders (e.g. AIDS, allergies,
CC asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease,
CC diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout,
CC Graves' disease, Hashimoto's thyroiditis, irritable bowel syndrome,
CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's
CC syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,
CC bacterial, fungal, parasitic, protozoan or helminthic infections. The
CC polynucleotides encoding MEPR are useful for creating transgenic animals
CC to model human disease. Sequences ABR82316-323 represent the human MEPR
CC polypeptides of the invention
XX

SO Sequence 575 AA;

Query Match 100.0%; Score 68; DB 6; Length 575;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYLGEYVAV 13
|||||
Db 543 YEKYLGEYVAV 555

RESULT 10

ABM83782
ID ABM83782 standard; protein; 609 AA.

XX ABM83782;

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic pprotein SEQ ID NO:4031.

KW gene therapy; human diagnostic and therapeutic polynucleotide; dtbp.

OS Homo sapiens.

XX WO2004023973-A2.

XX 25-MAR-2004.

PF 12-SEP-2003; 2003WO-US028227.

XX 12-SEP-2002; 2002US-0410259P.

PR 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthorn TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstlin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spito PA, Stewart EA, Wingrove J, Vilt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Pacury S, Shi X, Suarez CJ;

XX WPI; 2004-329368/30.
DR N-PSDB; ACN42434.

PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

XX Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dtbp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dtbp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dtbp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX

SO Sequence 609 AA;

Query Match 100.0%; Score 68; DB 8; Length 609;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYLGEYVAV 13
|||||
Db 577 YEKYLGEYVAV 589

RESULT 11

ABM83781
ID ABM83781 standard; protein; 627 AA.

XX ABM83781;

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic pprotein SEQ ID NO:4030.

KW gene therapy; human diagnostic and therapeutic polynucleotide; dtbp.

OS Homo sapiens.

XX WO2004023973-A2.

XX 25-MAR-2004.

PF 12-SEP-2003; 2003WO-US028227.

XX 12-SEP-2002; 2002US-0410259P.

PR 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthorn TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstlin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spito PA, Stewart EA, Wingrove J, Vilt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Pacury S, Shi X, Suarez CJ;

XX WPI; 2004-329368/30.
DR N-PSDB; ACN42433.

PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

PS Claim 27, Page: 190pp; English.

XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dthp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dthp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX
SQ Sequence 627 AA;

Query Match 100.0%; Score 68; DB 8; Length 627;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEERYKAV 13
|||
DB 595 YEKYLGEERYKAV 607

RESULT 12
ABM83779
ID ABM83779 standard; protein; 628 AA.

AC ABM83779;
XX
DT 18-NOV-2004 (first entry)

XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4028.

XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dthp.

XX
OS Homo sapiens.

XX
PN WO2004023973-A2.

XX
PD 25-MAR-2004.

XX
PF 12-SEP-2003; 2003WO-US028227.

XX
PR 12-SEP-2002; 2002US-0410259P.

XX
PR 12-SEP-2002; 2002US-0410260P.

XX
PA (INCY-) INCYTE CORP.

XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
PI Hartschorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV,
PI Mooney EM, Dejeane AM, Panesar IS, Banville SC, Reddy TP,
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH,
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kilton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patuty S, Shi X, Suarez CJ;

XX
DR MPI; 2004-329368/30.

XX
DR N-PSDB; ACN42431.

XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

XX
PS Claim 27, Page: 190pp; English.

XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dthp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dthp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX
SQ Sequence 628 AA;

Query Match 100.0%; Score 68; DB 8; Length 628;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEERYKAV 13
|||
DB 596 YEKYLGEERYKAV 608

RESULT 13
ABM83778
ID ABM83778 standard; protein; 643 AA.

AC ABM83778;
XX
DT 18-NOV-2004 (first entry)

XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4027.

XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dthp.

XX
OS Homo sapiens.

XX
PN WO2004023973-A2.

XX
PD 25-MAR-2004.

XX
PF 12-SEP-2003; 2003WO-US028227.

XX
PR 12-SEP-2002; 2002US-0410259P.

XX
PR 12-SEP-2002; 2002US-0410260P.

XX
PA (INCY-) INCYTE CORP.

XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
PI Hartschorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV,
PI Mooney EM, Dejeane AM, Panesar IS, Banville SC, Reddy TP,
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH,
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kilton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patuty S, Shi X, Suarez CJ;

XX
DR MPI; 2004-329368/30.

XX
DR N-PSDB; ACN42430.

XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

XX
PS Claim 27, Page: 190pp; English.

CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorder, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
CC
SQ Sequence 643 AA;
Query Match 100.0%; Score 68; DB 8; Length 643;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 YEKYLGEERYKAV 13
|||
Db 611 YEKYLGEERYKAV 623
RESULT 14
ABM83783
ID ABM83783 standard; protein; 645 AA.
XX
XX ABM83783;
AC
XX 18-NOV-2004 (first entry)
DT
XX Human diagnostic and therapeutic protein SEQ ID NO:4032.
DE
XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
KW
XX Homo sapiens.
OS
XX WO2004023973-A2.
PN
XX 25-MAR-2004.
PD
XX 12-SEP-2003; 2003WO-US028227.
PE
XX 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
XX (INCY-) INCYTE CORP.
PA
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
PI Hartsbome TA, Suchotelski MT, Alcus CM, Plets SJ, Elder LV,
PI Mooney EM, Deleagane AM, Panesar IS, Banville SC, Reddy TP,
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH,
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LU,
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kitron ES,
PI Xu Y, Kwong M, Politsky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,
PI Patucy S, Shi X, Suarez CJ;
PI
XX
XX WPI; 2004-329368/30.
DR N-PSDB; ACN42435.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
XX Claim 27; Page; 190pp; English.
PS
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC

CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorder, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
CC
SQ Sequence 645 AA;
Query Match 100.0%; Score 68; DB 8; Length 645;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 YEKYLGEERYKAV 13
|||
Db 613 YEKYLGEERYKAV 625
RESULT 15
AAU02938
ID AAU02938 standard; protein; 646 AA.
XX
XX AAU02938;
AC
XX 12-SEP-2001 (first entry)
DT
XX Angiotensin converting enzyme (ACEV) splice variant protein #38.
DE
XX
XX Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW platelet-derived endothelial cell growth factor; cardiovascular disease;
KW cellular tumour antigen p53; cyclin-dependent kinase inhibitor 1C;
KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW myocardial infarction; coronary arterial thrombosis; renal disease;
KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW nonaroidotic pulmonary granulomatous disease; endothelial abnormality;
KW vascular disorder; atherosclerosis.
KW
XX Homo sapiens.
OS
XX WO200136632-A2.
PN
XX 25-MAY-2001.
PD
XX 17-NOV-2000; 2000WO-IL000766.
PE
XX 17-NOV-1999; 99IL-00132978.
PR 10-DEC-1999; 99IL-00133455.
XX
XX (COMP-) COMPUGEN LTD.
PA
XX Levine Z, David A, Azar I, Khosravi R, Bernstein J;
PI
XX WPI; 2001-336004/35.
DR N-PSDB; AAS06038.
XX
XX Novel alternative splicing variants e.g. variant of angiotensin
PT converting enzyme (ACEV), useful in identifying candidate compounds
PT capable of binding to the variant and to detect anti-variant antibodies.
XX
XX Claim 4; Fig 38; 519pp; English.
PS
XX The sequence represents an angiotensin converting enzyme splice variant
CC

CC (ACEV) polypeptide. The polypeptides of the invention include variants of
CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
CC inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal
CC polypeptide receptor 2. The polypeptides and their associated nucleic
CC acids are useful for identification of variant sequences and detection of
CC candidate compounds capable of binding the molecules. The sequences of
CC the invention can be used in the treatment and diagnosis of various
CC disorders including cardiovascular diseases such as arteriosclerosis,
CC myocardial infarction and coronary arterial thrombosis, renal diseases
CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
CC immune disorders such as immune complex nephritis, multiple sclerosis,
CC cancer, sarcoidosis, nonrheumatic pulmonary granulomatous diseases such
CC as asbestosis and vascular pathologies involving an endothelial
CC abnormality such as deep vein thrombosis
XX

SQ Sequence 646 AA;

Query Match 100.0%; Score 68; DB 4; Length 646;

Best Local Similarity 100.0%; Pred. No. 0.021; Mismatches 0; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEKYLGEYVKAV 13

Db 614 YEKYLGEYVKAV 626

Search completed: November 1, 2005, 12:48:53
Job time : 74.3676 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:37:09 ; Search time 19.1176 Seconds
(without alignments)
50.761 Million cell updates/sec

Title: US-10-612-162A-4

Perfect score: 68

Sequence: 1 YEKYLGEYVKAV 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	100.0	696	5262177-4	Patent No. 5262177
2	68	100.0	696	5262177-4	Sequence No. 5262177
3	68	100.0	698	US-08-175-158A-2	Sequence 2, Appl1
4	68	100.0	698	US-09-439-740-2	Sequence 2, Appl1
5	68	100.0	1074	US-08-470-058-2	Sequence 2, Appl1
6	68	100.0	1074	US-09-037-188-2	Sequence 2, Appl1
7	68	100.0	1074	US-09-285-310-2	Sequence 2, Appl1
8	68	100.0	1410	US-08-470-058-4	Sequence 4, Appl1
9	68	100.0	1410	US-09-037-188-4	Sequence 4, Appl1
10	68	100.0	1410	US-09-285-310-4	Sequence 4, Appl1
11	56	82.4	703	US-08-145-681-6	Sequence 6, Appl1
12	56	82.4	703	US-08-453-703-6	Sequence 6, Appl1
13	56	82.4	703	US-08-456-106-6	Sequence 6, Appl1
14	56	82.4	703	US-08-456-108-6	Sequence 6, Appl1
15	56	82.4	703	US-09-265-577-6	Sequence 6, Appl1
16	56	82.4	703	US-09-265-577-6	Sequence 6, Appl1
17	51	75.0	708	US-08-633-733-6	Sequence 4, Appl1
18	51	75.0	708	US-08-145-681-4	Sequence 4, Appl1
19	51	75.0	708	US-08-453-703-4	Sequence 4, Appl1
20	51	75.0	708	US-08-456-106-4	Sequence 4, Appl1
21	51	75.0	708	US-08-456-108-4	Sequence 4, Appl1
22	51	75.0	708	US-09-265-577-4	Sequence 4, Appl1
23	51	75.0	708	US-09-265-577-4	Sequence 4, Appl1
24	48	70.6	694	US-08-724-586-2	Sequence 2, Appl1
25	48	70.6	694	US-09-421-632-2	Sequence 2, Appl1
26	48	70.6	694	US-09-932-190-2	Sequence 2, Appl1
27	48	70.6	705	US-08-655-640-2	Sequence 2, Appl1
	48	70.6	708	US-08-655-640-4	Sequence 4, Appl1

28	48	70.6	709	1	US-08-154-019-2	Sequence 2, Appl1
29	48	70.6	709	1	US-08-461-333-2	Sequence 2, Appl1
30	48	70.6	709	3	US-08-464-167-2	Sequence 2, Appl1
31	48	70.6	709	3	US-09-158-313-2	Sequence 2, Appl1
32	48	70.6	709	3	US-08-476-798-2	Sequence 2, Appl1
33	48	70.6	711	1	US-08-145-681-2	Sequence 2, Appl1
34	48	70.6	711	1	US-08-250-308-2	Sequence 2, Appl1
35	48	70.6	711	1	US-08-154-019-4	Sequence 4, Appl1
36	48	70.6	711	1	US-08-461-333-4	Sequence 4, Appl1
37	48	70.6	711	1	US-08-453-703-2	Sequence 2, Appl1
38	48	70.6	711	2	US-08-456-106-2	Sequence 2, Appl1
39	48	70.6	711	2	US-08-464-167-4	Sequence 4, Appl1
40	48	70.6	711	3	US-09-158-313-4	Sequence 4, Appl1
41	48	70.6	711	3	US-08-456-108-2	Sequence 2, Appl1
42	48	70.6	711	3	US-08-476-798-4	Sequence 2, Appl1
43	48	70.6	711	3	US-09-265-577-2	Sequence 2, Appl1
44	48	70.6	711	4	US-09-633-733-2	Sequence 2, Appl1
45	48	70.6	711	5	PCT-US93-03614-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
5262177-4
Patent No. 5262177
APPLICANT: BROWN, J. JOSEPH P.; ESTIN, CHARLES D.; PLOWMAN, GREGORY
D.; HELSTROM, KARL E.; ROSE, TIMOTHY M.; HELSTROM, INEGERD;
PURCHIO, ANTHONY F.; HU, SHU-LOK; PENNATHUR, SRIDHAR
TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HHUMAN
MELANOMA-ASSOCIATED ANTIGEN
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/7230
FILING DATE: 27-JAN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 827,313
FILING DATE: 07-FEB-1986
SEQ ID NO:4:
LENGTH: 696
5262177-4

Query Match 100.0%; Score 68; DB 6; Length 696;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
DB 664 YEKYLGEYVKAV 676

RESULT 2
5262177-4
Patent No. 5262177
APPLICANT: BROWN, J. JOSEPH P.; ESTIN, CHARLES D.; PLOWMAN, GREGORY
D.; HELSTROM, KARL E.; ROSE, TIMOTHY M.; HELSTROM, INEGERD;
PURCHIO, ANTHONY F.; HU, SHU-LOK; PENNATHUR, SRIDHAR
TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HHUMAN
MELANOMA-ASSOCIATED ANTIGEN
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/7230
FILING DATE: 27-JAN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 827,313
FILING DATE: 07-FEB-1986
SEQ ID NO:4:
LENGTH: 696
5262177-4

Query Match 100.0%; Score 68; DB 6; Length 696;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYLGEEYKAV 13
Db 664 YEKYLGEEYKAV 676

RESULT 3
US-08-175-158A-2

; Sequence 2, Application US/08175158A
; Patent No. 5386067
; GENERAL INFORMATION:
; APPLICANT: FUNK, Walter D.
; APPLICANT: MacGILLIVRAY, Rose T.A.
; APPLICANT: MASON, Anne B.
; APPLICANT: WOODWORTH, Robert C.
; TITLE OF INVENTION: RECOMBINANT TRANSFERRINS, TRANSFERRIN HALF-
; TITLE OF INVENTION: MOLECULES AND MUTANTS THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/175,158A
; FILING DATE: 26-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/832,029
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: UVI-005CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 698 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-175-158A-2

Query Match 100.0%; Score 68; DB 2; Length 698;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYLGEEYKAV 13
Db 666 YEKYLGEEYKAV 678

RESULT 4
US-09-439-740-2
; Sequence 2, Application US/09439740
; Patent No. 6825037
; GENERAL INFORMATION:
; APPLICANT: FUNK, Walter D.
; APPLICANT: MacGILLIVRAY, Rose T.A.
; APPLICANT: MASON, Anne B.
; APPLICANT: WOODWORTH, Robert C.
; TITLE OF INVENTION: RECOMBINANT TRANSFERRINS, TRANSFERRIN HALF-
; TITLE OF INVENTION: MOLECULES AND MUTANTS THEREOF
; NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/439,740
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/175,158
; FILING DATE:

ATTORNEY/AGENT INFORMATION:

; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: UVI-005CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 698 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-439-740-2

Query Match 100.0%; Score 68; DB 4; Length 698;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYLGEEYKAV 13
Db 666 YEKYLGEEYKAV 678

RESULT 5

US-08-470-058-2

; Sequence 2, Application US/08470058
; Patent No. 5817789
; GENERAL INFORMATION:
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Lemont, Jeffrey F.
; TITLE OF INVENTION: Chimeric Proteins For Use in Transport
; TITLE OF INVENTION: of a Selected Substance Into Cells
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,058
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: TKT93-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
STRADEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-058-2

Query Match 100.0%; Score 68; DB 2; Length 1074;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVAV 13
1042 YEKYLGEYVAV 1054

RESULT 6
US-09-037-188-2
Sequence 2, Application US/09037188
Patent No. 6027921
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,188
FILING DATE: 02-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34, 819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-037-188-2

Query Match 100.0%; Score 68; DB 3; Length 1074;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEKYLGEYVAV 13
1042 YEKYLGEYVAV 1054

DB 1042 YEKYLGEYVAV 1054

RESULT 7
US-09-285-310-2
Sequence 2, Application US/09285310
Patent No. 6262026
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,310
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/037,188
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34, 819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-285-310-2

Query Match 100.0%; Score 68; DB 3; Length 1074;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVAV 13
1042 YEKYLGEYVAV 1054

RESULT 8
US-08-470-058-4
Sequence 4, Application US/08470058
Patent No. 5817789
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
TITLE OF INVENTION: Chimeric Proteins For Use in Transport
TITLE OF INVENTION: of a Selected Substance into Cells
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA

ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TKT93-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-058-4

Query Match 100.0%; Score 68; DB 2; Length 1410;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEKYLGESEYKAV 13
|||
Db 1378 YEKYLGESEYKAV 1390

RESULT 9
US-09-037-188-4
Sequence 4, Application US/09037188
Patent No. 6027921
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,188
FILING DATE: 02-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Frazer, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-037-188-4

Query Match 100.0%; Score 68; DB 3; Length 1410;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEKYLGESEYKAV 13
|||
Db 1378 YEKYLGESEYKAV 1390

RESULT 10
US-09-285-310-4
Sequence 4, Application US/09285310
Patent No. 6262026
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,310
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/037,188
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Frazer, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-285-310-4

Query Match 100.0%; Score 68; DB 3; Length 1410;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEKYLGESEYKAV 13
|||
Db 1378 YEKYLGESEYKAV 1390

RESULT 11
US-08-145-681-6
Sequence 6, Application US/08145681

```
/ Patent No. 5571691
/ GENERAL INFORMATION:
/ APPLICANT: Conneely, Orla M.
/ APPLICANT: Heaton, Denis R.
/ APPLICANT: O'Malley, Bert W.
/ APPLICANT: May, Gregory S.
/ TITLE OF INVENTION: Production of Recombinant Lactoferrin
/ TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
/ TITLE OF INVENTION: Various Organisms
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Baker & Botts, L.L.P.
/ STREET: 910 Louisiana St
/ CITY: Houston
/ STATE: Texas
/ COUNTRY: USA
/ ZIP: 77002
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/145,681
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mcgregor, Martin L.
/ REGISTRATION NUMBER: 29,329
/ REFERENCE/DOCKET NUMBER: 19928-0125
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 713/229/1874
/ TELEFAX: 713/229/1522
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 703 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHEICAL: YES
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Sus scrofa
/ US-08-145-681-6

Query Match      82.4%; Score 56; DB 1; Length 703;
Best Local Similarity 76.9%; Pred. No. 0.13;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 YEKYLGEYVKAV 13
Db      671 YEKYLGEYVKAV 683

RESULT 12
US-08-453-703-6
/ Sequence 6, Application US/08453703
/ Patent No. 576939
/ GENERAL INFORMATION:
/ APPLICANT: Conneely, Orla M.
/ APPLICANT: Heaton, Denis R.
/ APPLICANT: O'Malley, Bert W.
/ APPLICANT: May, Gregory S.
/ TITLE OF INVENTION: Production of Recombinant Lactoferrin
/ TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
/ TITLE OF INVENTION: Various Organisms
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Penile & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
```

```
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/453,703
/ FILING DATE: Concurrently herewith
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/145,681
/ FILING DATE: October 28, 1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Albert P. Halluin
/ REGISTRATION NUMBER: 25,227
/ REFERENCE/DOCKET NUMBER: 8206-024
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-854-3660
/ TELEFAX: 415-854-3694
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 703 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHEICAL: YES
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Sus scrofa
/ US-08-453-703-6

Query Match      82.4%; Score 56; DB 1; Length 703;
Best Local Similarity 76.9%; Pred. No. 0.13;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 YEKYLGEYVKAV 13
Db      671 YEKYLGEYVKAV 683

RESULT 13
US-08-456-106-6
/ Sequence 6, Application US/08456106
/ Patent No. 5849881
/ GENERAL INFORMATION:
/ APPLICANT: Conneely, Orla M.
/ APPLICANT: Heaton, Denis R.
/ APPLICANT: O'Malley, Bert W.
/ APPLICANT: May, Gregory S.
/ TITLE OF INVENTION: Production of Recombinant Lactoferrin
/ TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
/ TITLE OF INVENTION: Various Organisms
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Penile & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/456,106
/ FILING DATE: Concurrently herewith
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/145,681
/ FILING DATE: October 28, 1993
```

ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8206-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 703 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Sus scrofa
US-08-456-106-6

Query Match 82.4%; Score 56; DB 2; Length 703;
Best Local Similarity 76.9%; Pred. No. 0.13;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YEKYLGEYVYKAV 13
|||||
Db 671 YEKYLGEYVYTAI 683

RESULT 14
US-08-456-108-6
Sequence 6, Application US/08456108
Patent No. 6100054
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Headon, Denis R.
APPLICANT: O'Malley, Bert W.
APPLICANT: May, Gregory S.
TITLE OF INVENTION: Production of Recombinant Lactoferrin
TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
TITLE OF INVENTION: Various Organisms
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,108
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/145,681
FILING DATE: October 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8206-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 703 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Sus scrofa
US-08-456-108-6

Query Match 82.4%; Score 56; DB 3; Length 703;
Best Local Similarity 76.9%; Pred. No. 0.13;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YEKYLGEYVYKAV 13
|||||
Db 671 YEKYLGEYVYTAI 683

RESULT 15
US-09-265-577-6
Sequence 6, Application US/09265577
Patent No. 6228614
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Headon, Denis R.
APPLICANT: O'Malley, Bert W.
APPLICANT: May, Gregory S.
TITLE OF INVENTION: PRODUCTION OF RECOMBINANT LACTOFERRIN
TITLE OF INVENTION: AND LACTOFERRIN POLYPEPTIDES USING cDNA SEQUENCES IN VARIOUS
TITLE OF INVENTION: ORGANISMS
FILE REFERENCE: 01380023US01
CURRENT APPLICATION NUMBER: US/09/265,577
CURRENT FILING DATE: 1999-03-09
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 703
TYPE: PRT
ORGANISM: Sus scrofa
US-09-265-577-6

Query Match 82.4%; Score 56; DB 3; Length 703;
Best Local Similarity 76.9%; Pred. No. 0.13;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YEKYLGEYVYKAV 13
|||||
Db 671 YEKYLGEYVYTAI 683

Search completed: November 1, 2005, 12:57:31
Job time: 19.1176 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:54:52 ; Search time 65.7647 Seconds
(without alignments)
82.636 Million cell updates/sec

Title: US-10-612-162A-4
Perfect score: 68
Sequence: 1 YEKYLGEERYKAV 13

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1865214 seqs, 418043040 residues
Total number of hits satisfying chosen parameters: 1865214

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubppaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubppaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubppaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*
- 22: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	13	US-10-612-162-4	Sequence 4, Appli
2	68	100.0	49	US-10-378-094-16	Sequence 16, Appli
3	68	100.0	49	US-10-384-060-38	Sequence 38, Appli
4	68	100.0	49	US-10-231-494-27	Sequence 27, Appli
5	68	100.0	137	US-10-383-201-12	Sequence 12, Appli
6	68	100.0	328	US-09-891-126-5	Sequence 5, Appli
7	68	100.0	328	US-10-266-745-5	Sequence 5, Appli
8	68	100.0	679	US-10-378-094-3	Sequence 3, Appli
9	68	100.0	679	US-10-384-060-3	Sequence 3, Appli
10	68	100.0	679	US-10-231-494-3	Sequence 3, Appli
11	68	100.0	679	US-10-429-482-4	Sequence 4, Appli

12	68	100.0	679	16	US-10-429-497-4	Sequence 4, Appli
13	68	100.0	679	16	US-10-429-515-4	Sequence 4, Appli
14	68	100.0	679	16	US-10-429-598-4	Sequence 4, Appli
15	68	100.0	679	16	US-10-429-635-4	Sequence 4, Appli
16	68	100.0	679	16	US-10-429-653-4	Sequence 4, Appli
17	68	100.0	679	16	US-10-429-659-4	Sequence 4, Appli
18	68	100.0	679	16	US-10-429-661-4	Sequence 4, Appli
19	68	100.0	679	16	US-10-429-660-4	Sequence 4, Appli
20	68	100.0	679	16	US-10-429-662-4	Sequence 4, Appli
21	68	100.0	679	16	US-10-429-655-4	Sequence 4, Appli
22	68	100.0	679	16	US-10-429-654-4	Sequence 4, Appli
23	68	100.0	698	10	US-09-935-642-6	Sequence 2, Appli
24	68	100.0	698	15	US-10-378-094-2	Sequence 2, Appli
25	68	100.0	698	15	US-10-384-060-2	Sequence 2, Appli
26	68	100.0	698	15	US-10-231-494-2	Sequence 2, Appli
27	68	100.0	698	15	US-10-383-201-10	Sequence 10, Appli
28	68	100.0	698	15	US-10-383-201-14	Sequence 14, Appli
29	68	100.0	698	17	US-10-887-711-2	Sequence 2, Appli
30	68	100.0	698	18	US-10-513-523-3	Sequence 3, Appli
31	68	100.0	1074	9	US-09-753-385-2	Sequence 2, Appli
32	68	100.0	1410	9	US-09-753-385-4	Sequence 4, Appli
33	68	100.0	1410	16	US-10-473-127-805	Sequence 805, App
34	68	100.0	1418	16	US-10-473-127-804	Sequence 804, App
35	56	82.4	15	16	US-10-769-514-14	Sequence 14, Appli
36	56	82.4	15	16	US-10-769-514-17	Sequence 47, Appli
37	56	82.4	703	17	US-10-620-256-6	Sequence 6, Appli
38	51	75.0	698	14	US-10-316-253-273	Sequence 273, App
39	51	75.0	698	14	US-10-316-253-275	Sequence 275, App
40	51	75.0	698	15	US-10-205-331-55	Sequence 35, Appli
41	51	75.0	708	14	US-10-169-297-8	Sequence 8, Appli
42	51	75.0	708	17	US-10-620-256-4	Sequence 4, Appli
43	51	75.0	708	18	US-10-513-523-2	Sequence 2, Appli
44	48	70.6	99	17	US-10-487-556-116	Sequence 116, App
45	48	70.6	323	9	US-09-891-126-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-612-162-4
; Sequence 4, Application US/10612162
; Publication No. US20040014145A1
; GENERAL INFORMATION:
; APPLICANT: Dade Behring Marburg GmbH
; TITLE OF INVENTION: Carboxydextran deficient transferrin (CDT)-specific
; FILE REFERENCE: 2002/B001
; CURRENT APPLICATION NUMBER: US/10/612,162
; PRIOR FILING DATE: 2003-07-03
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 03011334.4
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-162-4

Query Match 100.0%; Score 68; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEERYKAV 13
| | | | | | | | | | | | |
Db 1 YEKYLGEERYKAV 13

RESULT 2
US-10-378-094-16

```
/ Sequence 16, Application US/10378094
/ Publication No. US20030221201a1
/ GENERAL INFORMATION:
/ APPLICANT: PRIOR, Christopher P.
/ APPLICANT: LAI, Chai-Huei
/ APPLICANT: SADEGH, Homayoun
/ APPLICANT: TURNER, Andrew
/ TITLE OF INVENTION: MODIFIED TRANSFERRIN FUSION PROTEINS
/ FILE REFERENCE: 54710-5001-01-US
/ CURRENT APPLICATION NUMBER: US/10/378,094
/ CURRENT FILING DATE: 2003-03-04
/ PRIOR APPLICATION NUMBER: US 10/231,494
/ PRIOR FILING DATE: 2002-08-30
/ PRIOR APPLICATION NUMBER: US 60/334,059
/ PRIOR FILING DATE: 2001-11-30
/ PRIOR APPLICATION NUMBER: US 60/315,745
/ PRIOR FILING DATE: 2001-08-30
/ NUMBER OF SEQ ID NOS: 66
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 16
/ LENGTH: 49
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc.feature
/ OTHER INFORMATION: C2 subdomain of transferrin
US-10-378-094-16
```

```
Query Match      100.0%; Score 68; DB 15; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 YEKYLGEERYKAV 13
        |||||||
Db      37 YEKYLGEERYKAV 49
```

```
RESULT 3
US-10-384-060-38
/ Sequence 38, Application US/10384060
/ Publication No. US20030226155a1
/ GENERAL INFORMATION:
/ APPLICANT: SADEGH, Homayoun
/ APPLICANT: PRIOR, Christopher P.
/ APPLICANT: TURNER, Andrew
/ TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
/ FILE REFERENCE: 54710-5004-US
/ CURRENT APPLICATION NUMBER: US/10/384,060
/ CURRENT FILING DATE: 2003-03-10
/ PRIOR APPLICATION NUMBER: US 10/231,494
/ PRIOR FILING DATE: 2002-08-30
/ PRIOR APPLICATION NUMBER: US 60/334,059
/ PRIOR FILING DATE: 2001-11-30
/ PRIOR APPLICATION NUMBER: US 60/315,745
/ PRIOR FILING DATE: 2001-08-30
/ PRIOR APPLICATION NUMBER: US 60/406,977
/ PRIOR FILING DATE: 2002-08-30
/ NUMBER OF SEQ ID NOS: 80
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 38
/ LENGTH: 49
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: C2 domain of huma Tf
US-10-384-060-38
```

```
Query Match      100.0%; Score 68; DB 15; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 YEKYLGEERYKAV 13
        |||||||
```

```
Db      37 YEKYLGEERYKAV 49
```

```
RESULT 4
US-10-231-494-27
/ Sequence 27, Application US/10231494
/ Publication No. US20040023334a1
/ GENERAL INFORMATION:
/ APPLICANT: Prior, Christopher P.
/ TITLE OF INVENTION: Modified Transferrin Fusion Proteins
/ FILE REFERENCE: 54710-5001-US
/ CURRENT APPLICATION NUMBER: US/10/231,494
/ CURRENT FILING DATE: 2002-08-30
/ PRIOR APPLICATION NUMBER: US 60/315,745
/ PRIOR FILING DATE: 2001-08-30
/ PRIOR APPLICATION NUMBER: US 60/334,059
/ PRIOR FILING DATE: 2001-11-30
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 27
/ LENGTH: 49
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Transferrin
US-10-231-494-27
```

```
Query Match      100.0%; Score 68; DB 15; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 YEKYLGEERYKAV 13
        |||||||
Db      37 YEKYLGEERYKAV 49
```

```
RESULT 5
US-10-383-201-12
/ Sequence 12, Application US/10383201
/ Publication No. US20040029226a1
/ GENERAL INFORMATION:
/ APPLICANT: Alsobrook II, John et al.
/ TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
/ FILE REFERENCE: 21402-568A
/ CURRENT APPLICATION NUMBER: US/10/383,201
/ CURRENT FILING DATE: 2003-03-06
/ PRIOR APPLICATION NUMBER: 10/029020
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 60/365,984
/ PRIOR FILING DATE: 2002-03-20
/ PRIOR APPLICATION NUMBER: 60/372,022
/ PRIOR FILING DATE: 2002-04-12
/ PRIOR APPLICATION NUMBER: 60/389,143
/ PRIOR FILING DATE: 2002-06-14
/ PRIOR APPLICATION NUMBER: 60/391,779
/ PRIOR FILING DATE: 2002-06-26
/ PRIOR APPLICATION NUMBER: 60/410,755
/ PRIOR FILING DATE: 2002-09-13
/ PRIOR APPLICATION NUMBER: 60/412,957
/ PRIOR FILING DATE: 2002-09-23
/ PRIOR APPLICATION NUMBER: 10/051,874
/ PRIOR FILING DATE: 2002-01-16
/ PRIOR APPLICATION NUMBER: 60/366,928
/ PRIOR FILING DATE: 2002-03-22
/ PRIOR APPLICATION NUMBER: 10/055,877
/ PRIOR FILING DATE: 2002-01-22
/ NUMBER OF SEQ ID NOS: 155
/ SOFTWARE: CuraseqList version 0.1
/ SEQ ID NO 12
/ LENGTH: 137
/ TYPE: PRT
/ ORGANISM: Homo sapiens
```


US-10-383-201-12

Query Match 100.0%; Score 68; DB 15; Length 137;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEERYKAV 13
|||||
DB 105 YEKYLGEERYKAV 117

RESULT 6
US-09-891-126-5

; Sequence 5, Application US/09891126
; Patent No. US20020072596A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Transferrin Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT035PI
; CURRENT APPLICATION NUMBER: US/09/891,126
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: PCT/US00/34769
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/171,595
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-126-5

Query Match 100.0%; Score 68; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEERYKAV 13
|||||
DB 296 YEKYLGEERYKAV 308

RESULT 7

US-10-266-745-5
; Sequence 5, Application US/10266745
; Publication No. US20030149256A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Transferrin Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT035PI
; CURRENT APPLICATION NUMBER: US/10/266,745
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/891,126
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: PCT/US00/34769
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/171,595
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-266-745-5

Query Match 100.0%; Score 68; DB 14; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEERYKAV 13
|||||
DB 296 YEKYLGEERYKAV 308

RESULT 8
US-10-378-094-3

; Sequence 3, Application US/10378094
; Publication No. US20030221201A1
; GENERAL INFORMATION:
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: LAI, Char-Huei
; APPLICANT: SADEGH, Homayoun
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN FUSION PROTEINS
; FILE REFERENCE: 54710-5001-01-US
; CURRENT APPLICATION NUMBER: US/10/378,094
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: MISC FEATURE
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Mature Transferrin Protein
US-10-378-094-3

Query Match 100.0%; Score 68; DB 15; Length 679;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEERYKAV 13
|||||
DB 647 YEKYLGEERYKAV 659

RESULT 9

US-10-384-060-3
; Sequence 3, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGH, Homayoun
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: MISC FEATURE
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Mature Transferrin Protein
US-10-384-060-3

Query Match 100.0%; Score 68; DB 15; Length 679;

Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 YEKYLGEYVAV 13
Db 647 YEKYLGEYVAV 659

RESULT 10
US-10-231-494-3
; Sequence 3, Application US/10231494
; Publication No. US2004002334A1
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
; FILE REFERENCE: 54710-5001-US
; CURRENT APPLICATION NUMBER: US/10/231,494
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Mature transferrin protein
US-10-231-494-3

Query Match 100.0%; Score 68; DB 15; Length 679;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYLGEYVAV 13
Db 647 YEKYLGEYVAV 659

RESULT 11
US-10-429-482-4
; Sequence 4, Application US/10429482
; Publication No. US20040219097A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For The Diagnosis, Imaging and Treatment Of T
; FILE REFERENCE: 2537.000001
; CURRENT APPLICATION NUMBER: US/10/429,482
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-482-4

Query Match 100.0%; Score 68; DB 16; Length 679;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYLGEYVAV 13
Db 647 YEKYLGEYVAV 659

RESULT 12
US-10-429-497-4
; Sequence 4, Application US/10429497
; Publication No. US20040219098A1
; GENERAL INFORMATION:

; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For The Treatment of Tumors
; FILE REFERENCE: 2537.000006
; CURRENT APPLICATION NUMBER: US/10/429,497
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-497-4

Query Match 100.0%; Score 68; DB 16; Length 679;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYLGEYVAV 13
Db 647 YEKYLGEYVAV 659

RESULT 13
US-10-429-515-4
; Sequence 4, Application US/10429515
; Publication No. US20040219099A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For The Treatment Of Tumors
; FILE REFERENCE: 2537.000005
; CURRENT APPLICATION NUMBER: US/10/429,515
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-515-4

Query Match 100.0%; Score 68; DB 16; Length 679;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYLGEYVAV 13
Db 647 YEKYLGEYVAV 659

RESULT 14
US-10-429-598-4
; Sequence 4, Application US/10429598
; Publication No. US20040219100A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For The Treatment of Tumors
; FILE REFERENCE: 2537.000003
; CURRENT APPLICATION NUMBER: US/10/429,598
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-598-4

Query Match 100.0%; Score 68; DB 16; Length 679;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYLGEYVAV 13
Db 647 YEKYLGEYVAV 659

Db 647 YEKYLGEERYVKAV 659

RESULT 15
US-10-429-635-4
; Sequence 4, Application US/10429635
; Publication No. US20040219101A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For Treatment Of Tumors
; FILE REFERENCE: 2537.000007
; CURRENT APPLICATION NUMBER: US/10/429,635
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-635-4

Query Match 100.0%; Score 68; DB 16; Length 679;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEERYVKAV 13
Db 647 YEKYLGEERYVKAV 659

Search completed: November 1, 2005, 13:26:07
Job time : 65.7647 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:35:39 ; Search time 13.1912 Seconds
(without alignments)
94.822 Million cell updates/sec

Title: US-10-612-162A-4

Perfect score: 68

Sequence: 1 YEKILGEBRYKAV 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR79:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	100.0	698	1	TFHUP
2	58	83.3	694	1	TFRBP
3	56	82.4	703	2	A45543
4	55	80.9	708	2	JC2323
5	51	75.0	695	2	S49163
6	51	75.0	704	2	I47228
7	51	75.0	708	1	TFBOL
8	48	70.6	215	2	A60166
9	48	70.6	216	1	A39684
10	48	70.6	711	1	TFHUL
11	47	69.1	696	1	S01384
12	45	66.2	707	1	S33761
13	45	66.2	707	1	A28438
14	44	64.7	305	2	D64326
15	43	63.2	334	2	E75153
16	43	63.2	614	2	B83818
17	43	63.2	692	2	H70362
18	42	61.8	115	2	T50390
19	42	61.8	188	2	D64017
20	41	60.3	408	2	H97236
21	41	60.3	431	2	C86812
22	41	60.3	500	2	E89852
23	41	60.3	711	2	S37025
24	40	58.8	203	2	T39117
25	40	58.8	425	2	A99939
26	40	58.8	466	1	STECNT
27	40	58.8	466	2	AF0616
28	40	58.8	466	2	C85619
29	40	58.8	466	2	E90755

30	40	58.8	467	2	B96829	probable sugar tra
31	40	58.8	518	1	X1YHHA	homoserine O-acety
32	40	58.8	635	2	A42988	dnak-type molecule
33	40	58.8	738	1	TFHUM	melanotransferrin
34	39.5	58.1	328	1	B64478	hypothetical prote
35	39	57.4	311	2	A28446	transferrin - mous
36	39	57.4	334	1	DEOYG	glyceroldehyde-3-P
37	39	57.4	407	2	E70309	hypothetical prote
38	39	57.4	600	2	A49230	dnak-type molecula
39	39	57.4	605	2	I39837	dnak-type molecula
40	39	57.4	607	2	B95060	dnak protein limpo
41	39	57.4	607	2	G97928	hypothetical prote
42	39	57.4	661	2	A69252	3-hydroxycyl-CoA
43	39	57.4	728	2	S59964	procollagen-lysine
44	39	57.4	731	2	D71332	probable DNA copoi
45	39	57.4	883	2	T06848	phycobillosome link

ALIGNMENTS

RESULT 1

TFHUP

transferrin precursor [validated] - human

N.Alternate names: siderophilin

C.Species: Homo sapiens (man)

C.Date: 15-Oct-1982 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C.Accession: A20981; A92417; A94044; A29090; A32739; I51959; I63133; I54011; I68160; A03

R.Yang, F.; Lum, J.B.; McGill, J.R.; Moore, C.M.; Naylor, S.L.; van Bragt, P.H.; Baldwin

Proc. Natl. Acad. Sci. U.S.A. 81, 2752-2756, 1984

A>Title: Human transferrin: cDNA characterization and chromosomal localization.

A.Reference number: A20981; MUID:84194084; PMID:6585826

A.Contents: variant C

A.Accession: A20981

A.Molecule type: mRNA

A.Residues: 1-698 <YAN>

A.Cross-references: UNIPROT:P02787; EMBL:M12530; NID:G339452; PIDN:AAA61140.1; PID:G3394

A>Note: the authors translated the codon CAA for residue 203 as Glu

R.MacGillivray, R.T.A.; Mendez, E.; Shewale, J.G.; Sinha, S.K.; Lineback-Zins, J.; Brew,

J. Biol. Chem. 258, 3543-3553, 1983

A>Title: The primary structure of human serum transferrin. The structures of seven cyano

A.Reference number: A92417; MUID:83160878; PMID:6833213

A.Accession: A92417

A.Molecule type: protein

A.Residues: 20-263, 'E', 265-328, 'N', 330-379, 'SD', 382-435, 'D', 437-557, 'T', 559-560, 'P', 562-

A>Note: the sequence shown is the predominant electrophoretic genetic variant (C or TIC)

R.Park, I.; Schaeffer, E.; Sidoli, A.; Baralle, F.E.; Cohen, G.N.; Zakim, M.M.

Proc. Natl. Acad. Sci. U.S.A. 82, 3149-3153, 1985

A>Title: Organization of the human transferrin gene: direct evidence that it originated

A.Reference number: A94044; MUID:85216459; PMID:3858812

A.Accession: A94044

A.Molecule type: DNA

A.Residues: 73-263, 'E', 265-328, 'N', 330-562 <PAR>

A.Cross-references: EMBL:M1361

R.Adrjan, G.S.; Korinek, B.W.; Bowman, B.H.; Yang, F.

Gene 49, 167-175, 1986

A>Title: The human transferrin gene: 5' region contains conserved sequences which match

A.Reference number: A29090; MUID:87192006; PMID:3106157

A.Accession: A29090

A.Molecule type: DNA

A.Residues: 1-72; 291-300 <ADR>

A.Cross-references: EMBL:M15673

R.Uzan, G.; Frahn, M.; Park, I.; Beaumont, C.; Maessen, G.; Trepac, J.S.; Zakim, M.M.; Kah

Biochem. Biophys. Res. Commun. 119, 273-281, 1984

A>Title: Molecular cloning and sequence analysis of cDNA for human transferrin.

A.Reference number: A32739; MUID:84153910; PMID:6322780

A.Accession: A32739

A.Molecule type: mRNA

A.Residues: 422-690, 'G', 692-698 <UZA>

A.Cross-references: EMBL:M12525; NID:G339468; PIDN:AAA61142.1; PID:G339469

R.MacGillivray, R.T.A.; Mendez, E.; Sinha, S.K.; Sutton, M.R.; Lineback-Zins, J.; Brew, I

Proc. Natl. Acad. Sci. U.S.A. 79, 2504-2508, 1982

A>Title: The complete amino acid sequence of human serum transferrin.
A:Reference number: A93911; MUID:82222166; PMID:6955407
A:Contents: annotation; disulfide bonds
R:Hershenberger, C.L.; Larson, J.U.; Arnold, B.; Rosteck, P.R.
Ann. N. Y. Acad. Sci. 646, 140-154, 1991
A>Title: A cloned gene for human transferrin.
A:Reference number: I51959; MUID:92231399; PMID:1809186
A:Accession: I51959
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-698 <RES>
A:Cross-references: GB:S95936; NID:9248647; PIDN:AA52049.1; PID:9248648
R:Dupuid, J.R.; Bohmont, C.W.; Liu, N.G.; Tourtellicte, W.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 7260-7264, 1989
A>Title: Changes in brain gene expression shared by scrapie and Alzheimer disease.
A:Reference number: I48174; MUID:89386721; PMID:2780570
A:Accession: I63133
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 636-696 <RE2>
A:Cross-references: GB:M26641; NID:9339988; PIDN:AA61233.1; PID:9339989
R:Schaeffer, E.; Lucero, M.A.; Jelech, J.M.; Py, M.C.; Levin, M.J.; Chambon, P.; Cohen, Gene 56, 109-116, 1987
A>Title: Complete structure of the human transferrin gene. Comparison with analogous chi
A:Reference number: I54011; MUID:88056305; PMID:3678832
A:Accession: I54011
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-72 <RE3>
A:Cross-references: GB:M17611; NID:9339480; PIDN:AA61147.1; PID:9339485
A:Accession: I68160
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 564-698 <RE4>
A:Cross-references: GB:M17614; NID:9339483; PIDN:AA61148.1; PID:9339486
C:Comment: Each of the two repetitive domains binds a ferric ion and a bicarbonate anion
C:Genetics:
A:Gene: GDB:TF
A:Cross-references: GDB:120432; OMIM:190000
A:Map position: 3q21-3q21
A:Introns: 15/1; 72/3; 119/1; 168/1; 212/2; 231/1; 290/3; 350/1; 401/3; 433/1; 444/1; 45
C:Function:
A:Description: binds iron for delivery into cells
A:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; glycoprotein; iron transport; metal binding; plasma
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-698/Product: transferrin #status experimental <MAT>
F:20-350/Domain: transferrin repeat homology <TRH1>
F:355-666/Domain: transferrin repeat homology <TRH2>
F:28-67,38-58,137-213,156-350,177-193,180-196,190-198,246-260,358-615,364-396,374-387,42
F:432,630/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 100.0%; Score 68; DB 1; Length 698;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYLGEERYKAV 13
|||||
Db 666 YEKYLGEERYKAV 678

RESULT 2

TFRBP

transferrin precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 22-Jun-1999
C:Accession: S16246; A61239; C61573; S02694; A26504; S14653
R:Banfield, D.R.; Chow, B.K.C.; Funk, W.D.; Robertson, K.A.; Umetas, T.M.; Woodworth, R.
Biochim. Biophys. Acta 1089, 262-265, 1991
A>Title: The nucleotide sequence of rabbit liver transferrin cDNA.
A:Reference number: S16246; MUID:91274362; PMID:2054387
A:Accession: S16246
A:Molecule type: mRNA

A:Residues: 1-694 <BAN>
A:Cross-references: EMBL:X58533; NID:91750; PIDN:CA441424.1; PID:91751
R:Pierpoli, W.; Dall'Ara, A.; Yi, C.; Neri, P.; Santucci, A.; Choay, J.
Cell. Immunol. 134, 225-234, 1991
A>Title: Iron carrier proteins facilitate engraftment of allogeneic bone marrow and endu
A:Reference number: A61239; MUID:91191584; PMID:2013104
A:Accession: A61239
A:Molecule type: protein
A:Residues: 19-36 <PIE>
R:Chung, W.C.M.; Chan, S.L.; Shmizu, S.
Int. J. Biochem. 23, 609-616, 1991
A>Title: Purification of transferrin and lactoferrin using DEAE Affi-Gel Blue.
A:Reference number: A61573; MUID:91293379; PMID:2065820
A:Accession: C61573
A:Molecule type: protein
A:Residues: 19-26, 'X', 28-36, 'X', 38-53 <CHU>
R:Godovac-Zimmermann, J.
Biol. Chem. Hoppe-Seyler 369, 93-96, 1988
A>Title: Isolation, characterization and N-terminal amino-acid sequence of rabbit transf
A:Reference number: S00335; MUID:88209278; PMID:3365331
A:Accession: S00335
A:Molecule type: protein
A:Residues: 19-45, 'S', 47-48, 'Y', 50 <GOD>
R:Evans, R.W.; Altken, A.; Patel, K.J.
FEBS Lett. 238, 39-42, 1988
A>Title: Evidence for a single glycan moiety in rabbit serum transferrin and location of
A:Reference number: S02694; MUID:89005676; PMID:3169252
A:Accession: S02694
A:Molecule type: protein
A:Residues: 482-515, 'V', 517-544 <EVA>
A>Note: 516-ile was also found
R:Heaphy, S.; Williams, J.
Biochem. J. 205, 611-617, 1982
A>Title: The preparation and partial characterization of N-terminal and C-terminal iron-
A:Reference number: A26504; MUID:83074540; PMID:6816218
A:Accession: A26504
A:Molecule type: protein
A:Residues: 19-24, 'N', 26, 'X', 28-29, 'S' <HEA>
A:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; glycoprotein; iron transport; metal binding; plasma
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-694/Product: transferrin #status experimental <MAT>
F:19-349/Domain: transferrin repeat homology <TRH1>
F:355-662/Domain: transferrin repeat homology <TRH2>
F:27-66,37-57,136-212,155-349,176-192,179-195,189-197,245-259,357-611,363-395,373-386,42
F:508/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 85.3%; Score 58; DB 1; Length 694;
Best Local Similarity 76.9%; Pred. No. 0.062;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YEKYLGEERYKAV 13
|||||
Db 662 YEKYLGEERYKAV 674

RESULT 3

A45543

lactoferrin precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 17-Feb-1994 #sequence revision 17-Feb-1994 #text change 09-Jul-2004
C:Accession: A45543; S24173
R:Alexander, L.J.; Levine, W.B.; Teng, C.T.; Beattie, C.W.
Anim. Genet. 23, 251-256, 1992
A>Title: Cloning and sequencing of the porcine lactoferrin cDNA.
A:Reference number: A45543; MUID:92367939; PMID:11503255
A:Accession: A45543
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-703 <ALE>
A:Cross-references: UNIPROT:P14632
A:Experimental source: mammary gland
A>Note: sequence extracted from NCBI backbone (NCBIN:111151, NCBI:P:111153)

R.Lydon, J.P., O'Malley, B.R.; Saucedo, O.; Lee, T.; Headon, D.R.; Conneely, O.M.
 Biochim. Biophys. Acta 1132, 97-99, 1992
 A>Title: Nucleotide and primary amino acid sequence of porcine lactoferrin.
 A'Reference number: S24173; MUID:92379101; PMID:1511016
 A'Accession: S24173
 A'Molecule type: mRNA
 A'Residuals: 1-11, 'W', 13-50, 'I', 52-84, 'G', 86-120, 'L', 121-130, 'I', 132-282, 'S', 284-571, 'Q',
 A'Cross-references: EMBL:M92089; NID:g164613; PIDN:AAA31102.1; PID:g164614
 A'Experimental source: mammary gland
 C'Superfamily: transferrin; transferrin repeat homology
 C'Keywords: duplication; glycoprotein; iron; iron binding; metalloprotein; milk
 F:1-19/Domain: signal sequence #status predicted <Sig>
 F:20-703/Product: lactoferrin #status predicted <MAT>
 F:20-350/Domain: transferrin repeat homology <TRH1>
 F:36-48/Region: antimicrobial
 F:354-691/Domain: transferrin repeat homology <TRH2>
 F:28-62, 38-53, 129-212, 171-187, 184-195, 245-259, 362-394, 372-385, 419-698, 439-661, 471-546, 49
 F:177, 107, 206, 267/Binding site: iron (Asp, Tyr, Tyr, His) #status predicted
 F:103/Binding site: carbonate (Arg) #status predicted
 F:409, 447, 540, 609/Binding site: iron (Asp, Tyr, Tyr, His) #status predicted
 F:477/Binding site: carbonate (Arg) #status predicted
 F:490/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 82.4%; Score 56; DB 2; Length 703;
 Best Local Similarity 76.9%; Pred. No. 0.14;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKYLGESEYKAV 13
 Db 671 YEKYLGESEYKAV 683

RESULT 4

JC2323
 Lactoferrin - goat
 C'Species: Capra aegagrus hircus (domestic goat)
 C'Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
 A'Accession: JC2323
 R'Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
 Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
 A>Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus
 A'Reference number: JC2323; MUID:94380047; PMID:8093048
 A'Accession: JC2323
 A'Molecule type: mRNA
 A'Residuals: 1-708 <LRP>
 C'Superfamily: transferrin; transferrin repeat homology
 C'Keywords: duplication; glycoprotein
 F:359-696/Domain: transferrin repeat homology <TRH2>
 F:252, 300, 387, 495, 564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 80.9%; Score 55; DB 2; Length 708;
 Best Local Similarity 76.9%; Pred. No. 0.21;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKYLGESEYKAV 13
 Db 676 YEKYLGESEYKAV 688

RESULT 5

S49163
 transferrin precursor - rat
 N'Alternate names: lung-derived growth factor; siderophilin
 C'Species: Rattus norvegicus (Norway rat)
 C'Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
 A'Accession: S49163; S54980; A30014; A14679; A53289; A30512; I52203
 R'Eschbacher, H.; Pierce, A.; Codderville, B.; Gonzalez, F.; Benabisa, M.; Leger, D.; Wierus
 submitted to the EMBL Data Library, January 1994
 A'Description: Rat mammary gland transferrin: glycan structure, nucleotide sequence and
 A'Reference number: S49163
 A'Accession: S49163
 A'Status: preliminary
 A'Molecule type: mRNA

A'Residuals: 1-695 <ESC>
 A'Cross-references: UNIPROT:P12346; UNIPROT:Q63602; EMBL:X77158; NID:9510195; PIDN:CAAS-
 R'Eschbacher, H.; Pierce, A.; Codderville, B.; Gonzalez, F.; Benabisa, M.; Leger, D.; Wierus
 Biochem. J. 307, 47-55, 1995
 A>Title: Rat mammary-gland transferrin: nucleotide sequence, phylogenetic analysis and
 A'Reference number: S49163; MUID:95234054; PMID:7717992
 A'Accession: S49163
 A'Status: preliminary
 A'Molecule type: mRNA
 A'Residuals: 1-695 <ES2>
 A'Cross-references: EMBL:X77158; NID:9510195; PIDN:CAAS4403.1; PID:9510196
 R'Hugueny, J.; Idzerda, R.L.; Haywood, L.; Lee, D.C.; McKnight, G.S.; Griswold, M.D.
 Endocrinology 120, 332-340, 1987
 A>Title: Transferrin messenger ribonucleic acid: molecular cloning and hormonal regula
 A'Reference number: A30014; MUID:87053639; PMID:3023031
 A'Accession: A30014
 A'Molecule type: mRNA
 A'Residuals: 518-687, 'D', 689-692, 'TA', 695 <HUG>
 A'Cross-references: GB:M27966; NID:9207439; PIDN:AAA42267.1; PID:9207440
 R'Schreiber, G.; Dryburgh, H.; Millership, A.; Matsuda, Y.; Inglis, A.; Phillips, J.; Ek
 J. Biol. Chem. 254, 12013-12019, 1979
 A>Title: The synthesis and secretion of rat transferrin.
 A'Reference number: A14679; MUID:80049855; PMID:500689
 A'Accession: A14679
 A'Molecule type: protein
 A'Residuals: 20-47 <SCH>
 R'Cavanaugh, P.G.; Nicolson, G.L.
 J. Cell. Biochem. 47, 261-271, 1991
 A>Title: Lung-derived growth factor that stimulates the growth of lung-metastasizing tun
 A'Reference number: A53289; MUID:92165927; PMID:1791188
 A'Accession: A53289
 A'Status: preliminary
 A'Molecule type: protein
 A'Residuals: 89, 'Y', 91, 'A', 93-99, 'V', 101-102, 'N', 233, 'AN', 236-243, 401-406, 'N', 408 <CAV>
 A'Experimental source: lung
 A>Note: sequence extracted after extraction from NCBI backbone (NCBIP:86115, NCBIP:86114)
 R'Putres, L.R.; Putres, M.; Linton, N.; Brand, W.; Johnson, G.; Jacobs, P.
 Biochim. Biophys. Acta 966, 318-327, 1998
 A>Title: Properties of the transferrin associated with rat intestinal mucosa.
 A'Reference number: A30512; MUID:88327006; PMID:104665
 A'Accession: A30512
 A'Molecule type: protein
 A'Residuals: 20-30, 639-643, 'KD', 646, 'LRACD', <PUR>
 R'Alfred, A.R.; Howlett, G.J.; Schreiber, G.
 Biochem. Biophys. Res. Commun. 122, 960-965, 1984
 A>Title: Synthesis of rat transferrin in Escherichia coli containing a recombinant bacte
 A'Reference number: I52203; MUID:84307580; PMID:6236811
 A'Accession: I52203
 A'Status: preliminary; translated from GB/EMBL/DBJ
 A'Molecule type: mRNA
 A'Residuals: 7-25, 'X', 27-56, 'A', 58-64, 267-295 <RES>
 A'Cross-references: GB:M26113; NID:9207437; PIDN:AAA42266.1; PID:9207438
 C'Genetics:
 A'Gene: TF
 C'Superfamily: transferrin; transferrin repeat homology
 C'Keywords: duplication
 F:20-348/Domain: transferrin repeat homology <TRH1>

Query Match 75.0%; Score 51; DB 2; Length 695;
 Best Local Similarity 69.2%; Pred. No. 0.99;
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEKYLGESEYKAV 13
 Db 663 YEKYLGESEYKAV 675

RESULT 6

I47228
 carbonic anhydrase II inhibitor (transferrin homolog) precursor - pig
 C'Species: Sus scrofa domestica (domestic pig)
 C'Date: 21-Feb-1997 #sequence_revision 12-Feb-1997 #text_change 09-Jul-2004

closely resembles the C-terminal duplication in transferrin. This protein is nearly identical to the C-terminal duplication in transferrin. This protein is nearly identical to the C-terminal duplication in transferrin.

C:Superfamily: hemiferrin; transferrin repeat homology

C:Keywords: glycoprotein; transferrin repeat homology

F:1-215/Domain: transferrin repeat homology #status atypical <TRH2>

Query Match 70.6%; Score 48; DB 2; Length 215;

Best Local Similarity 53.8%; Pred. No. 0.97;

Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEKYLGEERYVAV 13

DB 183 YDSYLGDDVVRAM 195

RESULT 9

A39684

hemiferrin - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #ext_change 09-Jul-2004

C:Accession: A39684

R:Stallard, B.J.; Collard, M.W.; Griswold, M.D.

Mol. Cell. Biol. 11, 1448-1453, 1991

A:Title: A transferrin-like (hemiferrin) mRNA is expressed in the germ cells of rat testis

A:Reference number: A39684; MUID:91141493; PMID:1996102

A:Accession: A39684

A:Molecule type: mRNA

A:Residues: 1-216 <STA>

A:Cross-references: UNIPROT:Q64599; GB:M60388

C:Superfamily: hemiferrin; transferrin repeat homology

C:Keywords: glycoprotein; transferrin repeat homology

F:1-204/Domain: transferrin repeat homology #status atypical <TRH2>

Query Match 70.6%; Score 48; DB 1; Length 216;

Best Local Similarity 53.8%; Pred. No. 0.97;

Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEKYLGEERYVAV 13

DB 184 YDSYLGDDVVRAM 196

RESULT 10

TFHUL

lactotransferrin precursor [validated] - human

N:Alternate names: lactoferrin

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1992 #sequence_revision 21-Nov-1997 #ext_change 08-Dec-2000

C:Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74

R:Cho, Y.

submitted to the EMBL Data Library, March 1994

A:Reference number: G06820

A:Accession: G01394

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Cross-references: EMBL:U07643; NID:g467236; PIDN:AA660324.1; PID:g467237

R:Rey, M.W.; Woloshuk, S.L.; DeBeer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A:Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A:Reference number: S11228; MUID:90384839; PMID:2402455

A:Accession: S11228

A:Molecule type: mRNA

A:Residues: 1-148, 'T', 150-422, 'C', 424-711 <REY>

A:Cross-references: EMBL:X53961; NID:g34415; PIDN:CAA37914.1; PID:g34416

R:Yang, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A:Title: Differential molecular mechanism of the estrogen action that regulates lactoferrin

A:Reference number: A45401; MUID:93125571; PMID:1480183

A:Accession: A45401

A:Molecule type: DNA

A:Residues: 1-15 <TEN>

A:Cross-references: GB:S52659; NID:g263311; PIDN:AA824877.1; PID:g263312

A:Experimental source: placenta

A>Note: sequence extracted from NCBI backbone (NCBI:122202)

R:Powell, M.J.; Ogden, J.B.

Nucleic Acids Res. 18, 4013, 1990

A:Title: Nucleotide sequence of human lactoferrin cDNA.

A:Reference number: S10324; MUID:90326549; PMID:2374734

A:Accession: S10324

A:Molecule type: mRNA

A:Residues: 3-711 <POW>

A:Cross-references: EMBL:X52941; NID:g34411; PIDN:CAA37116.1; PID:g34412

R:Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A:Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A:Reference number: S15853; MUID:91264786; PMID:2049066

A:Accession: S15853

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 20-31 <ST1>

A:Accession: S20841

A:Molecule type: protein

A:Residues: 20-28, 'X', 30-31 <ST2>

R:Rado, T.A.; Mei, X.; Benz Jr., E.J.

Blood 70, 989-993, 1987

A:Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA

A:Reference number: S07160; MUID:88001031; PMID:3477300

A:Accession: S07160

A:Molecule type: mRNA

A:Residues: 436-487, 'A', 489-711 <RAD>

A:Cross-references: EMBL:M18642; NID:g18615; PIDN:AA86665.1; PID:g386855

R:Panelia, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.

Cancer Res. 51, 3037-3043, 1991

A:Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes

A:Reference number: A61169; MUID:91235214; PMID:1674448

A:Accession: A61169

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 3-701, 'SMKPVN' <PAN>

A:Experimental source: normal breast tissue

R:Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.

Bur. J. Biochem. 145, 659-666, 1984

A:Title: Human lactotransferrin: amino acid sequence and structural comparisons with other

A:Reference number: A31000; MUID:85076667; PMID:6510420

A:Accession: A31000

A:Molecule type: protein

A:Residues: 20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-4

A>Note: This is the final paper in a series

R:Houen, G.; Hoegdal, E.V.; Barkholt, V.; Nørskov, L.

Bur. J. Biochem. 241, 303-308, 1996

A:Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affinity

A:Reference number: S74119; MUID:97054624; PMID:8898921

A:Accession: S74119

A:Molecule type: protein

A:Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>

A:Experimental source: neutrophil granulocytes

A:Gene: GDB: LTF

A:Cross-references: GDB:119368; OMIM:150210

A:Map position: 3q21-3q23

C:Superfamily: transferrin; transferrin repeat homology

C:Keywords: duplication; glycoprotein; iron binding; milk

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-711/Product: lactotransferrin #status experimental <MAT>

F:21-356/Domain: transferrin repeat homology <TRH1>

F:360-699/Domain: transferrin repeat homology <TRH2>

F:729-653/Domain: transferrin repeat homology <TRH3>

F:729-653/Domain: transferrin repeat homology <TRH4>

F:729-653/Domain: transferrin repeat homology <TRH5>

F:729-653/Domain: transferrin repeat homology <TRH6>

F:729-653/Domain: transferrin repeat homology <TRH7>

F:729-653/Domain: transferrin repeat homology <TRH8>

F:729-653/Domain: transferrin repeat homology <TRH9>

F:729-653/Domain: transferrin repeat homology <TRH10>

F:729-653/Domain: transferrin repeat homology <TRH11>

F:729-653/Domain: transferrin repeat homology <TRH12>

F:729-653/Domain: transferrin repeat homology <TRH13>

F:729-653/Domain: transferrin repeat homology <TRH14>

F:729-653/Domain: transferrin repeat homology <TRH15>

F:729-653/Domain: transferrin repeat homology <TRH16>

F:729-653/Domain: transferrin repeat homology <TRH17>

F:729-653/Domain: transferrin repeat homology <TRH18>

F:729-653/Domain: transferrin repeat homology <TRH19>

F:729-653/Domain: transferrin repeat homology <TRH20>

F:729-653/Domain: transferrin repeat homology <TRH21>

F:729-653/Domain: transferrin repeat homology <TRH22>

F:729-653/Domain: transferrin repeat homology <TRH23>

F:729-653/Domain: transferrin repeat homology <TRH24>

F:729-653/Domain: transferrin repeat homology <TRH25>

F:729-653/Domain: transferrin repeat homology <TRH26>

F:729-653/Domain: transferrin repeat homology <TRH27>

F:729-653/Domain: transferrin repeat homology <TRH28>

Db 679 YEKYLGPQYVAGI 691

RESULT 11

501384

transferrin - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: S01384; A60520; A61573

R:Bailewin, G.S.; Weinstein, J.

Nucleic Acids Res. 16, 8720, 1988

A:Title: Nucleotide sequence of porcine liver transferrin.

A:Reference number: S01384; PMID:88335629; PMID:3419934

A:Accession: S01384

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-696 <BAL>

A:Cross-references: UNIPROT:P09571; EMBL:X12386; NID:g2126; PID:CAA30943.1; PID:g833800

A>Note: 308-Arg was also found

R:Bailewin, G.S.; Baile, T.; Chandler, R.; Grego, B.; Pedersen, J.; Simpson, R.J.; Toh, H

Comp. Biochem. Physiol. B 95, 261-268, 1990

A:Title: Isolation of transferrin from porcine gastric mucosa: comparison with porcine B

A:Reference number: A60520; PMID:90227903; PMID:2328566

A:Accession: A60520

A:Molecule type: protein

A:Residues: 1-8; 'X', 10-11, 'X', 13-15 <BA2>

A:Experimental source: gastric mucosa

A>Note: the authors suggest transferrin from gastric mucosa may act in dietary iron upta

R:Chung, M.C.M.; Chan, S.L.; Shmidt, S.

Int. J. Biochem. 23, 609-616, 1991

A:Title: Purification of transferrins and lactoferrin using DEAE Affi-Gel Blue.

A:Reference number: A61573; PMID:91293379; PMID:2065820

A:Accession: A61573

A:Molecule type: protein

A:Residues: 1-8, 'X', 10-18, 'XE' <CHU>

C:Superfamily: transferrin; transferrin repeat homology

C:Keywords: duplication; glycoprotein; iron transport; plasma

F:1-696/Product: transferrin #status predicted <MAT>

F:1-335/Domain: transferrin repeat homology <TRH>

Query Match 69.1%; Score 47; DB 1; Length 696;

Best Local Similarity 61.5%; Pred. No. 4.8;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 YEKYLGEYVKA 13

Db 655 YESYLGADYITAV 667

RESULT 12

S33761

transferrin precursor - horse

N:Alternate names: growth-promoting factor

C:Species: Equus caballus (domestic horse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C:Accession: S33761; S02145

R:Carpenter, M.A.; Broad, T.E.

Biochim. Biophys. Acta 1173, 230-232, 1993

A:Title: The cDNA sequence of horse transferrin.

A:Reference number: S33761; PMID:93277958; PMID:8504171

A:Accession: S33761

A:Molecule type: mRNA

A:Residues: 1-706 <CAR>

A:Cross-references: UNIPROT:P27425; EMBL:M69020; NID:g164242; PID:AAA30958.1; PID:g1642

A:Experimental source: liver; developmental stage adult

R:Yoshinari, K.; Yuasa, K.; Iga, F.; Mamura, A.

Biochim. Biophys. Acta 1010, 28-34, 1989

A:Title: A growth-promoting factor for human myeloid leukemia cells from horse serum ide

A:Reference number: S02145; PMID:89076897; PMID:2909248

A:Accession: S02145

A:Molecule type: protein

A:Residues: 20-35, 'X', 37, 'X', 39-40, 'X', 43-44 <YOS>

C:Complex: monomer

C:Superfamily: transferrin; transferrin repeat homology

C:Keywords: duplication; glycoprotein; iron transport; metal binding; plasma

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-706/Product: transferrin #status experimental <MAT>

F:358-694/Domain: transferrin repeat homology <TRH>

F:26-64, 36-55, 134-215, 174-190, 177-198, 187-200, 248-262, 360-623, 366-398, 376-389, 423-701, 44

Query Match 66.2%; Score 45; DB 2; Length 706;

Best Local Similarity 61.5%; Pred. No. 11;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 YEKYLGEYVKA 13

Db 674 YKYLGEKYLTVAV 686

RESULT 13

A28438

lactoferrin precursor - mouse

N:Alternate names: lactotransferrin

C:Species: Mus musculus (house mouse)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A28438; A41205

R:Penhagoc, B.T.; Teng, C.T.

J. Biol. Chem. 262, 10134-10139, 1987

A:Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secre

A:Reference number: A92596; PMID:87280033; PMID:3611056

A:Accession: A28438

A:Molecule type: mRNA

A:Residues: 3-707 <PEN>

A:Cross-references: EMBL:J03298

R:Lin, Y.; Teng, C.T.

J. Biol. Chem. 266, 21880-21885, 1991

A:Title: Characterization of estrogen-responsive mouse lactoferrin promoter.

A:Reference number: A41205; PMID:92042099; PMID:1939212

A:Accession: A41205

A:Molecule type: DNA

A:Residues: 1-15 <LIN>

A:Cross-references: GB:M74778

C:Superfamily: transferrin; transferrin repeat homology

C:Keywords: duplication; glycoprotein

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-707/Product: lactotransferrin #status predicted <MAT>

F:358-695/Domain: transferrin repeat homology <TRH>

F:494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 66.2%; Score 45; DB 1; Length 707;

Best Local Similarity 81.8%; Pred. No. 11;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 EKYLGEEYVKA 12

Db 676 EKYLGKEVYTA 686

RESULT 14

D64326

UDPglucose 4-epimerase (EC 5.1.3.2) - Methanococcus jannaschii

C:Species: Methanococcus jannaschii

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C:Accession: D64326

R:Bull, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, ';

Reich, C.I.; Overbeek, R.; Kirsch, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;

rsom, J.D.; Sadow, P.M.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Huret, M.A.

Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Bordovsky, M.; Klenk, H.P.; Frazer, C.M.; Smith, H.O.; Weese, C

A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii

A:Reference number: A64300; PMID:96337999; PMID:8688087

A:Accession: D64326

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-305 <BUJ>

A:Cross-references: UNIPROT:Q57664; GB:U67477; GB:L77117; NID:g1590949; PID:AA898196.1;

C:Genetics:

A:Map position: FOR202715-203632

C:Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology

C:Keywords: Isomerase

F/2-305/Domain: UDPglucose 4-epimerase homology <UDP>

Query Match

64.7%; Score 44; DB 2; Length 305;

Best Local Similarity 77.8%; Pred. No. 6.8;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KYLGEEYVK 11

Db 144 KYVGEEYIK 152

RESULT 15

E75153

glyceraldehyde 3-phosphate dehydrogenase (gap) PAB0257 - Pyrococcus abyssi (strain Orsay

C:Species: Pyrococcus abyssi

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C:Accession: E75153

R:anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru

A:Reference number: A75001

A:Accession: E75153

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-334 <KAW>

A:Cross-references: UNIPROT:Q9V1P1; GB:AJ248284; GB:AL096836; NID:G5457730; PIDN:CAB4930

A:Experimental source: strain Orsay

C:Genetics:

A:Gene: gap; PAB0257

C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase

Query Match

63.2%; Score 43; DB 2; Length 334;

Best Local Similarity 61.5%; Pred. No. 11;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YEKYLGEERYKAV 13

Db 127 YEKALGKSYVRVY 139

Search completed: November 1, 2005, 12:55:51
Job time : 14.1912 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:34:09, Search time 63.6618 Seconds
(without alignments)
104.569 Million cell updates/sec

Title: US-10-612-162a-4
Perfect score: 68
Sequence: 1 YEKYIGEEYKAV 13

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	698	1 TRFE_HUMAN	P02787 homo sapien
2	58	85.3	695	1 TRFE_RABIT	P19134 oryctolagus
3	56	82.4	304	2 Q6YST2	Q6YST2 sus scrofa
4	56	82.4	694	2 Q7TSX8	Q7TSX8 martora mon
5	56	82.4	704	1 TRFL_PIG	P14632 sus scrofa
6	56	82.4	704	2 Q8MNN8	Q8MNN8 sus scrofa
7	56	82.4	704	2 Q6Y7J3	Q6Y7J3 sus scrofa
8	56	82.4	704	2 Q7YS20	Q7YS20 sus scrofa
9	55	80.9	708	1 TRFL_CAPHI	Q29477 capra hircu
10	51	75.0	355	2 Q8M1I0	Q8M1I0 bos taurus
11	51	75.0	681	2 Q6LBN7	Q6LBN7 bos taurus
12	51	75.0	698	1 TRFE_RAT	P12346 rattus norv
13	51	75.0	698	2 Q7TNX0	Q7TNX0 rattus norv
14	51	75.0	704	1 ICA_PIG	Q29545 sus scrofa
15	51	75.0	708	1 TRFL_BOVIN	P24627 bos taurus
16	51	75.0	708	1 TRFL_BUBU	Q77698 bubalus bub
17	51	75.0	708	2 Q6LEC7	Q6LEC7 bos taurus
18	51	75.0	711	2 Q9XT72	Q9XT72 trichosurus
19	51	75.0	979	2 Q7TMC7	Q7TMC7 rattus norv
20	51	75.0	980	2 Q7TTP4	Q7TTP4 rattus norv
21	49	72.1	695	1 TRFL_HORSE	Q77611 equus cabal
22	48	70.6	216	2 Q64599	Q64599 rattus norv
23	48	70.6	704	1 TRFE_BOVIN	Q29443 bos taurus
24	48	70.6	708	1 TRFL_CAMDR	Q92443 camelus dro
25	47	70.6	711	1 TRFL_HUMAN	P02788 homo sapien
26	47	69.1	696	1 TRFE_PIG	P09571 sus scrofa
27	45	66.2	63	2 Q9TOR4	Q9TOR4 equus cabal
28	45	66.2	697	1 TRFE_MOUSE	Q92111 mus musculi
29	45	66.2	706	1 TRFE_HORSE	P27425 equus cabal
30	45	66.2	707	1 TRFL_MOUSE	P08071 mus musculi
31	45	66.2	707	2 Q8CBA0	Q8CBA0 mus musculi

32	44	64.7	300	2 Q8ZT13	Q8ZT13 pyrobaculum
33	44	64.7	305	1 GALE_METJA	Q57664 methanococ
34	44	64.7	738	1 TRFM_MOUSE	Q91071 mus musculi
35	43	63.2	238	2 Q9DPK5	Q9DPK5 gillichthys
36	43	63.2	301	2 Q97AH2	Q97AH2 thermoplas
37	43	63.2	334	1 GIP_PIRAB	Q97B21 pyrococcus
38	43	63.2	501	2 Q6C8P2	Q6C8P2 kluyveromyc
39	43	63.2	613	1 DNK_BACHD	Q9K472 bacillus ha
40	43	63.2	671	2 Q6CUQ3	Q6CUQ3 kluyveromyc
41	43	63.2	671	2 Q707Z3	Q707Z3 kluyveromyc
42	43	63.2	691	2 Q6UPC0	Q6UPC0 acanthopagr
43	43	63.2	692	1 PHSG_AQUAE	Q66932 aquifex aeo
44	42	61.8	115	2 Q9P7Y2	Q9P7Y2 schizosach
45	42	61.8	188	1 Y966_HAEIN	P44085 haemophilus

ALIGNMENTS

RESULT 1
TRFE_HUMAN
ID TRFE_HUMAN STANDARD; PRT; 698 AA.
AC P02787; Q43890; Q9NQB8; Q9UHV0;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Serotransferrin precursor (transferrin) (Siderophilin) (Beta-1-metal
binding globulin) (PRO1400).
GN Name=TF;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS TF*B2; TF*CHI AND TF*DI.
RX MEDLINE=84194084; PubMed=6585826;
RA Yang F., Lum J.B., McGill J.R., Moore C.M., Naylor S.L.,
van Bragt P.H., Baldwin W.D., Bowman B.H.;
RT "Human transferrin: cDNA characterization and chromosomal
localization.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:2752-2756(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88056305; PubMed=3678832; DOI=10.1016/0378-1119(87)90163-6;
RA Scheffer E., Lucero M.A., Jeltsch U.-M., Py M.-C., Levin M.O.,
Chandon P., Cohen G.N., Zakim M.W.;
RT "Complete structure of the human transferrin gene. Comparison with
RT analogous chicken gene and human pseudogene.";
RN Gene 56:109-116(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Herberberger C.L., Larson J.L., Arnold B., Rostack P.R. Jr.,
Williams P., Dehoff B., Dunn P., O'Neal K.L., Riemen M.W., Tice P.A.;
RT "A cloned gene for human transferrin.";
RN Ann. N.Y. Acad. Sci. 646:140-154(1991).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT ATRANSFERRINEMIA PRO-477.
RX MEDLINE=20563920; PubMed=1110675;
RA Beutler E., Gelbart T., Lee P.L., Trevino R., Fernandez M.A.,
Palbans V.F.;
RT "Molecular characterization of a case of atransferrinemia.";
RN Blood 96:4071-4074(2000).
RN [5]
RP SEQUENCE FROM N.A.
RX Rieder M.J., Carlington D.P., da Ponte S.H., Hastings N.C.,
Abern M.O., Kulanek S.A., Rajkumar N., Toth E.J., Yi Q.,
Nickeron D.A.;
RT "SeattlesNPB. NHBI H166682 program for genomic applications. WA-
PHCC, Seattle, WA (URL: http://pga.gs.washington.edu)."
RN Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
[6]

RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Scheffen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [17]
RP SEQUENCE OF 99-698 FROM N.A.
RC TISSUE=Fetal liver;
RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M.,
RA He F.;
RT "Functional prediction of the coding sequences of 33 new genes deduced
RT by analysis of cDNA clones from human fetal liver.";
RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
RN [18]
RP SEQUENCE OF 422-698 FROM N.A.
RX MEDLINE=8415310; PubMed=6322780;
RA Uzan G., Fraim M., Park I., Beemond C., Maessen G., Trepac J.S.,
RA Zakim M.W., Kahn A.;
RT "Molecular cloning and sequence analysis of cDNA for human
RT transferrin.";
RL Biochem. Biophys. Res. Commun. 119:273-281(1984).
RN [19]
RP SEQUENCE OF 20-698.
RX MEDLINE=83160878; PubMed=6833213;
RA McGillivray R.T.A., Mendez E., Shewale J.G., Sinha S.K.,
RA Lineback-Zins J., Brew K.;
RT "The primary structure of human serum transferrin. The structures of
RT seven cyanogen bromide fragments and the assembly of the complete
RT structure.";
RL J. Biol. Chem. 258:3543-3553(1983).
RN [10]
RP SEQUENCE OF 73-698 FROM N.A.
RX MEDLINE=85216459; PubMed=3858612;
RA Park J., Schaeffer E., Sidoli A., Baralle F.E., Cohen G.N.,
RA Zakim M.W.;
RT "Organization of the human transferrin gene: direct evidence that it
RT originated by gene duplication.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:3149-3153(1985).
RN [11]
RP SEQUENCE OF 1-14 FROM N.A.
RX MEDLINE=87066744; PubMed=3786138;
RA Lucero M.A., Schaeffer E., Cohen G.N., Zakim M.W.;
RT "The 5' region of the human transferrin gene: structure and potential
RT regulatory sites.";
RL Nucleic Acids Res. 14:8692-8692(1986).
RN [12]
RP SEQUENCE OF 1-72 AND 291-300 FROM N.A.
RX MEDLINE=87192006; PubMed=3106157; DOI=10.1016/0378-1119(86)90277-5;
RA Adrian G.S., Korinek B.W., Bowman B.R., Yang F.;
RT "The human transferrin gene: 5' region contains conserved sequences
RT which match the control elements regulated by heavy metals,
RT glucocorticoids and acute phase reaction.";
RL Gene 49:167-175(1986).
RN [13]
RP SEQUENCE OF 45-72 FROM N.A.

RX MEDLINE=20392111; PubMed=10931525;
RX DOI=10.1002/1097-4547(20000815)61:4<388::AID-JNRS53.0.CO;2-O;
RA de Arriba Zepa G.A., Saleh M.-C., Fernandez P.M., Guillou F.,
RA Espinosa de los Monteros A., de Vellis J., Zakim M.W., Baron B.;
RT "Alternative splicing prevents transferrin secretion during
RT differentiation of a human oligodendrocyte cell line.";
RL J. Neurosci. Res. 61:388-395(2000).
RN [14]
RP SEQUENCE OF 564-624 FROM N.A., AND VARIANT TP*C2.
RC TISSUE=Brain;
RX MEDLINE=97418135; PubMed=9272172;
RA Namekata K., Oyama F., Imagawa M., Ihara Y.;
RT "Human transferrin (Tf): a single mutation at codon 570 determines Tf
RT C1 or Tf C2 variant.";
RL Hum. Genet. 100:457-458(1997).
RN [15]
RP SEQUENCE OF 564-624 FROM N.A.
RA Teuchida S., Ikemoto S., Kajii E.;
RL Submitted (APR-1998) to the EMBL/Genbank/DBJ databases.
RN [16]
RP SEQUENCE OF 636-696 FROM N.A.
RX MEDLINE=89386721; PubMed=2780570;
RA Duguid J.R., Belmont C.W., Liu N.G., Tourtelotte W.W.;
RT "Changes in brain gene expression shared by scrapie and Alzheimer
RT disease.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:7260-7264(1989).
RN [17]
RP SEQUENCE OF 263-266, 454-458, 531-538 AND 589-595.
RC TISSUE=Heart;
RX MEDLINE=96007936; PubMed=7498159;
RA Kovalyov L.I., Shishkin S.S., Efimochkin A.S., Kovalyova M.A.,
RA Ershova E.S., Egorov T.A., Muralymov A.K.;
RT "The major protein expression profile and two-dimensional protein
RT database of human heart.";
RL Electrophoresis 16:1160-1169(1995).
RN [18]
RP DISULFIDE BONDS.
RX MEDLINE=8222166; PubMed=6953407;
RA McGillivray R.T.A., Mendez E., Sinha S.K., Sutton M.R.,
RA Lineback-Zins J., Brew K.;
RT "The complete amino acid sequence of human serum transferrin.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2504-2508(1982).
RN [19]
RP MUTAGENESIS.
RX MEDLINE=92031536; PubMed=1932003;
RA Woodworth R.C., Mason A.B., Funk W.D., McGillivray R.T.A.;
RT "Expression and initial characterization of five site-directed mutants
RT of the N-terminal half-molecule of human transferrin.";
RL Biochemistry 30:10824-10829(1991).
RN [20]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 22-350.
RX MEDLINE=98272665; PubMed=9609685; DOI=10.1021/b198035j;
RA McGillivray R.T.A., Moore S.A., Chen J., Anderson B.F., Baker H.,
RA Luo Y., Bewley M.C., Smith C.A., Murphy M.B.P., Wang Y., Mason A.B.,
RA Woodworth R.C., Breyer G.D., Baker E.N.;
RT "Two high-resolution crystal structures of the recombinant N-lobe of
RT human transferrin reveal a structural change implicated in iron
RT release.";
RL Biochemistry 37:7919-7928(1998).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-350.
RX MEDLINE=98434369; PubMed=9760232; DOI=10.1021/b19812064;
RA Jeffrey P.D., Bewley M.C., McGillivray R.T.A., Mason A.B.,
RA Woodworth R.C., Baker E.N.;
RT "Ligand-induced conformational change in transferrin: crystal
RT structure of the open form of the N-terminal half-molecule of human
RT transferrin.";
RL Biochemistry 37:13978-13986(1998).
RN [22]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 23-352.
RX MEDLINE=99155227; PubMed=10029548; DOI=10.1021/b1982454j;
RA Bewley M.C., Tam B.M., Grewal J., He S., Shewly S., Murphy M.E.P.,
RA Mason A.B., Woodworth R.C., Baker E.N., McGillivray R.T.A.;

RT "X-ray crystallography and mass spectroscopy reveal that the N-lobe of
RT human transferrin expressed in *Pichia pastoris* is folded correctly but
Query Match 100.0%; Score 68; DB 1; Length 698;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 YEKYLGEERYVKAV 13
Db 666 YEKYLGEERYVKAV 678
RESULT 2
TRFE_RABIT STANDARD; RPT; 695 AA.
AC P19134; O46514;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Serotransferrin precursor (transferrin) (Siderophilin) (Beta-1-metal
binding globulin).
CN Name="TF";
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxId=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91274362; PubMed=2054387; DOI=10.1016/0167-4781(91)90021-D;
RA Banfield D.K., Chow B.K.-C., Funk W.D., Robertson K.A., Umels T.M.,
RA Woodworth R.C., Macgillivray R.T.A.;
RT "The nucleotide sequence of rabbit liver transferrin cDNA.";
RL Biochim. Biophys. Acta 1089:262-265(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white;
RA Chareeb B.A.A., Thepot D., Pulesant C., Cajero-Juarez M.,
RA Houdebine L.M.;
RT "Cloning and structural organisation of the rabbit transferrin encoding
gene.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 20-51.
RX MEDLINE=89209278; PubMed=3355331;
RA Godovac-Zimmermann J.;
RT "Isolation, characterization and N-terminal amino-acid sequence of
rabbit transferrin.";
RL Biol. Chem. Hoppe-Seyler 369:93-96(1988).
RN [4]
RP SEQUENCE OF 483-545.
RX MEDLINE=89005676; PubMed=3169252; DOI=10.1016/0014-5793(88)80221-7;
RA Evans R.W., Aitken A., Patel K.J.;
RT "Evidence for a single glycan moiety in rabbit serum transferrin and
location of the glycan within the polypeptide chain.";
RL FEBS Lett. 238:39-42(1988).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).
RC TISSUE=Plasma;
RX MEDLINE=89026775; PubMed=3179277;
RA Bailey S., Evans R.W., Garratt R.C., Gorinsky B., Hasnain S.,
RA Horburgh C., Jhoti H., Lindley P.F., Mydin A., Sarrat R., Watson J.L.;
RT "Molecular structure of serum transferrin at 3.3-A resolution.";
RL Biochemistry 27:5804-5812(1988).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RA Sarrat R., Garratt R.C., Gorinsky B., Jhoti H., Lindley P.F.;
RT "High-resolution X-ray studies on rabbit serum transferrin:
preliminary structure analysis of the N-terminal half-molecule at 2.3-
A resolution.";
RL Acta Crystallogr. B 46:763-771(1990).
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
can bind two atoms of ferric iron in association with the binding

CC of an anion, usually bicarbonate. It is responsible for the
CC transport of iron from sites of absorption and heme degradation to
CC those of storage and utilization. Serum transferrin may also have
CC a further role in stimulating cell proliferation.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -1- DOMAIN: Composed of two homologous domains.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
CC or send an email to license@ebi.ac.uk).
CC -----
CC DR EMBL; X58533; CAA41424.1; -;
DR EMBL; AF031625; AAB94136.1; -;
DR EMBL; AF031611; AAB94136.1; JOINED.
DR EMBL; AF031612; AAB94136.1; JOINED.
DR EMBL; AF031613; AAB94136.1; JOINED.
DR EMBL; AF031614; AAB94136.1; JOINED.
DR EMBL; AF031615; AAB94136.1; JOINED.
DR EMBL; AF031616; AAB94136.1; JOINED.
DR EMBL; AF031617; AAB94136.1; JOINED.
DR EMBL; AF031618; AAB94136.1; JOINED.
DR EMBL; AF031619; AAB94136.1; JOINED.
DR EMBL; AF031620; AAB94136.1; JOINED.
DR EMBL; AF031621; AAB94136.1; JOINED.
DR EMBL; AF031622; AAB94136.1; JOINED.
DR EMBL; AF031623; AAB94136.1; JOINED.
DR EMBL; AF031624; AAB94136.1; JOINED.
DR PDB; 1JNF; X-ray; A=20-695.
DR PDB; 1TFD; X-ray; @=20-323.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW 3D-structure; Direct protein sequencing; Glycoprotein; Iron transport;
KW Metal-binding; Repeat; Signal; Transport.
FT CHAIN 1 695
FT SIGNAL 1 19
FT REPEAT 20 355 Serotransferrin.
FT REPEAT 356 695 1.
FT DISULFID 38 67 2.
FT DISULFID 38 58
FT DISULFID 137 213
FT DISULFID 156 350
FT DISULFID 177 193
FT DISULFID 180 196
FT DISULFID 190 198
FT DISULFID 246 260
FT DISULFID 358 364
FT DISULFID 364 396
FT DISULFID 374 387
FT DISULFID 421 690
FT DISULFID 436 653
FT DISULFID 468 539
FT DISULFID 492 681
FT DISULFID 502 516
FT DISULFID 513 522
FT DISULFID 579 593
FT DISULFID 631 636
FT CARBOHYD 509 509
FT METAL 82 82 N-linked (GLCNAC. . .).
FT METAL 114 114 Iron 1.
FT METAL 207 207 Iron 1.
FT METAL 268 268 Iron 1.

```

FT METAL 411 411 Iron 2.
FT METAL 444 444 Iron 2.
FT METAL 533 533 Iron 2.
FT METAL 601 601 Iron 2.
FT BINDING 139 139 Carbonate 1.
FT BINDING 143 143 Carbonate 1.
FT BINDING 145 145 Carbonate 1 (via amide nitrogen).
FT BINDING 146 146 Carbonate 1 (via amide nitrogen).
FT BINDING 470 470 Carbonate 2.
FT BINDING 474 474 Carbonate 2.
FT BINDING 476 476 Carbonate 2 (via amide nitrogen).
FT BINDING 477 477 Carbonate 2 (via amide nitrogen).
FT VARIANT 517 517 V -> I.
FT CONFLICT 7 7 Missing (in Ref. 1).
FT CONFLICT 47 47 K -> S (in Ref. 3).
FT STRAND 50 50 P -> Y (in Ref. 3).
FT HELIX 24 30
FT TURN 31 48
FT TURN 51 52
FT STRAND 55 61
FT HELIX 64 72
FT TURN 73 74
FT STRAND 78 81
FT HELIX 83 90
FT TURN 92 94
FT STRAND 96 104
FT STRAND 111 111
FT STRAND 113 121
FT TURN 122 123
FT HELIX 128 130
FT TURN 132 133
FT STRAND 136 138
FT TURN 141 142
FT TURN 144 147
FT HELIX 148 154
FT HELIX 155 157
FT HELIX 165 172
FT STRAND 176 177
FT TURN 179 180
FT TURN 183 185
FT HELIX 187 190
FT TURN 191 192
FT TURN 194 195
FT TURN 200 201
FT TURN 203 204
FT HELIX 206 215
FT TURN 216 217
FT STRAND 221 225
FT TURN 226 227
FT HELIX 228 232
FT HELIX 236 239
FT TURN 240 241
FT STRAND 242 245
FT TURN 247 248
FT STRAND 251 253
FT HELIX 254 256
FT TURN 257 258
FT STRAND 263 266
FT STRAND 269 273
FT HELIX 279 293
FT TURN 303 304
FT TURN 307 308
FT TURN 316 317
FT STRAND 320 323
FT TURN 326 327
FT HELIX 330 334
FT HELIX 336 346
FT TURN 347 348

Query Match      85.3%; Score 58; DB 1; Length 695;
Best Local Similarity 76.9%; Pred. No. 0.99;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 YEKYLGEYKAV 13
Db 663 YEKYLGEYKAV 675

RESULT 3
ID Q6YST2 PRELIMINARY; PRT; 304 AA.
AC Q6YST2;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DR 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Lactoferrin (Fragment).
GN Name-LTF;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: Transferrins are iron binding transport proteins which
CC bind ferric iron in association with the binding of an anion,
CC usually bicarbonate (By similarity).
CC -! SIMILARITY: Belongs to the transferrin family.
CC EMBL; AP006435; BAD08658.1; -.
DR HSSP; O8TCD2; 1B0L.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_PER. 1.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 1.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
KM Iron transport; Metal-binding; transport.
SQ NON_TER 1
SQ SEQUENCE 304 AA; 3315 MW; 16C0B1675D8722A8 CRC64;

Query Match      82.4%; Score 56; DB 2; Length 304;
Best Local Similarity 76.9%; Pred. No. 0.98;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKYLGEYKAV 13
Db 272 YEKYLGEYKAV 284

RESULT 4
ID Q7TSX8 PRELIMINARY; PRT; 694 AA.
AC Q7TSX8;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DR 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Transferrin.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Rinaldo J.A.S., Gerin J.L.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: Transferrins are iron binding transport proteins which
CC bind ferric iron in association with the binding of an anion,
CC usually bicarbonate (By similarity).

```



```

CC -1- DOMAIN: Composed of two homologous domains (By similarity).
CC -1- SIMILARITY: Belongs to the transferrin family.
DR EMBL, AY288100; AAP37129.1; -.
DR HSP, P19134; 1JNF.
DR GO, GO:0005576; C:cytoregulatory; IEA.
DR GO, GO:0008199; F:ferritin binding; IEA.
DR GO, GO:0006879; P:iron ion homeostasis; IEA.
DR GO, GO:0006826; P:iron ion transport; IEA.
DR InterPro, IPR001156; Peptidase_S60.
DR Pfam, PF00405; Transferrin; 2.
DR SMART, SM00094; TR_FER; 2.
DR PROSITE, PS00205; TRANSFERRIN_1; 2.
DR PROSITE, PS00206; TRANSFERRIN_2; 2.
DR PROSITE, PS00207; TRANSFERRIN_3; 2.
DR Iron transport; Metal-binding; Transport.
KW SEQUENCE 694 AA; 76466 MW; 40053F7DC1CFCA87 CRC64;

Query Match 82.4%; Score 56; DB 2; Length 694;
Beet Local Similarity 84.6%; Pred. No. 2.1;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKYLGEYKAV 13
DB 662 YEKYLGEYKAV 674

RESULT 5
TRFL_PIG STANDARD; PRT; 704 AA.
AC P14632; Q29557;
DT 01-APR-1990 (Rel. 14, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin).
GN Name-LTF;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Suid.
OX NCBI_TaxId=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92379101; PubMed=1511016; DOI=10.1016/0167-4781(92)90061-4;
RA Lyndon J.P., O'Malley B.R., Saucedo O., Lee T., Headon D.R.,
RA Connolly O.W.;
RT "Nucleotide and primary amino acid sequence of porcine lactoferrin.";
RL Blochm. Biophys. Acta 1132:97-99(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92367939; PubMed=1503259;
RA Alexander L.J., Levine W.B., Teng C.T., Beattie C.W.;
RT "Cloning and sequencing of the porcine lactoferrin cDNA.";
RL Anim. Genet. 23:251-256(1992).
RN [3]
RP SEQUENCE OF 20-49.
RX MEDLINE=90105538; PubMed=2605266;
RA Hutchens T.W., Magnuson J.S., Yip T.-T.;
RT "Rapid purification of porcine colostral whey lactoferrin by affinity
chromatography on single-stranded DNA-agarose. Characterization, amino
acid composition and N-terminal amino acid sequence.";
RL Blochm. Biophys. Acta 999:323-329(1989).
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
can bind two atoms of ferric iron in association with the binding
of an anion, usually bicarbonate.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: Composed of two homologous domains.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

```

```

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, M92089; AAA31102.1; -.
DR EMBL, M81327; AAA31059.1; -.
DR PIR, A45543; A45543.
DR HSP, Q9TUM0; 1DT2.
DR InterPro, IPR001156; Peptidase_S60.
DR Pfam, PF00405; Transferrin; 2.
DR PRINTS, PR00422; TRANSFERRIN.
DR SMART, SM00094; TR_FER; 2.
DR PROSITE, PS00205; TRANSFERRIN_1; 2.
DR PROSITE, PS00206; TRANSFERRIN_2; 2.
DR PROSITE, PS00207; TRANSFERRIN_3; 1.
KW Direct protein sequencing; Glycoprotein; Iron transport;
KW Metal-binding; Repeat; Signal; Transport.
FT SIGNAL 1
FT CHAIN 20 704
FT REPEAT 20 359
FT DISULFID 28 62
FT DISULFID 38 53
FT DISULFID 130 213
FT DISULFID 172 188
FT DISULFID 185 196
FT DISULFID 246 260
FT DISULFID 363 395
FT DISULFID 373 386
FT DISULFID 420 699
FT DISULFID 472 547
FT DISULFID 496 680
FT DISULFID 506 520
FT DISULFID 517 530
FT DISULFID 588 602
FT DISULFID 640 645
FT METAL 77
FT METAL 107
FT METAL 207
FT METAL 268
FT METAL 410
FT METAL 448
FT METAL 541
FT METAL 610
FT BINDING 132 132
FT BINDING 136 136
FT BINDING 138 138
FT BINDING 139 139
FT BINDING 474 474
FT BINDING 478 478
FT BINDING 480 480
FT BINDING 481 481
FT CARBOHYD 385 385
FT CARBOHYD 491 491
FT CONFLICT 12 12
FT CONFLICT 46 48
FT CONFLICT 51 51
FT CONFLICT 85 85
FT CONFLICT 121 121
FT CONFLICT 132 132
FT CONFLICT 284 284
FT CONFLICT 573 573
FT CONFLICT 590 590
FT CONFLICT 625 625
FT CONFLICT 662 662
FT CONFLICT 686 704
SQ SEQUENCE 704 AA; 77625 MW; 932615FD08A0358 CRC64;

Query Match 82.4%; Score 56; DB 1; Length 704;

```

Best Local Similarity 76.9%; Pred. No. 2.1;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YEKYLGEYVAV 13
Db 672 YEKYLGEYVAV 684

RESULT 6

Q8MWN8 PRELIMINARY; PRT; 704 AA.
AC Q8MWN8;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Lactoferrin (Fragment).
GN Name=Lf;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Wang S.-R., Lin T.-Y., Weng C.-N.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
bind ferric iron in association with the binding of an anion,
usually bicarbonate (By similarity).
CC -1- DOMAIN: Composed of two homologous domains (By similarity).
CC -1- SIMILARITY: Belongs to the transferrin family.
DR EMBL; L77887; AAL40161.1; -.
DR HSSP; P24627; INKX.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
KW Iron transport; Metal-binding; Transport.
FT NON TER 1
SQ SEQUENCE 704 AA; 77681 MW; 64BE769F7503CC32 CRC64;

Query Match 82.4%; Score 56; DB 2; Length 704;
Best Local Similarity 76.9%; Pred. No. 2.1;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YEKYLGEYVAV 13
Db 672 YEKYLGEYVAV 684

RESULT 7

Q6Y739 PRELIMINARY; PRT; 704 AA.
AC Q6Y739;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Lactotransferrin.
GN Name=Lf;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;

Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Transferrins are iron binding transport proteins which
bind ferric iron in association with the binding of an anion,
usually bicarbonate (By similarity).
CC -1- DOMAIN: Composed of two homologous domains (By similarity).
CC -1- SIMILARITY: Belongs to the transferrin family.
DR EMBL; AP006185; BAD08651.1; -.
DR HSSP; Q29477; LFW1.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
KW Iron transport; Metal-binding; Transport.
SQ SEQUENCE 704 AA; 77611 MW; 10DFBA3C136D5DA CRC64;

Query Match 82.4%; Score 56; DB 2; Length 704;
Best Local Similarity 76.9%; Pred. No. 2.1;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YEKYLGEYVAV 13
Db 672 YEKYLGEYVAV 684

RESULT 8

Q7YS20 PRELIMINARY; PRT; 704 AA.
AC Q7YS20;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Lactoferrin.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Pecorini C., Fogher C., Baldi A.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
bind ferric iron in association with the binding of an anion,
usually bicarbonate (By similarity).
CC -1- DOMAIN: Composed of two homologous domains (By similarity).
CC -1- SIMILARITY: Belongs to the transferrin family.
DR EMBL; AY306198; AAF0487.1; -.
DR HSSP; P24627; INKX.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR Pfam; PF00405; Transferrin; 2.
DR InterPro; IPR001156; Peptidase_S60.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 1.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
KW Iron transport; Metal-binding; Transport.
SQ SEQUENCE 704 AA; 77522 MW; AAC8B176E5BF6A CRC64;

Query Match 82.4%; Score 56; DB 2; Length 704;
Best Local Similarity 76.9%; Pred. No. 2.1;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKYIGEEYKAV 13
 DB 672 YEKYIGEEYKAV 684

RESULT 9
 TRFL_CAPRI
 ID TRFL_CAPRI STANDARD, PRT, 708 AA.
 AC Q29477, Q29479, (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Lactoferrin precursor (Lactoferrin).
 GN Name-LTF;
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Capra.
 OC NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Lee T., Yu S., Kim S., Lee K., Yu D.;
 RL Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA MEDLINE=94380047; PubMed=8093048;
 RA le Provost F., Nocard M., Guerin G., Martin P.;
 RT "Characterization of the goat lactoferrin cDNA. Assignment of the
 RT relevant locus to bovine U2 synteny group".
 RL Biochem. Biophys. Res. Commun. 203:1334-1332(1994).
 CC -1- FUNCTION: Transferrins are iron binding proteins which
 CC can bind two atoms of ferric iron in association with the binding
 CC of an anion, usually bicarbonate.
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: Composed of two homologous domains.
 CC -1- SIMILARITY: Belongs to the transferrin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use. By non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL, US3857; AAA97958.1; -
 DR EMBL, X78902; CA55517.1; -
 DR PDB, 1UW1; X-ray; A=20-708.
 DR InterPro; IPR001156; Peptidase_S60.
 DR Pfam; PF00405; Transferrin; 2.
 DR SMART; SMO0094; TR_PRR; 2.
 DR PROSITE; PS00205; TRANSFERRIN_1; 2.
 DR PROSITE; PS00206; TRANSFERRIN_2; 2.
 DR 3D-structure; Glycoprotein; Iron transport; Metal-binding; Repeat;
 KW Signal; Transport.
 FT SIGNAL 1 19 By similarity.
 FT CHAIN 20 708 Lactotransferrin.
 FT REPEAT 20 363 1.
 FT REPEAT 364 708 2.
 FT DISULFID 28 64 By similarity.
 FT DISULFID 38 55 By similarity.
 FT DISULFID 134 217 By similarity.
 FT DISULFID 176 192 By similarity.
 FT DISULFID 189 200 By similarity.
 FT DISULFID 250 264 By similarity.
 FT DISULFID 367 399 By similarity.
 FT DISULFID 377 390 By similarity.

FT DISULFID 424 703 By similarity.
 FT DISULFID 444 666 By similarity.
 FT DISULFID 476 551 By similarity.
 FT DISULFID 500 694 By similarity.
 FT DISULFID 510 524 By similarity.
 FT DISULFID 521 534 By similarity.
 FT DISULFID 592 606 By similarity.
 FT DISULFID 644 649 By similarity.
 FT METAL 79 79 Iron 1 (By similarity).
 FT METAL 111 111 Iron 1 (By similarity).
 FT METAL 211 211 Iron 1 (By similarity).
 FT METAL 272 272 Iron 2 (By similarity).
 FT METAL 414 414 Iron 2 (By similarity).
 FT METAL 452 452 Iron 2 (By similarity).
 FT METAL 545 545 Iron 2 (By similarity).
 FT METAL 614 614 Carbonate 1 (By similarity).
 FT BINDING 140 140 Carbonate 1 (By similarity).
 FT BINDING 142 142 Carbonate 1 (via amide nitrogen) (By similarity).
 FT BINDING 143 143 Carbonate 1 (via amide nitrogen) (By similarity).
 FT BINDING 478 478 Carbonate 2 (By similarity).
 FT BINDING 482 482 Carbonate 2 (By similarity).
 FT BINDING 484 484 Carbonate 2 (via amide nitrogen) (By similarity).
 FT BINDING 485 485 Carbonate 2 (via amide nitrogen) (By similarity).
 FT CARBOHYD 252 252 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 300 300 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 387 387 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 495 495 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 554 554 I -> V (in Ref. 2).
 FT CONFLICT 56 56 L -> R (in Ref. 2).
 FT CONFLICT 88 88 Q -> K (in Ref. 2).
 FT CONFLICT 124 124 F -> P (in Ref. 2).
 FT CONFLICT 154 154 S -> R (in Ref. 2).
 FT CONFLICT 304 304 D -> G (in Ref. 2).
 FT CONFLICT 414 414
 SQ SEQUENCE 708 AA; 77358 MW; F2EDA3C83539960D CRC64;

Query Match
 Best Local Similarity 80.9%; Score 55; DB 1; Length 708;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKYIGEEYKAV 13
 DB 676 YEKYIGEEYKAV 688

RESULT 10
 Q8MTIO PRELIMINARY; PRT, 355 AA.
 AC Q8MTIO;
 DT 01-OCT-2002 (TRENBLREL. 22, Created)
 DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
 DE Lactotransferrin (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=91160550; PubMed=2001696;
 RA Pierce A., Colavizza D., Benalissa M., Maes P., Tartar A.,
 RA Montreuil J., Spik G.;
 RT "Molecular cloning and sequence analysis of bovine lactotransferrin".
 RL Eur. J. Biochem. 196:177-184(1991).
 CC -1- FUNCTION: Transferrins are iron binding transport proteins which
 CC bind ferric iron in association with the binding of an anion,
 CC usually bicarbonate (By similarity).
 CC -1- SIMILARITY: Belongs to the transferrin family.

```
DR EMBL; X17066; CAA34912.1; -.
DR HSSP; P24627; IBLF.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin_1.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 1.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 1.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
DR Iron transport; Metal-binding; Transport.
KW NON_TER
FT
SQ SEQUENCE 355 AA; 38861 MW; 92CF0C274EBC6893 CRC64;
Query Match 75.0%; Score 51; DB 2; Length 355;
Best Local Similarity 69.2%; Pred. No. 7.1;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 YEKYLGEYVYKAV 13
DB 323 YEKYLGEYVYTAI 335
RESULT 11
06LBN7 PRELIMINARY; PRT; 681 AA.
AC 06LBN7.
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Lactoferrin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary;
RZ MEDLINE=91086328; PubMed=2263492;
RA Mead P.E.; Tweedle J.W.;
RT "cDNA and protein sequence of bovine lactoferrin.";
RL Nucleic Acids Res. 18:7167-7167(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary;
RA Tweedle J.;
RL Submitted (JUN-1991) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC bind ferric iron in association with the binding of an anion,
CC usually bicarbonate (By similarity).
CC -1- DOMAIN: Composed of two homologous domains (By similarity).
CC EMBL; X54801; CAA38572.1; -.
DR HSSP; Q29477; IHW1.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin_2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW Iron transport; Metal-binding; Transport.
FT
CHAIN <1 681 Bovine Lactoferrin.
```

```
SQ SEQUENCE 681 AA; 75181 MW; 4927DE88144D99BA CRC64;
Query Match 75.0%; Score 51; DB 2; Length 681;
Best Local Similarity 69.2%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 YEKYLGEYVYKAV 13
DB 649 YEKYLGEYVYTAI 661
RESULT 12
TRFE_RAT STANDARD; PRT; 698 AA.
ID TRFE_RAT
AC P1346; O63602; O64628; O64630;
DT 01-OCT-1989 (Rel. 12, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Sero-transferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal
DE binding globulin).
GN Name=Trf;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RX [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=Mistar; TISSUE=Mammary gland;
RX MEDLINE=95234054; PubMed=7717992;
RA Becerra H., Pierce A., Coddeville B., Gonzalez F., Benaisa M.,
RA Leger D., Wieruszewski J.M., Spik G., Pambianco M.;
RT "Rat mammary-gland transferrin: nucleotide sequence, phylogenetic
RT analysis and glycan structure.";
RL Biochem. J. 307:47-55(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=Mistar; TISSUE=Liver;
RX MEDLINE=96208933; PubMed=8829802; DOI=10.1016/0305-0491(95)02068-3;
RA Hosino A., Hisayasu S., Shimada T.;
RT "Complete sequence analysis of rat transferrin and expression of
RT transferrin but not lactoferrin in the digestive glands.";
RL Comp. Biochem. Physiol. 113B:491-497(1996).
RN [3]
RP SEQUENCE OF 7-295 FROM N.A. (ISOFORM 2).
RX MEDLINE=84307580; PubMed=6236811;
RA Aldred A.R., Howlett G.J., Schreiber G.;
RT "Synthesis of rat transferrin in Escherichia coli containing a
RT recombinant bacteriophage.";
RL Biochem. Biophys. Res. Commun. 122:960-965(1984).
RN [4]
RP SEQUENCE OF 521-698 FROM N.A.
RX MEDLINE=87053639; PubMed=3023031;
RA Huggenvik J.T., Idzerda R.L., Haywood L., Lee D.C., McKnight G.S.,
RA Grissold M.D.;
RT "Transferrin messenger ribonucleic acid: molecular cloning and
RT hormonal regulation in rat Sertoli cells.";
RL Endocrinology 120:332-340(1987).
RN [5]
RP SEQUENCE OF 20-47.
RX MEDLINE=80049855; PubMed=500689;
RA Schreiber G., Dryburgh H., Millerlship A., Matsuda Y., Inglis A.,
RA Phillips J., Edwards K., Mages J.;
RT "The synthesis and secretion of rat transferrin.";
RL J. Biol. Chem. 254:12013-12019(1979).
RN [6]
RP SEQUENCE OF 20-30 AND 642-653.
RX PubMed=3046665;
RA Purves L.R., Purves M., Linton N., Brandt W., Johnson G., Jacobs P.;
RT "Properties of the transferrin associated with rat intestinal
RT mucosa.";
RL Biochim. Biophys. Acta 966:318-327(1988).
RN [7]
RP SEQUENCE OF 89-102; 232-243 AND 404-411.
```

CC PubMed:1791189; Cavanaugh P.G., Nicolson G.L.;
 RA "Lung-derived growth factor that stimulates the growth of lung-
 RT metastasizing tumor cells: identification as transferrin.";
 RL J. Cell. Biochem. 47:261-271(1991).
 CC -1- FUNCTION: Transferrins are iron binding transport proteins which
 can bind two atoms of ferric iron in association with the binding
 of an anion, usually bicarbonate. It is responsible for the
 transport of iron from sites of absorption and heme degradation to
 those of storage and utilization. Serum transferrin may also have
 a further role in stimulating cell proliferation.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS: Secreted.
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P12346-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P12346-2; Sequence=VSP_011840;
 CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
 CC -1- DOMAIN: Composed of two homologous domains.
 CC -1- SIMILARITY: Belongs to the transferrin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X77158; CA54403.1; -
 DR EMBL: D38380; BAA07458.1; -
 DR EMBL: M26113; AAA42266.1; -
 DR EMBL: M27966; AAA42267.1; -
 DR PIR: S49163; S49163.
 DR HSP: P19134; 1TFD.
 DR GlycoSuiteDB: P12346; -
 DR InterPro: IPR001156; Peptidase_S60.
 DR Pfam: PF00405; Transferrin; 2.
 DR PRINTS: PR00442; TRANSFERRIN.
 DR SMART: SMO0094; TR_PER; 2.
 DR PROSITE: PS00205; TRANSFERRIN_1; 1.
 DR PROSITE: PS00207; TRANSFERRIN_2; 2.
 DR PROSITE: PS00206; TRANSFERRIN_3; 2.
 KM Alternative splicing; Direct protein sequencing; Glycoprotein;
 iron transport; Metal-binding; Repeat; Signal; Transport.
 FT SIGNAL 1 19
 FT CHAIN 20 698 Serotransferrin..
 FT REPEAT 20 355 1.
 FT REPEAT 356 698 2.
 FT DISULFID 28 67 By similarity.
 FT DISULFID 38 58 By similarity.
 FT DISULFID 137 213 By similarity.
 FT DISULFID 156 350 By similarity.
 FT DISULFID 177 193 By similarity.
 FT DISULFID 180 196 By similarity.
 FT DISULFID 190 198 By similarity.
 FT DISULFID 246 260 By similarity.
 FT DISULFID 363 395 By similarity.
 FT DISULFID 373 336 By similarity.
 FT DISULFID 420 693 By similarity.
 FT DISULFID 435 656 By similarity.
 FT DISULFID 471 542 By similarity.
 FT DISULFID 495 684 By similarity.
 FT DISULFID 505 519 By similarity.
 FT DISULFID 516 525 By similarity.
 FT DISULFID 582 596 By similarity.
 FT DISULFID 634 639 By similarity.
 FT METAL 82 82 Iron 1 (By similarity).
 FT METAL 114 114 Iron 1 (By similarity).
 FT METAL 207 207 Iron 1 (By similarity).
 FT METAL 268 268 Iron 1 (By similarity).

FT METAL 410 410 Iron 2 (By similarity).
 FT METAL 447 447 Iron 2 (By similarity).
 FT METAL 536 536 Iron 2 (By similarity).
 FT METAL 604 604 Iron 2 (By similarity).
 FT BINDING 139 139 Carbonate 1 (By similarity).
 FT BINDING 143 143 Carbonate 1 (By similarity).
 FT BINDING 145 145 Carbonate 1 (via amide nitrogen) (By
 similarity).
 FT BINDING 146 146 Carbonate 1 (via amide nitrogen) (By
 similarity).
 FT BINDING 473 473 Carbonate 2 (By similarity).
 FT BINDING 477 477 Carbonate 2 (By similarity).
 FT BINDING 479 479 Carbonate 2 (via amide nitrogen) (By
 similarity).
 FT BINDING 480 480 Carbonate 2 (via amide nitrogen) (By
 similarity).
 FT CARBOHYD 512 512 N-linked (GlcNAc...) (Potential).
 FT VARSPLIC 65 266 Missing (in isoform 2).
 FT CONFLICT 57 57 A -> P (in Ref. 1).
 FT CONFLICT 110 110 P -> R (in Ref. 1).
 FT CONFLICT 318 354 ARGCGVPEPRMDYRLVGHSTYTAIRMGEGVCPEAS ->
 RGLRLAPKDGQAVPRPQLCHSKSKAGSCPDA (in
 Ref. 1).
 FT CONFLICT 380 380 S -> G (in Ref. 1).
 FT CONFLICT 691 691 E -> D (in Ref. 4).
 FT CONFLICT 696 697 HK -> TA (in Ref. 4).
 SQ SEQUENCE 698 AA; 76363 MW; DDF2C1918B2A1B0E CRC64;
 Query Match Score 51; DB 1; Length 698;
 Best Local Similarity 69.2%; Pred. No. 13;
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YEKYLGEYKAV 13
 DB 666 YEEYLGAEYLGAV 678
 RESULT 13
 Q7TNXO PRELIMINARY; PRT; 698 AA.
 AC Q7TNXO;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Liver regeneration-related protein LRKG03.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Xu C.S., Li W.Q., Li Y.C., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,
 RA Yang K.J., Yan H.M., Chang C.F., Zhao L.F., Ma H., Wang L., Wang S.F.,
 RA Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
 RL Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Transferrins are iron binding transport proteins which
 bind ferric iron in association with the binding of an anion,
 usually bicarbonate (By similarity).
 CC -1- DOMAIN: Composed of two homologous domains (By similarity).
 CC -1- SIMILARITY: Belongs to the transferrin family.
 CC EMBL: AY327504; AAP97736.1; -
 DR HSP: P02787; 1BP9.
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0008199; F:ferric iron binding; IEA.
 DR GO: GO:0006879; P:iron ion homeostasis; IEA.
 DR GO: GO:0006826; P:iron ion transport; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR001156; Peptidase_S60.
 DR Pfam: PF00405; Transferrin; 2.
 DR SMART: SMO0094; TR_PER; 2.
 DR PROSITE: PS00205; TRANSFERRIN_1; 1.
 DR PROSITE: PS00206; TRANSFERRIN_2; 2.

DR PROSITE: PS00207; TRANSFERRIN_3; 2.
 KM Iron transport; Metal-binding; Transport.
 SQ SEQUENCE 698 AA; 76395 MW; B91ABB41C447194 CRC64;
 Query Match 75.0%; Score 51; DB 2; Length 698;
 Best Local Similarity 69.2%; Pred. No. 13;
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 YEKYLGEYKAV 13
 ||:|||||:
 DB 666 YEKYLGEYKAV 678

RESULT 14
 ICA_PIG STANDARD; PRT; 704 AA.
 AC Q29545;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Inhibitor of carbonic anhydrase precursor.
 GN Name=ICA;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=97254619; PubMed=9100029; DOI=10.1021/b19627424;
 RA Wuebbens M.W., Roush E.D., Decastro C.M., Fierke C.A.;
 RT "Cloning, sequencing, and recombinant expression of the porcine
 RT inhibitor of carbonic anhydrase: a novel member of the transferrin
 RT family";
 RL Biochemistry 36:4327-4336(1997).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=93099129; PubMed=1463741;
 RA Roush E.D., Fierke C.A.;
 RT "Purification and characterization of a carbonic anhydrase II
 RT inhibitor from porcine plasma";
 RL Biochemistry 31:12536-12542(1992).
 CC -1- FUNCTION: Specifically binds and inhibits carbonic anhydrase II
 CC with nanomolar affinity.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Plasma.
 CC -1- DOMAIN: Composed of two homologous domains.
 CC -1- PTM: N-glycosylated.
 CC -1- SIMILARITY: Belongs to the transferrin family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: U36916; AA58956.1; -.
 DR PIR: I47228; I47228.
 DR HSBP: P09571; I4728.
 DR InterPro: IPR001156; Peptidase_S60.
 DR Pfam: PF00405; Transferrin; 2.
 DR PRINTS: PR00422; TRANSFERRIN.
 DR SMART: SM00094; TR_FER; 2.
 DR PROSITE: PS00205; TRANSFERRIN_1; 2.
 DR PROSITE: PS00206; TRANSFERRIN_2; 1.
 DR PROSITE: PS00207; TRANSFERRIN_3; 2.
 KW Direct protein sequencing; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 704 Inhibitor of carbonic anhydrase.
 FT REPEAT 20 351 1.
 FT REPEAT 352 704 2.

FT DISULFID 28 67 By similarity.
 FT DISULFID 38 58 By similarity.
 FT DISULFID 137 213 By similarity.
 FT DISULFID 172 188 By similarity.
 FT DISULFID 175 196 By similarity.
 FT DISULFID 185 198 By similarity.
 FT DISULFID 246 260 By similarity.
 FT DISULFID 360 392 By similarity.
 FT DISULFID 370 383 By similarity.
 FT DISULFID 417 699 By similarity.
 FT DISULFID 440 662 By similarity.
 FT DISULFID 472 549 By similarity.
 FT DISULFID 496 690 By similarity.
 FT DISULFID 506 520 By similarity.
 FT DISULFID 517 532 By similarity.
 FT DISULFID 589 603 By similarity.
 FT CARBOHYD 491 491 By similarity.
 SQ SEQUENCE 704 AA; 77634 MW; 16BBO651931E336 CRC64; (Potential).

OY 1 YEKYLGEYKAV 13
 ||:|||||:
 DB 672 YEKYLGEYKAV 684

Query Match 75.0%; Score 51; DB 1; Length 704;
 Best Local Similarity 61.5%; Pred. No. 13;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

RESULT 15
 TRFL_BOVIN STANDARD; PRT; 708 AA.
 ID TRFL_BOVIN Q29629; Q9MZX3;
 AC P24627; Q29629; Q9MZX3;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Lactotransferrin precursor (lactoferrin) [Contains: lactoferricin B
 DE (Lactin B)].
 GN Name=LTF;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Submaxillary gland;
 RX MEDLINE=91160550; PubMed=2001696;
 RA Pierce A., Colavizza D., Benalissa M., Maes P., Tartar A.,
 RA Montreuil J., Spik G.;
 RT "Molecular cloning and sequence analysis of bovine lactotransferrin";
 RL Eur. J. Biochem. 196:177-184(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92028986; PubMed=1718281;
 RA Goodman R.E., Schanbacher F.L.;
 RT "Bovine lactoferrin mRNA: sequence, analysis, and expression in the
 RT mammary gland";
 RL Biochem. Biophys. Res. Commun. 180:75-84(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Tsang T.C., Burns D.K., Wang F., Pan Y.C.E., Schmidt A.M., Stern D.;
 RT "Cloning of a 80-kD advanced glycosylated end product (AGE) binding
 RT protein from bovine lung";
 RL FASEB J. 6:233-233(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood; and Mammary gland;
 RX MEDLINE=94266164; PubMed=8206385; DOI=10.1016/0378-1119(94)90108-2;
 RA Seyfert H.-M., Tuckoritz A., Interthal H., Koczan D., Hobom G.;
 RT "Structure of the bovine lactoferrin-encoding gene and its promoter";
 RL Gene 143:265-269(1994).
 RN [5]

CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
 CC alcohols. The antibodies allow direct detection of CDT in solution,
 CC eliminating the need for immobilizing it on a solid phase (as required
 CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
 CC fragments used in the method of the invention.

CC Sequence 13 AA;

Query Match 100.0%; Score 68; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00036; Mismatches 0; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYLGEERYV 13
 |||||
 DB 1 YEKYLGEERYV 13

RESULT 2
 AAAY24760
 ID AAAY24760 standard; peptide; 12 AA.

AC AAAY24760;

DT 24-AUG-1999 (first entry)

DE Lactoferrin duodecapeptide #10.

KM Lactoferrin; LF; human; monoclonal antibody; hybridoma cell line; IGM;

KM Immunoglobulin M; HIV-1; AIDS.

OS Synthetic.

PN MO9926656-A1.

PD 03-JUN-1999.

PF 24-NOV-1998; 98WO-US025258.

PR 24-NOV-1997; 97US-0066464P.

PA (HUMA-) INST HUMAN GENETICS & BIOCHEMISTRY.

PI Rodman TC;

DR WPI. 1999-394785/33.

PT New hybridoma cell lines producing monoclonal human natural IGM
 PT antibodies.

PS Example 2; Page 15; 52pp; English.

CC The present invention describes hybridoma cell lines having the following
 CC accession numbers: (a) ATCC CRU-12431 (I); (b) ATCC CRU 12477 (II); and
 CC (c) ATCC CRU 12472 (III), producing monoclonal forms of human natural IGM
 CC antibodies. These are useful for treating HIV-1 infected individuals.
 CC Methods from the present invention can be used treating, or increasing
 CC CD4+T cells, in a patient suffering from an infection caused by HIV-1, by
 CC administering the human IGM monoclonal antibodies produced by (II) and
 CC (III) cells individually or together. The antibodies can be used as
 CC positive controls in assays for prognosing the onset of AIDS. The present
 CC sequence represents a lactoferrin peptide from an example of the present
 CC invention

CC Sequence 12 AA;

Query Match 67.6%; Score 46; DB 2; Length 12;
 Best Local Similarity 80.0%; Pred. No. 1.2; Mismatches 1; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YEKYLGEERYV 10
 |||||
 DB 2 YEKYLGEERYV 11

RESULT 3
 ADR15983
 ID ADR15983 standard; peptide; 8 AA.

AC ADR15983;

DT 04-NOV-2004 (first entry)

DE Transferrin peptide fragment #141.

KM glycosylation; proteolytic enzyme; proteolysis; detection; transferrin.

OS Synthetic.

PN WO2004070389-A1.

PD 19-AUG-2004.

PF 06-FEB-2004; 2004WO-GB000480.

PR 06-FEB-2003; 2003GB-00002740.

PA (AXIS-) AXIS-SHIELD ASA.

PI Rye PD;

DR WPI; 2004-625547/60.

PT Assay for differentiating protein isoforms to determine their
 PT concentrations in sample e.g. blood, involves contacting the sample with
 PT proteolytic enzyme to produce peptide fragment by proteolysis followed by
 PT detecting.

PS Disclosure; Page 18; 30pp; English.

CC The present invention describes an assay for a protein having at least
 CC two isoforms with different glycosylation patterns. The assay involves
 CC contacting a sample containing the protein with a proteolytic enzyme,
 CC followed by detecting the content or relative content of at least one
 CC peptide fragment produced by proteolysis. Also described is a kit for the
 CC assay method comprising the proteolytic enzyme and a substrate bound
 CC specific binding partner (S1) for at least 2 of the isoforms of the
 CC proteins. The method can be used for assaying isoforms of proteins
 CC according to their glycosylation pattern to determine their concentration
 CC or relative concentration in the sample or material (e.g. blood). The
 CC method avoids use of antibodies for distinguishing between glycosylated
 CC isoforms of the proteins. The present sequence represents a transferrin
 CC peptide fragment which is used in the exemplification of the present
 CC invention.

CC Sequence 8 AA;

Query Match 63.2%; Score 43; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 YLGEERYV 11
 |||||
 DB 1 YLGEERYV 8

RESULT 4
 ADR15928
 ID ADR15928 standard; peptide; 8 AA.

AC ADR15928;

DT 04-NOV-2004 (first entry)

DE Transferrin peptide fragment #86.

KM glycosylation; proteolytic enzyme; proteolysis; detection; transferrin.

XX OS Synthetic.
XX PN WO2004070389-A1.
XX PD 19-AUG-2004.
XX PF 06-FEB-2004; 2004WO-GB000480.
XX PR 06-FEB-2003; 2003GB-00002740.
XX PA (AXIS-) AXIS-SHIELD ASA.
XX PI Rye PD;
XX DR WPI; 2004-625547/60.
XX PT Assay for differentiating protein isoforms to determine their
PT concentrations in sample e.g. blood, involves contacting the sample with
PT proteolytic enzyme to produce peptide fragment by proteolysis followed by
PT detecting.
XX PS Disclosure; Page 16; 30pp; English.
XX CC The present invention describes an assay for a protein having at least
CC two isoforms with different glycosylation patterns. The assay involves
CC contacting a sample containing the protein with a proteolytic enzyme,
CC followed by detecting the content or relative content of at least one
CC peptide fragment produced by proteolysis. Also described is a kit for the
CC assay method comprising the proteolytic enzyme and a substrate bound
CC specific binding partner (S1) for at least 2 of the isoforms of the
CC proteins. The method can be used for assaying isoforms of proteins
CC according to their glycosylation pattern to determine their concentration
CC or relative concentration in the sample or material (e.g. blood). The
CC method avoids use of antibodies for distinguishing between glycosylated
CC isoforms of the proteins. The present sequence represents a transferrin
CC peptide fragment which is used in the exemplification of the present
CC invention.
XX CC
XX SQ Sequence 8 AA;
XX
XX Query Match 63.2%; Score 43; DB 8; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 YLGEYVK 11
XX |||||
XX 1 YLGEYVK 8
XX DB
XX
XX RESULT 5
XX ADS13391
XX ID ADS13391 standard; peptide; 8 AA.
XX AC ADS13391;
XX XX
XX DT 16-DEC-2004 (first entry)
XX DE Human rheumatoid arthritis marker peptide - SEQ ID 182.
XX KM Rheumatoid arthritis; marker; antiinflammatory; antiarthritic.
XX OS Homo sapiens.
XX PN WO2004082617-A2.
XX PD 30-SEP-2004.
XX PF 15-MAR-2004; 2004WO-US007880.
XX PR 14-MAR-2003; 2003US-0455037P.
XX PA (SURR-) SURROMED INC.

XX PI Kantor AB, Becker CH, Schulman H;
XX DR WPI; 2004-690929/67.
XX PT New isolated marker for rheumatoid arthritis, useful in preparing a
XX PT composition for diagnosing or treating rheumatoid arthritis.
XX PS Claim 1; SEQ ID NO 182; 184pp; English.
XX CC The invention relates to a novel isolated marker for rheumatoid arthritis
XX CC selected from one of many (around 400) markers defined in the
XX CC specification. Rheumatoid arthritis is a chronic inflammatory disorder of
XX CC the small joints which is estimated to affect 2.1 million people in the
XX CC United States alone. Current approaches to treat the disease include the
XX CC use of non-steroidal antiinflammatory drugs (NSAIDs), which may reduce
XX CC pain, swelling and inflammation, and disease-modifying anti-rheumatic
XX CC drugs (DMARDs), which act to slow the progression of the disease and
XX CC avoid further joint injury. These drugs are associated with a number of
XX CC serious side effects and the search for improved therapeutics is a
XX CC subject of active research. The marker of the invention demonstrates
XX CC antiarthritic activity and may be useful in preparing a composition for
XX CC diagnosing or treating rheumatoid arthritis. The current sequence is that
XX CC of a human rheumatoid arthritis marker peptide of the invention.
XX
XX SQ Sequence 8 AA;
XX
XX Query Match 63.2%; Score 43; DB 8; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 YLGEYVK 11
XX |||||
XX 1 YLGEYVK 8
XX DB
XX
XX RESULT 6
XX ABP99131
XX ID ABP99131 standard; peptide; 12 AA.
XX AC ABP99131;
XX XX
XX DT 18-MAR-2003 (first entry)
XX DE ErbB2 cell overexpression EOP1-120 peptide SEQ ID NO:241.
XX KM ErbB2; cancer; oncogene; ErbB2 overexpression-associated protein isoform;
XX KM EOP1; EOP; ErbB2 overexpression feature; cytosstatic; vaccine;
XX KM gene therapy.
XX OS Homo sapiens.
XX PN WO200290991-A2.
XX PD 14-NOV-2002.
XX PF 02-MAY-2002; 2002WO-GB002047.
XX PR 03-MAY-2001; 2001GB-00010886.
XX PR 23-NOV-2001; 2001GB-00028183.
XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX PI Herath HMAc, Page MJ;
XX DR WPI; 2003-103531/09.
XX PT Diagnosing and treating ErbB2-related cancer, comprises generating ErbB2
XX PT Overexpression Features (EOPs) from test samples from a subject by
XX PT electrophoresis, and comparing the EOPs in the sample with a
XX PT predetermined reference range.
XX PS Claim 3; Page 22; 106pp; English.

XX The present invention describes a method for screening or diagnosing
CC ErbB2-related cancer. The method comprises generating ErbB2
CC overexpression features (EOPs) from test samples of body fluid from the
CC subject by electrophoresis, and comparing the EOPs in the test sample
CC with that from normal subjects or with an expression reference feature
CC (ERP) in the test sample. Also described: (1) an antibody capable of
CC immunospecific binding to an ErbB2 overexpression protein isoform (EOP1);
CC (2) pharmaceutical compositions comprising an EOP1, a nucleic acid
CC encoding an EOP1, an amount of the above antibody or its fragment, and a
CC carrier; (3) a kit comprising one or more antibodies and/or EOPs cited
CC above, other reagents and instructions for use; (4) methods of treating
CC or preventing ErbB2-related cancer; (5) methods of screening for or
CC identifying agents that interact with or modulate the expression or
CC activity of one or more EOPs; EOP1 fragment, EOP1-related polypeptides,
CC or EOP1-fusion proteins; (6) a method for modulating the activity of one
CC or more of the ErbB2 EOPs, comprising administering to a subject an
CC agent identified by the method of (5); and (7) a method for identifying
CC targets for therapeutic modulation of ErbB2-related cancer. EOPs have
CC cytostatic activity and can be used in vaccines and gene therapy. The
CC method is useful in screening, diagnosing, preventing or treating ErbB2-
CC related cancer, determining the stage or severity of ErbB2-related
CC cancer, identifying a subject at risk of developing ErbB2-related cancer,
CC monitoring the effect of therapy administered to a subject with ErbB2-
CC related cancer, and for drug screening or drug development. The kit is
CC useful in carrying out the above methods. ABP98940 to ABP99206 represent
CC specifically claimed EOPs from the present invention

XX Sequence 12 AA;

Query Match 63.2%; Score 43; DB 6; Length 12;
Best Local Similarity 54.5%; Pred. No. 3.7;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 YEKYIGSEYVK 11
|:|:|:|:|:
Db 2 YDSYLGDDYVR 12

RESULT 7

AAV41865 ID AAV41865 standard; peptide; 12 AA.

AC AAV41865;

DT 09-DEC-1999 (first entry)

XX Rheumatoid arthritis diagnostic protein isoform peptide #16.

XX Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection;

KW rheumatoid arthritis diagnostic feature; ERP1; synovial fluid;

KM rheumatoid arthritis diagnostic protein isoform; screening;

XX expression reference protein isoform; prognosis.

XX Homo sapiens.

OS WO9947925-A2.

PN 23-SEP-1999.

PF 15-MAR-1999; 99WO-GB000763.

PR 13-MAR-1998; 98GB-00005477.

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Parekh RB, Patel TP, Townsend RR;

XX WPI; 1999-571871/48.

PT Diagnosis of human rheumatoid arthritis by two-dimensional
XX electrophoresis.

PS Disclosure; Page 18; 157pp; English.

XX A method has been developed for the diagnosis of human rheumatoid
CC arthritis (RA) using two-dimensional electrophoresis to generate a two-
CC dimensional array of features. The method can be used for screening,
CC diagnosis and prognosis of RA in a subject or for monitoring the effect
CC of an anti-RA drug or therapy administered to a subject. The method
CC comprises: (a) analysing a sample of serum or plasma and optionally
CC synovial fluid by two-dimensional electrophoresis, to generate a two-
CC dimensional array of features; (b) identifying at least one chosen
CC feature whose relative abundance correlates with the presence or absence
CC of RA; and (c) comparing the abundance of each chosen feature in the
CC sample with the abundance of that chosen feature in serum or plasma from
CC one or more persons without RA, where the relative abundance of the
CC chosen feature or features in the sample indicates the presence or
CC absence of RA in the subject. The method can also be used in clinical
CC studies for testing drugs for therapy of RA, for purification of RA-
CC diagnostic protein isoforms (RPIs), and for production of antibodies to
CC RPIs. The RA-diagnostic feature (RADF) proteins can be used to identify
CC compounds that promote or inhibit their activity, which are then used as
CC RA drugs. Nucleic acid encoding RADFs can be used in gene therapy
CC protocols. AAV41844 to AAV42100 represent RPI peptides, AAV42101 to
CC AAV42103 represent expression reference protein isoform peptides and
CC AA225066 to AA225068 represent degenerate probes for RPIs, which are all
CC used in the exemplification of the present invention

XX Sequence 12 AA;

Query Match 54.4%; Score 37; DB 2; Length 12;
Best Local Similarity 70.0%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 YLGEYVKAV 13
|:|:|:|:|:
Db 2 YLGEYVTAI 11

RESULT 8

AAV41864 ID AAV41864 standard; peptide; 12 AA.

AC AAV41864;

DT 09-DEC-1999 (first entry)

XX Rheumatoid arthritis diagnostic protein isoform peptide #15.

XX Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection;

KW rheumatoid arthritis diagnostic feature; ERP1; synovial fluid;

KM rheumatoid arthritis diagnostic protein isoform; screening;

XX expression reference protein isoform; prognosis.

XX Homo sapiens.

OS WO9947925-A2.

PN 23-SEP-1999.

PF 15-MAR-1999; 99WO-GB000763.

PR 13-MAR-1998; 98GB-00005477.

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Parekh RB, Patel TP, Townsend RR;

XX WPI; 1999-571871/48.

PT Diagnosis of human rheumatoid arthritis by two-dimensional
XX electrophoresis.

PS Disclosure; Page 18; 157pp; English.

CC A method has been developed for the diagnosis of human rheumatoid
CC arthritis (RA) using two-dimensional electrophoresis to generate a two-
CC dimensional array of features. The method can be used for screening,
CC diagnosis and prognosis of RA in a subject or for monitoring the effect
CC of an anti-RA drug or therapy administered to a subject. The method
CC comprises: (a) analyzing a sample of serum or plasma and optionally
CC synovial fluid by two-dimensional electrophoresis, to generate a two-
CC dimensional array of features; (b) identifying at least one chosen
CC feature whose relative abundance correlates with the presence or absence
CC of RA; and (c) comparing the abundance of each chosen feature in the
CC sample with the abundance of that chosen feature in serum or plasma from
CC one or more persons without RA, where the relative abundance of the
CC chosen feature or features in the sample indicates the presence or
CC absence of RA in the subject. The method can also be used in clinical
CC studies for testing drugs for therapy of RA, for purification of RA-
CC diagnostic protein isoforms (RPIs), and for production of antibodies to
CC RPIs. The RA-diagnostic feature (RADF) proteins can be used to identify
CC compounds that promote or inhibit their activity, which are then used as
CC RA drugs. Nucleic acid encoding RADFs can be used in gene therapy
CC protocols. AA141844 to AA142100 represent RPI peptides, AA142101 to
CC AA142103 represent expression reference protein isoform peptides and
CC AA225066 to AA225068 represent degenerate probes for RPIs, which are all
CC used in the exemplification of the present invention
XX

SQ Sequence 12 AA;

Query Match 54.4%; Score 37; DB 2; Length 12;
Best Local Similarity 70.0%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 YIGSEYVYKAV 13
Db 2 YIGSEYVYTAI 11

RESULT 9
AD15914

ID AD15914 standard; peptide; 12 AA.

XX AD15914;

XX 04-NOV-2004 (first entry)

XX DE Transferrin peptide fragment #72.

XX glycosylation; proteolytic enzyme; proteolysis; detection; transferrin.

XX Synthetic.

XX WO2004070389-A1.

XX 19-AUG-2004.

XX 06-FEB-2004; 2004WO-GB000480.

XX 06-FEB-2003; 2003GB-00002740.

XX (AXIS-) AXIS-SHIELD ASA.

XX Rye PD;

XX MPI; 2004-625547/60.

XX Assay for differentiating protein isoforms to determine their

XX concentrations in sample e.g. blood, involves contacting the sample with

XX proteolytic enzyme to produce peptide fragment by proteolysis followed by

XX detecting.

XX Disclosure; Page 15; 30pp; English.

XX The present invention describes an assay for a protein having at least

XX two isoforms with different glycosylation patterns. The assay involves

XX contacting a sample containing the protein with a proteolytic enzyme,

CC followed by detecting the content or relative content of at least one
CC peptide fragment produced by proteolysis. Also described is a kit for the
CC assay method comprising the proteolytic enzyme and a substrate bound
CC specific binding partner (S1) for at least 2 of the isoforms of the
CC proteins. The method can be used for assaying isoforms of proteins
CC according to their glycosylation pattern to determine their concentration
CC or relative concentration in the sample or material (e.g. blood). The
CC method avoids use of antibodies for distinguishing between glycosylated
CC isoforms of the proteins. The present sequence represents a transferrin
CC peptide fragment which is used in the exemplification of the present
XX invention.

SQ Sequence 12 AA;

Query Match 54.4%; Score 37; DB 8; Length 12;
Best Local Similarity 70.0%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 YIGSEYVYKAV 13
Db 2 YIGSEYVYTAI 11

RESULT 10
AD13240

ID AD13240 standard; peptide; 12 AA.

XX AD13240;

XX 16-DEC-2004 (first entry)

XX DE Human rheumatoid arthritis marker peptide - SEQ ID 31.

XX rheumatoid arthritis; marker; antiinflammatory; antiarthritic.

XX Homo sapiens.

XX WO2004082617-A2.

XX 30-SEP-2004.

XX 15-MAR-2004; 2004WO-US007880.

XX 14-MAR-2003; 2003US-0455037P.

XX (SURR-) SURROMED INC.

XX Kantor AB, Becker CH, Schulman H;

XX MPI; 2004-690929/67.

XX New isolated marker for rheumatoid arthritis, useful in preparing a

XX composition for diagnosing or treating rheumatoid arthritis.

XX Claim 1; SEQ ID NO 31; 184pp; English.

CC The invention relates to a novel isolated marker for rheumatoid arthritis
CC selected from one of many (around 400) markers defined in the
CC specification. Rheumatoid arthritis is a chronic inflammatory disorder of
CC the small joints which is estimated to affect 2.1 million people in the
CC United States alone. Current approaches to treat the disease include the
CC use of non-steroidal antiinflammatory drugs (NSAIDs), which may reduce
CC pain, swelling and inflammation, and disease-modifying anti-rheumatic
CC drugs (DMARDs), which act to slow the progression of the disease and
CC avoid further joint injury. These drugs are associated with a number of
CC serious side effects and the search for improved therapeutics is a
CC subject of active research. The marker of the invention demonstrates
CC antiarthritic activity and may be useful in preparing a composition for
CC diagnosing or treating rheumatoid arthritis. The current sequence is that
CC of a human rheumatoid arthritis marker peptide of the invention.

SQ Sequence 12 AA;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 4 YLGEEYKAV 13
||| |||
DB 2 YLGHSYVTAL 11

RESULT 13

AAAB14919
ID AAB14919 standard; peptide; 10 AA.

AAAB14919;

DT 11-JAN-2001 (first entry)

DE Random 27-mer library peptide R6-52.

KM RNA-protein fusion; protein library; protein isolation; gene cloning;

KW myc epitope tag.

OS Synthetic.

PN WO200047775-A1.

PD 17-AUG-2000.

PF 01-FEB-2000; 2000WO-US002589.

PR 09-FEB-1999; 99US-00247190.

PA (GENO) GEN HOSPITAL CORP.

PI Szoetbak JW, Roberts RW, Liu R;

DR WPI; 2000-533022/48.

PT Producing protein or DNA libraries which are useful for improving
PT existing proteins, by in vitro translating protein coding sequences to
PT produce RNA-protein fusions and incubating these protein fusions under
PT high salt conditions.

PS Disclosure; Fig 22; 121pp; English.

XX The present sequence was isolated from an RNA-protein fusion library
CC following selection for peptides that bound to a c-myc monoclonal
CC antibody. RNA-protein fusions comprise a protein covalently linked to the
CC 3' end of its own mRNA. The fusions are made by synthesis and in vitro or
CC in situ translation of an mRNA molecule with a peptide acceptor attached
CC to its 3' end. The RNA-protein fusions are incubated under high salt
CC conditions to produce a protein library. This method is useful for
CC improving or altering existing proteins, as well as for isolating new
CC proteins and nucleic acid or small molecule targets. It may also be used
CC to improve human or humanised single-chain antibodies for the treatment
CC of a number of diseases. The method is useful for the isolation of
CC proteins with specific binding properties, for screening cDNA libraries
CC and cloning new genes on the basis of protein-protein interactions.
CC Unlike prior art, the new method does not rely on maintaining the
CC integrity of an mRNA:ribosome:nascent chain ternary complex, which is
CC very fragile and is therefore of limited use. The method does not rely on
CC topological links between the protein and the nucleic acid so that the
CC information of the protein is retained and can be recovered in readable,
CC nucleic acid form

XX Sequence 10 AA;

Query Match 44.1%; Score 30; DB 3; Length 10;

Best Local Similarity 66.7%; Pred. No. 3.8e+02;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 EKYLGEEYV 10
|:|:|:|:|
DB 1 EBYLVSEYV 9

RESULT 14

AAAY04623

ID AAY04623 standard; peptide; 10 AA.

AAAY04623;

DT 22-JUN-1999 (first entry)

DE Factor VII catalytic domain-interacting peptide #23.

KM Receptor; catalytic domain; Factor VII; epidermal growth factor-2; EGF-2;

KW tissue factor; blood clotting disorder; thrombosis; restenosis;

KW myocardial infarction; angina; reoclusion; cerebrovascular disease;

KW peripheral arterial occlusive disease; hypercoagulability;

KW pulmonary embolism; anticoagulant; cyclic.

OS Synthetic.

PN WO9913063-A1.

PD 18-MAR-1999.

PF 08-SEP-1998; 98WO-GB002701.

PR 09-SEP-1997; 97GB-00019162.

PA (NYCO-) NYCOMED IMAGING AS.

PI (MATT/) MATTHEWS D P.

PI Sakariassen KS, Orning L, Fischer PM;

DR WPI; 1999-229234/19.

PT New anticoagulant compounds for coagulating blood clotting disorders.
PT Claim 10; Page 37; 46pp; English.

XX Peptides AAY04601-Y04623 represent claimed compounds which are capable of
CC interacting with an internal receptor in the catalytic domain of Factor
CC VII (FVII) defined by the residues Leu263, Pro264, Glu265, Phe268,
CC Ser269, Tyr357 and Arg353 or a ligand defined by residues Cys98-Cys102 of
CC the epidermal growth factor-2 (EGF-2) domain of FVIIa/tissue factor (TF)
CC complex, with the exclusion of the peptide from amino acids 82-128 of
CC FVII. The compounds can be used to prevent the formation of a functional
CC FVIIa/TF complex, so can be used to combat or prevent blood clotting
CC disorders, e.g. thrombosis (particularly vascular thrombosis or deep vein
CC thrombosis), acute myocardial infarction, restenosis, angina, reoclusion,
CC cerebrovascular disease, peripheral arterial occlusive disease,
CC hypercoagulability or pulmonary embolism. They can also be used to
CC prevent the occurrence of blood clotting disorders caused by e.g.
CC grafting surgery, vessel wall potency restoration or sepsis

XX Sequence 10 AA;

Query Match 42.6%; Score 29; DB 2; Length 10;

Best Local Similarity 62.5%; Pred. No. 5.6e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 EKYLGEEYV 9
|:|:|:|:|
DB 2 EBYGSGSY 9

RESULT 15

```

AAy04647
ID  AAy04647 standard, peptide, 10 AA.
XX
AC  AAy04647;
XX
DT  22-JUN-1999 (first entry)
XX
DE  Factor IXa/Xa catalytic domain-interacting peptide #23.
XX
KM  Receptor, catalytic domain, Factor IXa, Factor Xa, tissue factor, angina,
KM  blood clotting disorder; thrombosis; restenosis; myocardial infarction;
KM  reclosure; cerebrovascular disease; hypercoagulability; anticoagulant;
KM  peripheral arterial occlusive disease; pulmonary embolism; cyclic.
XX
OS  Synthetic.
XX
FH  Key
FH  Modified-site
FT  1
FT  /note= "peptide is cyclic due to a lactam bond between
FT  the side chains of residues 1 and 10"
FT  10
FT  /note= "peptide is cyclic due to a lactam bond between
FT  the side chains of residues 1 and 10"
XX
PN  WO9913062-A1.
XX
PD  18-MAR-1999.
XX
PF  08-SEP-1998; 98WO-GB002700.
XX
PR  09-SEP-1997; 97GB-00019157.
XX
PA  (NYCO-) NYCOMED IMAGING AS.
XX  (MATT/) MATTHEWS D P.
XX
PI  Sakariassen KS, Fischer PM,
XX
DR  WPI, 1999-215061/18.
XX
PT  New anticoagulant compounds for treating blood clotting disorder capable
PT  of interacting with internal receptor.
XX
PS  Claim 10; Page 38; 50pp; English.
XX
CC  Peptides AAy04625-Y04647 represent claimed compounds which are capable of
CC  interacting with an internal receptor in the catalytic domain of Factor
CC  IXa (FIXa) or Factor X (FX) defined by the residues Ile290, Ala291,
CC  Asp292, Tyr293, Thr294, Glu374 and Phe378 of FIXa, and Leu300, Pro301,
CC  Glu302, Tyr305, Ala306, Lys385 and Phe389 of FXa, or the ligand defined
CC  by residues Cys95-Cys99 of FIXa or Cys96-Cys100 of FXa. The compounds can
CC  be used to prevent the formation of a functional FVIIa/FIXa or
CC  FVIIa/FXa complex, so can be used to combat or prevent blood clotting
CC  disorders, e.g. thrombosis (particularly vascular thrombosis or deep vein
CC  thrombosis), acute myocardial infarction, restenosis, angina, reclosure,
CC  cerebrovascular disease, peripheral arterial occlusive disease,
CC  hypercoagulability or pulmonary embolism. They can also be used to
CC  prevent the occurrence of blood clotting disorders caused by e.g.
CC  grafting surgery, vessel wall potency restoration or sepsis
XX
SQ  Sequence 10 AA;

Query Match 42.6%; Score 29; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. NO. 5.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY  2 EKYLGEEY 9
    | : | | | : |
DB  2 EYGGGEQY 9

```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 14:26:15 ; Search time 42 seconds
(without alignments)
23.106 Million cell updates/sec

Title: US-10-612-162A-4
Perfect score: 68
Sequence: 1 YEKYLGEYVAV 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 143084

Minimum DB seq length: 0
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/pdata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/pdata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/pdata/1/1aa/5A_COMB.pep:*
- 4: /cgn2_6/pdata/1/1aa/5B_COMB.pep:*
- 5: /cgn2_6/pdata/1/1aa/PCTUS_COMB.pep:*
- 6: /cgn2_6/pdata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	ID	Description
1	46	67.6	12	4	US-09-462-118-22
2	29	42.6	12	1	US-07-954-213-24
3	28	41.2	11	4	US-10-053-485-21
4	28	41.2	12	4	US-09-462-118-21
5	27	39.7	10	3	US-09-187-859-1150
6	27	39.7	10	4	US-09-839-542B-1150
7	27	39.7	11	1	US-08-082-844-8
8	27	39.7	11	5	PCT-US94-07040-8
9	27	39.7	12	4	US-08-728-742A-41
10	27	39.7	12	4	US-08-728-742A-68
11	26	38.2	9	3	US-09-171-654-65
12	26	38.2	9	3	US-09-171-654-66
13	26	38.2	10	4	US-09-755-630B-185
14	26	38.2	12	1	US-07-954-213-11
15	26	38.2	12	1	US-07-954-213-17
16	26	38.2	12	1	US-07-954-213-18
17	26	38.2	12	1	US-07-954-213-19
18	26	38.2	12	1	US-07-954-213-20
19	26	38.2	12	1	US-07-954-213-21
20	26	38.2	12	1	US-07-954-213-22
21	26	38.2	12	1	US-07-954-213-23
22	26	38.2	12	1	US-08-196-989B-6
23	26	38.2	12	4	US-08-760-935-6
24	26	38.2	12	4	US-09-225-024-6
25	25	36.8	8	3	US-09-187-859-1102
26	25	36.8	8	3	US-09-187-859-1230
27	25	36.8	8	4	US-09-839-542B-1102

28	25	36.8	8	4	US-09-839-542B-1230	Sequence 1230, Ap
29	25	36.8	10	3	US-09-187-859-1104	Sequence 1104, Ap
30	25	36.8	10	3	US-09-187-859-1192	Sequence 1192, Ap
31	25	36.8	10	3	US-09-187-859-1232	Sequence 1232, Ap
32	25	36.8	10	3	US-09-187-859-2361	Sequence 2361, Ap
33	25	36.8	10	4	US-09-839-542B-1104	Sequence 1104, Ap
34	25	36.8	10	4	US-09-839-542B-1192	Sequence 1192, Ap
35	25	36.8	10	4	US-09-839-542B-1232	Sequence 1232, Ap
36	25	36.8	10	4	US-09-839-542B-2361	Sequence 2361, Ap
37	25	36.8	12	4	US-09-091-071-8	Sequence 8, Appl
38	24	35.3	9	1	US-08-266-514-30	Sequence 30, Appl
39	24	35.3	9	2	US-08-654-604-30	Sequence 30, Appl
40	24	35.3	9	3	US-08-341-018-40	Sequence 40, Appl
41	24	35.3	9	3	US-08-470-335-216	Sequence 216, App
42	24	35.3	9	3	US-08-470-335-216	Sequence 216, App
43	24	35.3	9	4	US-08-467-602-410	Sequence 410, App
44	24	35.3	9	4	US-08-411-295F-35	Sequence 35, Appl
45	24	35.3	9	4	US-08-411-295F-89	Sequence 89, Appl

ALIGNMENTS

RESULT 1
US-09-462-118-22
; Sequence 22, Application US/09462118
; Patent No. 6610833
; GENERAL INFORMATION:
; APPLICANT: Rodman, Toby C.
; TITLE OF INVENTION: Monoclonal Human Natural Antibodies
; FILE REFERENCE: 4436/1C074-US1
; CURRENT APPLICATION NUMBER: US/09/462,118
; CURRENT FILING DATE: 1999-12-18
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Human
US-09-462-118-22

Query Match 67.6%; Score 46; DB 4; Length 12;
Best Local Similarity 80.0%; Pred. No. 0.089;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEKYLGEYV 10
DB 2 YEKYLGPQYV 11

RESULT 2
US-07-954-213-24
; Sequence 24, Application US/07954213
; Patent No. 5387504
; GENERAL INFORMATION:
; APPLICANT: Mumford, Richard A.
; APPLICANT: Lark, Michael W.
; APPLICANT: Bayne, Ellen B.K.
; APPLICANT: Heitner, Lori A.
; TITLE OF INVENTION: MONOSPECIFIC ANTIBODIES AND ASSAY SYSTEM
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/954,213
FILING DATE: 19920930
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W. III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 18842
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4720
TELEFAX: (908) 594-3905
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-954-213-24

Query Match 42.6%; Score 29; DB 1; Length 12;
Best Local Similarity 55.6%; Pred. No. 84;
Matches 5; Conservative 2; Mismatches 2; Gaps 0;

OY 4 YLGEYVKA 12
| | | | |
Db 1 YTGEDVDA 9

RESULT 3
US-10-053-485-21
Sequence 21, Application US/10053485
Patent No. 6576896
GENERAL INFORMATION:
APPLICANT: Figeys, Daniel
APPLICANT: Aebersold, Ruedi
TITLE OF INVENTION: ELECTROSMOTIC FLUIDIC DEVICE AND RELATED METHODS
FILE REFERENCE: UMOT118617
CURRENT APPLICATION NUMBER: US/10/053,485
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: US 09/209,880
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: US 60/069,398
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 21
LENGTH: 11
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-10-053-485-21

Query Match 41.2%; Score 28; DB 4; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 KYLGEYVYK 11
| | | | |
Db 3 KDLGEHFK 11

RESULT 4
US-09-462-118-21
Sequence 21, Application US/09462118
Patent No. 6610833
GENERAL INFORMATION:
APPLICANT: Rodman, Toby C.
TITLE OF INVENTION: Monoclonal Human Natural Antibodies
FILE REFERENCE: 4436/1C074-US1
CURRENT APPLICATION NUMBER: US/09/462,118
CURRENT FILING DATE: 1999-12-18
NUMBER OF SEQ ID NOS: 36

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 21
LENGTH: 12
TYPE: PRT
ORGANISM: Human
US-09-462-118-21

Query Match 41.2%; Score 28; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYL 5
| | | | |
Db 8 YEKYL 12

RESULT 5
US-09-187-859-1150
Sequence 1150, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gout, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1150
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence
US-09-187-859-1150

Query Match 39.7%; Score 27; DB 3; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 EKYLGEYVYK 11
| | | | |
Db 1 EFKLEBYTK 10

RESULT 6
US-09-839-542B-1150
Sequence 1150, Application US/09839542B
Patent No. 6569996
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Gout, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100086.407D1
CURRENT APPLICATION NUMBER: US/09/839,542B
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1150
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence
US-09-839-542B-1150

Query Match 39.7%; Score 27; DB 4; Length 10;

Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EKYLGEEYK 11
| : | | | |
Db 1 EYFLLEBYTK 10

RESULT 7

US-08-082-844-8
Sequence 8, Application US/08082844
Patent No. 5443978

GENERAL INFORMATION:

APPLICANT: Ellenberger, Suzanne R.
APPLICANT: Peiser, Galen D.
APPLICANT: Bell, Russell N.
APPLICANT: Husey Jr., Charles E.
APPLICANT: Shatuck-Bidens, Donna M.
APPLICANT: Swedlund, Bradley D.
TITLE OF INVENTION: Chrysanthenyl Diphosphate Synthase,
TITLE OF INVENTION: Corresponding Genes and Use in Pyrethrin Synthesis
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: United States of America
ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,844
FILING DATE: 19930625

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Caruthers, Jennie M.
REGISTRATION NUMBER: 34,464
REFERENCE/DOCKET NUMBER: 22-90A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
TELEX: 823189

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..11
OTHER INFORMATION: /label=Xaa
OTHER INFORMATION: /note="Xaa equals residues which could not be
OTHER INFORMATION: identified with certainty."
US-08-082-844-8

Query Match 39.7%; Score 27; DB 1; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YEKYLGEEY 9
| | | | |
Db 3 YEDYESNEY 11

RESULT 8
PCT-US94-07040-8
Sequence 8, Application PC/TUS9407040

GENERAL INFORMATION:
APPLICANT: Ellenberger, Suzanne R.
APPLICANT: Peiser, Galen D.
APPLICANT: Bell, Russell N.
APPLICANT: Husey Jr., Charles E.
APPLICANT: Shatuck-Bidens, Donna M.
APPLICANT: Swedlund, Bradley D.
TITLE OF INVENTION: Chrysanthenyl Diphosphate Synthase,
TITLE OF INVENTION: Corresponding Genes and Use in Pyrethrin Synthesis
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: United States of America
ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07040
FILING DATE: 21-JUNE-1994

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/082,844
FILING DATE: 25-JUNE-1993

ATTORNEY/AGENT INFORMATION:

NAME: Caruthers, Jennie M.
REGISTRATION NUMBER: 34,464
REFERENCE/DOCKET NUMBER: 22-90A PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
TELEX: 823189

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..11
OTHER INFORMATION: /label=Xaa
OTHER INFORMATION: /note="Xaa equals residues which could not be
OTHER INFORMATION: identified with certainty."
PCT-US94-07040-8

Query Match 39.7%; Score 27; DB 5; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YEKYLGEEY 9
| | | | |
Db 3 YEDYESNEY 11

RESULT 9

US-08-728-742A-41
Sequence 41, Application US/08728742A
Patent No. 6579695

GENERAL INFORMATION:

APPLICANT: Ralph H. Lambalot, Amy M. Gehring, Ralph Reid and Christopher T. Wals
TITLE OF INVENTION: PHOSPHOPANTETHEINYL TRANSFERASES AND USES THEREOF
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESSES:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston

STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,742A
FILING DATE: October 11, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,152
FILING DATE: October 13, 1995
APPLICATION NUMBER: 60/021,650
FILING DATE: July 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: HMI-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
US-08-728-742A-41

Query Match 39.7%; Score 27; DB 4; Length 12;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 EBYKAV 13
| : || :
Db 5 ESYIKAI 11

RESULT 10
US-08-728-742A-68
Sequence 68, Application US/08728742A
Patent No. 6579695
GENERAL INFORMATION:
APPLICANT: Ralph H. Lambalot, Amy M. Gehring, Ralph Reid and Christopher T. Wales
TITLE OF INVENTION: PHOSPHOPANTHETHEINYL TRANSFERASES AND USES THEREOF
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,742A
FILING DATE: October 11, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,152
FILING DATE: October 13, 1995
APPLICATION NUMBER: 60/021,650
FILING DATE: July 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: HMI-015

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
US-08-728-742A-68

Query Match 39.7%; Score 27; DB 4; Length 12;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 EBYKAV 13
| : || :
Db 5 ESYIKAI 11

RESULT 11
US-09-171-654-65
Sequence 65, Application US/09171654A
Patent No. 6239107
GENERAL INFORMATION:
APPLICANT: FRIDKIN, Matilyahu
TITLE OF INVENTION: CONJUGATES OF LIPOPHILIC MOETIES AND FRAGMENTS OF
FILE REFERENCE: GOZES-4
CURRENT APPLICATION NUMBER: US/09/171,654A
CURRENT FILING DATE: 1999-04-29
EARLIER APPLICATION NUMBER: PCT/IL97/00129
EARLIER FILING DATE: 1997-04-18
EARLIER APPLICATION NUMBER: IL 118003
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 65
LENGTH: 9
TYPE: PPT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism:Artificial
OTHER INFORMATION: the C-terminal residue is amidated;
OTHER INFORMATION: residue 5 is aminocaproic acid.
US-09-171-654-65

Query Match 38.2%; Score 26; DB 3; Length 9;
Best Local Similarity 44.4%; Pred. No. 4.1e+05;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 EBYLGEYV 10
: ||| : :
Db 1 KXYLKKYL 9

RESULT 12
US-09-171-654-66
Sequence 66, Application US/09171654A
Patent No. 6239107
GENERAL INFORMATION:
APPLICANT: GOZES, Illana
APPLICANT: FRIDKIN, Matilyahu
TITLE OF INVENTION: CONJUGATES OF LIPOPHILIC MOETIES AND FRAGMENTS OF
FILE REFERENCE: GOZES-4
CURRENT APPLICATION NUMBER: US/09/171,654A
CURRENT FILING DATE: 1999-04-29
EARLIER APPLICATION NUMBER: PCT/IL97/00129

```
/ EARLIER FILING DATE: 1997-04-18
/ EARLIER APPLICATION NUMBER: IL 118003
/ EARLIER FILING DATE: 1996-04-23
/ NUMBER OF SEQ ID NOS: 80
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO: 66
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism: Artificial
/ FEATURE:
/ OTHER INFORMATION: The N-terminus is modified with a stearyl moiety;
/ OTHER INFORMATION: the C-terminal residue is amidated;
/ OTHER INFORMATION: residue 5 is aminoisauric acid.
US-09-171-654-66

Query Match          38.2%; Score 26; DB 3; Length 9;
Best Local Similarity 44.4%; Pred. No. 4.1e+05;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      2 EKYLGEEYV 10
       :|||:|:|:
Db      1 KKYLKXKYL 9

RESULT 13
US-09-755-630B-185
/ Sequence 185, Application US/09755630B
/ Patent No. 6639054
/ GENERAL INFORMATION:
/ APPLICANT: ALIBHAI, MURTAZA F.
/ APPLICANT: ASTWOOD, JAMES D.
/ APPLICANT: SAMPSON, HUGH A.
/ APPLICANT: MCHESTER, CHARLES A.
/ TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTINS
/ FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
/ CURRENT APPLICATION NUMBER: US/09/755,630B
/ CURRENT FILING DATE: 2001-01-05
/ PRIOR APPLICATION NUMBER: US 60/174,669
/ PRIOR FILING DATE: 2000-01-06
/ NUMBER OF SEQ ID NOS: 295
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO: 185
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic polypeptide
US-09-755-630B-185

Query Match          38.2%; Score 26; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 EKYLGEEYV 11
       :|||:|:|:
Db      1 EKYTAQCCK 10

RESULT 14
US-07-954-213-11
/ Sequence 11, Application US/07954213
/ Patent No. 5387504
/ GENERAL INFORMATION:
/ APPLICANT: Mumford, Richard A.
/ APPLICANT: Lark, Michael W.
/ APPLICANT: Bayne, Ellen B.K.
/ APPLICANT: Hoerner, Lori A.
/ TITLE OF INVENTION: MONOSPECIFIC ANTIBODIES AND ASSAY SYSTEM
/ TITLE OF INVENTION: FOR DETECTING STROMELYSIN CLEAVAGE PRODUCTS
/ NUMBER OF SEQUENCES: 24
/ CORRESPONDENCE ADDRESS:
```

```
/ ADDRESSEE: Merck & Co., Inc.
/ STREET: 126 E. Lincoln Avenue
/ CITY: Rahway
/ STATE: NJ
/ COUNTRY: USA
/ ZIP: 07065
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/954,213
/ FILING DATE: 19920930
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Wallien, John W. III
/ REGISTRATION NUMBER: 35,403
/ REFERENCE/DOCKET NUMBER: 18842
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (908) 594-3905
/ TELEFAX: (908) 594-4720
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 amino acids
/ TYPE: AMINO ACID
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-07-954-213-11

Query Match          38.2%; Score 26; DB 1; Length 12;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      4 YLGEDEV 10
       :|||:|:|:
Db      1 YTGEDFV 7

RESULT 15
US-07-954-213-17
/ Sequence 17, Application US/07954213
/ Patent No. 5387504
/ GENERAL INFORMATION:
/ APPLICANT: Mumford, Richard A.
/ APPLICANT: Lark, Michael W.
/ APPLICANT: Bayne, Ellen B.K.
/ APPLICANT: Hoerner, Lori A.
/ TITLE OF INVENTION: MONOSPECIFIC ANTIBODIES AND ASSAY SYSTEM
/ TITLE OF INVENTION: FOR DETECTING STROMELYSIN CLEAVAGE PRODUCTS
/ NUMBER OF SEQUENCES: 24
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Merck & Co., Inc.
/ STREET: 126 E. Lincoln Avenue
/ CITY: Rahway
/ STATE: NJ
/ COUNTRY: USA
/ ZIP: 07065
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/954,213
/ FILING DATE: 19920930
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Wallien, John W. III
/ REGISTRATION NUMBER: 35,403
/ REFERENCE/DOCKET NUMBER: 18842
/ TELECOMMUNICATION INFORMATION:
```

Tue Nov 1 17:05:18 2005

TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-954-213-17

Query Match 38.2%; Score 26; DB 1; Length 12;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 YLGEYV 10
| | | | |
Db 1 YTGEDFV 7

Search completed: November 1, 2005, 14:41:34
Job time : 43 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 14:32:10 ; Search time 162 Seconds

(without alignments)
33.547 Million cell updates/sec

Title: US-10-612-162a-4

Perfect score: 68

Sequence: 1 YEKYLGEYVKAV 13

Scoring table: BLOSUM62

Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 285352

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Database : Published Applications AA.*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	13	US-10-612-162-4	Sequence 4, Appli
2	46	67.6	12	US-10-247-946-22	Sequence 22, Appli
3	46	67.6	12	US-10-251-526-22	Sequence 22, Appli
4	43	63.2	8	US-10-801-990-182	Sequence 182, App
5	43	63.2	12	US-10-700-330-241	Sequence 241, App
6	37	54.4	12	US-10-801-990-31	Sequence 31, Appli
7	34	50.0	12	US-10-033-741-41	Sequence 41, Appli
8	34	50.0	12	US-10-033-662-41	Sequence 41, Appli
9	30	44.1	13	US-10-823-253-3	Sequence 3, Appli
10	30	44.1	13	US-10-823-810-3	Sequence 3, Appli
11	28	41.2	9	US-10-482-284A-11	Sequence 11, Appli

12	28	41.2	9	US-10-482-284A-25	Sequence 25, Appli
13	28	41.2	9	US-10-482-284A-28	Sequence 28, Appli
14	28	41.2	9	US-10-505-929-8	Sequence 8, Appli
15	28	41.2	10	US-10-464-576-1	Sequence 1, Appli
16	28	41.2	11	US-10-053-485-21	Sequence 21, Appli
17	28	41.2	12	US-09-991-800-2	Sequence 2, Appli
18	28	41.2	12	US-10-247-946-21	Sequence 21, Appli
19	28	41.2	12	US-10-251-526-21	Sequence 21, Appli
20	27	39.7	10	US-10-006-869-1150	Sequence 1150, Ap
21	27	39.7	10	US-10-395-032-1150	Sequence 1150, Ap
22	27	39.7	10	US-11-004-107-1150	Sequence 1150, Ap
23	26	38.2	9	US-10-948-707-221	Sequence 221, App
24	26	38.2	10	US-09-572-404B-976	Sequence 976, App
25	26	38.2	10	US-09-755-630A-185	Sequence 185, App
26	26	38.2	10	US-10-209-372-36	Sequence 36, App
27	26	38.2	10	US-10-658-180-185	Sequence 185, App
28	26	38.2	11	US-10-239-313A-76	Sequence 76, Appli
29	26	38.2	13	US-10-280-139-11	Sequence 11, Appli
30	25	36.8	8	US-10-006-869-1102	Sequence 1102, Ap
31	25	36.8	8	US-10-006-869-1230	Sequence 1230, Ap
32	25	36.8	8	US-10-395-032-1102	Sequence 1102, Ap
33	25	36.8	8	US-10-395-032-1230	Sequence 1230, Ap
34	25	36.8	8	US-11-004-107-1102	Sequence 1102, Ap
35	25	36.8	8	US-11-004-107-1230	Sequence 1230, Ap
36	25	36.8	9	US-10-119-536A-109	Sequence 109, App
37	25	36.8	9	US-10-128-520-29	Sequence 29, Appli
38	25	36.8	9	US-10-275-652-50	Sequence 50, Appli
39	25	36.8	9	US-10-948-707-682	Sequence 682, App
40	25	36.8	10	US-09-840-277-128	Sequence 128, App
41	25	36.8	10	US-10-006-869-1104	Sequence 1104, Ap
42	25	36.8	10	US-10-006-869-1192	Sequence 1192, Ap
43	25	36.8	10	US-10-006-869-1232	Sequence 1232, Ap
44	25	36.8	10	US-10-006-869-2361	Sequence 2361, Ap
45	25	36.8	10	US-10-395-032-1104	Sequence 1104, Ap

ALIGNMENTS

RESULT 1
US-10-612-162-4
; Sequence 4, Application US/10612162
; Publication No. US20040014145A1
; GENERAL INFORMATION:
; APPLICANT: Dade Behring Marburg GmbH
; TITLE OF INVENTION: Carbohydrate deficient transferrin (CDT) -specific
; FILE REFERENCE: 2002/B001
; CURRENT APPLICATION NUMBER: US/10/612,162
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 10230550.1
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 03011334.4
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-162-4

Query Match 100.0%; Score 68; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
| | | | | | | | | | | | |
Db 1 YEKYLGEYVKAV 13

RESULT 2
US-10-247-946-22

```
; Sequence 22, Application US/10247946
; Publication No. US20030144485A1
; GENERAL INFORMATION:
; APPLICANT: Rodman, Toby C.
; TITLE OF INVENTION: Monoclonal Human Natural Antibodies
; FILE REFERENCE: 4436/1C074-US1
; CURRENT APPLICATION NUMBER: US/10/247,946
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/462,118
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Human
US-10-247-946-22
```

```
Query Match      67.6% Score 46; DB 14; Length 12;
Best Local Similarity 80.0%; Pred. No. 0.72;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy 1 YEKYLGEERYV 10
    |||||:
Db 2 YEKYLGPQYV 11
```

RESULT 3
US-10-251-526-22

```
; Sequence 22, Application US/10251526
; Publication No. US20030144486A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Rodman, Toby C.
; TITLE OF INVENTION: Monoclonal Human Natural Antibodies
; FILE REFERENCE: 4436/1C074-US1
; CURRENT APPLICATION NUMBER: US/10/251,526
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/462,118
; PRIOR FILING DATE: 1999-12-18
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Human
US-10-251-526-22
```

```
Query Match      67.6% Score 46; DB 14; Length 12;
Best Local Similarity 80.0%; Pred. No. 0.72;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy 1 YEKYLGEERYV 10
    |||||:
Db 2 YEKYLGPQYV 11
```

RESULT 4
US-10-801-990-182

```
; Sequence 182, Application US/10801990
; Publication No. US20050048574A1
; GENERAL INFORMATION:
; APPLICANT: Kantor, Aaron B.
; APPLICANT: Schulman, Howard
; APPLICANT: Becker, Christopher
; TITLE OF INVENTION: BIOMARKERS FOR RHEUMATOID ARTHRITIS
; FILE REFERENCE: SURR.121
; CURRENT APPLICATION NUMBER: US/10/801,990
; PRIOR FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US 60/455,037
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 182
```

```
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-801-990-182
```

```
Query Match      63.2% Score 43; DB 17; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 4 YLGEERYK 11
    |||||
Db 1 YLGEERYK 8
```

RESULT 5
US-10-700-330-241

```
; Sequence 241, Application US/10700330
; Publication No. US20040203022A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Mudiyanselage Alhula Chandrasiri Herath
; APPLICANT: Page, Martin John
; TITLE OF INVENTION: Proteins and Genes for Diagnosis And Treatment of ErbB2-Related C
; FILE REFERENCE: 2543-1-031
; CURRENT APPLICATION NUMBER: US/10/700,330
; PRIOR FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: GB 0110886.9
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: GB 0128183.1
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 241
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-700-330-241
```

```
Query Match      63.2% Score 43; DB 16; Length 12;
Best Local Similarity 54.5%; Pred. No. 2.3;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy 1 YEKYLGEERYK 11
    |||||:
Db 2 YDSYLGDDYVR 12
```

RESULT 6
US-10-801-990-31

```
; Sequence 31, Application US/10801990
; Publication No. US20050048574A1
; GENERAL INFORMATION:
; APPLICANT: Kantor, Aaron B.
; APPLICANT: Schulman, Howard
; APPLICANT: Becker, Christopher
; TITLE OF INVENTION: BIOMARKERS FOR RHEUMATOID ARTHRITIS
; FILE REFERENCE: SURR.121
; CURRENT APPLICATION NUMBER: US/10/801,990
; PRIOR FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US 60/455,037
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-801-990-31
```

```
Query Match      54.4% Score 37; DB 17; Length 12;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy 4 YLGEERYKAV 13
```


Db 2 YLGEYVTAI 11

RESULT 7
US-10-033-741-41
; Sequence 41, Application US/10033741
; Publication No. US20030049640A1
; GENERAL INFORMATION:
; APPLICANT: Herman, et al.
; TITLE OF INVENTION: Proteins, Genes and Their Use For Diagnosis and Treatment of Vasc
; FILE REFERENCE: 9195-079
; CURRENT APPLICATION NUMBER: US/10/033,741
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-033-741-41

Query Match 50.0%; Score 34; DB 14; Length 12;
Best Local Similarity 60.0%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 YLGEYVKAV 13
Db 2 YLGHSTVTAI 11

RESULT 8
US-10-033-662-41
; Sequence 41, Application US/10033662
; Publication No. US20030092197A1
; GENERAL INFORMATION:
; APPLICANT: Herman, et al.
; TITLE OF INVENTION: Proteins, Genes and Their Use For Diagnosis and Treatment of Card
; FILE REFERENCE: 9195-081
; CURRENT APPLICATION NUMBER: US/10/033,662
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-033-662-41

Query Match 50.0%; Score 34; DB 14; Length 12;
Best Local Similarity 60.0%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 YLGEYVKAV 13
Db 2 YLGHSTVTAI 11

RESULT 9
US-10-823-253-3
; Sequence 3, Application US/10823253
; Publication No. US20050002934A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Jennifer
; TITLE OF INVENTION: RECOMBINANT IL-9 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 10271-112-999
; CURRENT APPLICATION NUMBER: US/10/823,253
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: 60/462,259
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/477,797

; PRIOR FILING DATE: 2003-06-10
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-823-253-3

Query Match 44.1%; Score 30; DB 17; Length 13;
Best Local Similarity 62.5%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 YLGEYVK 11
Db 3 YYGSDYVK 10

RESULT 10
US-10-823-810-3
; Sequence 3, Application US/10823810
; Publication No. US20050147607A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Jennifer
; TITLE OF INVENTION: METHODS OF PREVENTING OR TREATING RESPIRATORY CONDITIONS
; FILE REFERENCE: 10271-113-999
; CURRENT APPLICATION NUMBER: US/10/823,810
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: 60/462,307
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/477,801
; PRIOR FILING DATE: 2003-06-10
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-823-810-3

Query Match 44.1%; Score 30; DB 18; Length 13;
Best Local Similarity 62.5%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 YLGEYVK 11
Db 3 YYGSDYVK 10

RESULT 11
US-10-482-284A-11
; Sequence 11, Application US/10482284A
; Publication No. US20050019344A1
; GENERAL INFORMATION:
; APPLICANT: KHANNA, Rajiv
; APPLICANT: ELKINGTON, Rebecca A.
; APPLICANT: WALKER, Susan J.
; TITLE OF INVENTION: Novel human cytomegalovirus (HCMV) cytotoxic T cell epitopes, ct
; TITLE OF INVENTION: polypeptides, compositions comprising same and diagnostic and ct
; FILE REFERENCE: 47-203
; CURRENT APPLICATION NUMBER: US/10/482,284A
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: AU PR5931
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 318
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human cytomegalovirus pp65 C

OTHER INFORMATION: epitope peptide
US-10-482-284A-11

Query Match 41.2%; Score 28; DB 17; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 5 LGEEYVK 11
:|::|||
Db 2 IGDQYVK 8

RESULT 12
US-10-482-284A-25

Sequence 25, Application US/10482284A
Publication No. US20050019344A1

GENERAL INFORMATION:

APPLICANT: KHANNA, Rajiv

APPLICANT: ELKINGTON, Rebecca A.

APPLICANT: WALKER, Susan J.

TITLE OF INVENTION: Novel human cytomegalovirus (HCMV) cytotoxic T cell epitopes,

TITLE OF INVENTION: polypeptides, compositions comprising same and diagnostic and th

FILE REFERENCE: 47-203

CURRENT APPLICATION NUMBER: US/10/482,284A

PRIOR FILING DATE: 2003-12-29

PRIOR APPLICATION NUMBER: AU PR5931

PRIOR FILING DATE: 2001-06-26

NUMBER OF SEQ ID NOS: 318

SOFTWARE: PatentIn version 3.2

SEQ ID NO 25

LENGTH: 9

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: human cytomegalovirus pp65

US-10-482-284A-25

Query Match 41.2%; Score 28; DB 17; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 5 LGEEYVK 11
:|::|||
Db 1 IGDQYVK 7

RESULT 13
US-10-482-284A-28

Sequence 28, Application US/10482284A
Publication No. US20050019344A1

GENERAL INFORMATION:

APPLICANT: KHANNA, Rajiv

APPLICANT: ELKINGTON, Rebecca A.

APPLICANT: WALKER, Susan J.

TITLE OF INVENTION: Novel human cytomegalovirus (HCMV) cytotoxic T cell epitopes,

TITLE OF INVENTION: polypeptides, compositions comprising same and diagnostic and th

FILE REFERENCE: 47-203

CURRENT APPLICATION NUMBER: US/10/482,284A

PRIOR FILING DATE: 2003-12-29

PRIOR APPLICATION NUMBER: AU PR5931

PRIOR FILING DATE: 2001-06-26

NUMBER OF SEQ ID NOS: 318

SOFTWARE: PatentIn version 3.2

SEQ ID NO 28

LENGTH: 9

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: human cytomegalovirus pp65

US-10-482-284A-28

Query Match 41.2%; Score 28; DB 17; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 5 LGEEYVK 11
:|::|||
Db 3 IGDQYVK 9

RESULT 14
US-10-505-929-8

Sequence 8, Application US/10505929
Publication No. US20050221381A1

GENERAL INFORMATION:

APPLICANT: KLADE, CHRISTOF

APPLICANT: SCHALICH, JULIANE

APPLICANT: VYTYTSKA, ORESTA

APPLICANT: AICHINGER, GERALD

APPLICANT: OTAVA, ALEXANDER

APPLICANT: MATTER, FRANK

TITLE OF INVENTION: METHOD FOR ISOLATING LIGANDS

FILE REFERENCE: SONN:055US

CURRENT APPLICATION NUMBER: US/10/505,929

PRIOR FILING DATE: 2004-08-27

PRIOR APPLICATION NUMBER: PCT/EP03/02005

PRIOR FILING DATE: 2003-02-27

PRIOR APPLICATION NUMBER: A 316/2002

PRIOR FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: A 1376/2002

PRIOR FILING DATE: 2002-09-13

NUMBER OF SEQ ID NOS: 584

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 8

LENGTH: 9

TYPE: PRT

ORGANISM: Cytomegalovirus

US-10-505-929-8

Query Match 41.2%; Score 28; DB 18; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 5 LGEEYVK 11
:|::|||
Db 2 IGDQYVK 8

RESULT 15
US-10-464-576-1

Sequence 1, Application US/10464576
Publication No. US20040188603A1

GENERAL INFORMATION:

APPLICANT: Bateman, Robert H

APPLICANT: Bateman, Robert H

APPLICANT: Langridge, James I

APPLICANT: McKenna, Therese

APPLICANT: Richardson, Keith

TITLE OF INVENTION: Method of Mass Spectrometry and a Mass Spectrometer

FILE REFERENCE: deH055

CURRENT APPLICATION NUMBER: US/10/464,576

PRIOR FILING DATE: 2003-06-19

PRIOR APPLICATION NUMBER: uk 0217146.0

PRIOR FILING DATE: 2002-07-24

PRIOR APPLICATION NUMBER: uk 0218719.3

PRIOR FILING DATE: 2002-08-12

PRIOR APPLICATION NUMBER: uk 0221914.5

PRIOR FILING DATE: 2002-09-20

PRIOR APPLICATION NUMBER: uk 0305796.5

PRIOR FILING DATE: 2003-03-13

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIn version 3.2

SEQ ID NO 1
 LENGTH: 10
 TYPE: PRT
 ORGANISM: unknown
 FEATURE:
 OTHER INFORMATION: Chemically synthesized
 US-10-464-576-1

Query Match 41.2%; Score 28; DB 16; Length 10;
 Best Local Similarity 66.7%; Pred. No. 5.6e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KYLGEEYVK 11
 | |||:
 Db 2 KDLGSEHFK 10

Search completed: November 1, 2005, 14:46:02
 Job time : 163 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 14:21:39 ; Search time 38 Seconds
(without alignments)
32.916 Million cell updates/sec

Title: US-10-612-162a-4

Sequence: 1 YEKYLGEYVKAV 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1828

Minimum DB seq length: 0
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79 : *
1: PIR1 : *
2: PIR2 : *
3: PIR3 : *
4: PIR4 : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	26	38.2	12	2 PH0746	T-cell receptor be
2	26	38.2	12	2 PH0771	T-cell receptor be
3	26	38.2	13	2 PH1479	T-cell receptor be
4	23	33.8	9	2 PH0108	late G1-69 protein
5	23	33.8	12	2 S25056	Ig heavy chain - m
6	20	29.4	10	2 PT0215	T-cell receptor be
7	20	29.4	11	2 PT0214	T-cell receptor be
8	20	29.4	13	2 S47359	T-cell antigen rec
9	20	29.4	13	2 S47361	T-cell antigen rec
10	20	29.4	13	2 S47365	T-cell antigen rec
11	20	29.4	13	2 S47368	T-cell antigen rec
12	20	29.4	13	2 S47372	T-cell antigen rec
13	20	29.4	13	2 S47383	T-cell antigen rec
14	20	29.4	13	2 S47384	T-cell antigen rec
15	20	29.4	13	2 S47374	T-cell antigen rec
16	19	27.9	11	2 A58838	hemolysin - Porphy
17	19	27.9	13	2 E60396	antigen 7H8/2 - ma
18	18	26.5	9	2 S70334	endospore protein,
19	18	26.5	9	2 PT0324	Ig heavy chain CRD
20	18	26.5	10	2 S62880	polygalacturonase
21	18	26.5	10	2 A24867	scyllosporin I - s
22	18	26.5	11	2 S68392	H+-transporting tw
23	18	26.5	11	2 I60434	68kDa neurofilamen
24	18	26.5	12	2 C49315	urease (EC 3.5.1.5
25	18	26.5	13	2 A32734	enkephalin precurs
26	18	26.5	13	2 G44644	neurotoxin-associa
27	17	25.0	6	2 S11556	hydrogensulfite re
28	17	25.0	8	2 PN0043	phosphatidylethano
29	17	25.0	9	2 PT0315	Ig heavy chain CRD

30	17	25.0	10	2 A13687	caerulein-like pep
31	17	25.0	11	2 B60769	Ig H2 chain - Pac1
32	17	25.0	12	2 S18722	mark protein - bee
33	17	25.0	12	2 PH1466	T-cell receptor be
34	17	25.0	13	2 PT0263	Ig heavy chain CRD
35	17	25.0	13	2 PT0290	Ig heavy chain CRD
36	17	25.0	13	2 S47373	T-cell antigen rec
37	16	23.5	7	2 A38081	amine oxidase (cop
38	16	23.5	9	2 E41978	callifMRamide 5 -
39	16	23.5	9	2 F41978	callifMRamide 6 -
40	16	23.5	9	2 G41978	callifMRamide 7 -
41	16	23.5	9	2 A37027	macrophage chemotr
42	16	23.5	11	2 PH1375	T antigen variant
43	16	23.5	12	2 PH1308	Ig heavy chain DJ
44	16	23.5	12	2 S23168	Z protein - guinea
45	16	23.5	12	2 T46794	hypothetical prote

ALIGNMENTS

RESULT 1
PH0746
T-cell receptor beta chain (B28) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C/Accession: PH0746
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-related allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; MUID:92078846; PMID:1836010
A/Accession: PH0746
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>
A/Cross-references: EMBL:X60837; NID:950098; PIDN:CAA43230.1; PID:950099
A/Experimental source: T lymphocyte
C/Keywords: T-cell receptor

Query Match
Best Local Similarity 38.2%; Score 26; DB 2; Length 12;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEKYL 6
DB 7 YEQYFG 12
RESULT 2
PH0771
T-cell receptor beta chain (P25.1.1) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C/Accession: PH0771
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-related allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; MUID:92078846; PMID:1836010
A/Accession: PH0771
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>
A/Cross-references: EMBL:X60865; NID:953624; PIDN:CAA43255.1; PID:953625
A/Experimental source: T lymphocyte
C/Keywords: T-cell receptor

Query Match
Best Local Similarity 38.2%; Score 26; DB 2; Length 12;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 3
PH1479
T-cell receptor beta chain (clone A3/72.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004
C:Accession: PH1479
R:Caenova, J.L.; Marillon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Kc
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatih
A:Reference number: PH1430; MUID:93171821; PMID:8436911
A:Accession: PH1479
A:Molecule type: mRNA
A:Residues: 1-13 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Keywords: receptor; T-cell

Query Match 38.2%; Score 26; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 YEKYIG 6
||:|
Db 8 YEQYFG 13

RESULT 4
PH0108
late G1-69 protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH0108
R:Nikaido, T.; Bradley, D.W.; Pardee, A.B.
Exp. Cell Res. 192, 102-109, 1991
A:Title: Molecular cloning of transcripts that accumulate during the late G1 phase in cu
A:Reference number: PH0108; MUID:91078351; PMID:1984406
A:Accession: PH0108
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-9 <NTK>

Query Match 33.8%; Score 23; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GEY 9
|||
Db 6 GEY 9

RESULT 5
S25056
Ig heavy chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 20-Jun-2000
C:Accession: S25056
R:Jacob, J.; Kelsce, G.
submitted to the EMBL Data Library, July 1992
A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitropheny
A:Reference number: S25024
A:Accession: S25056
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-12 <TAC>
A:Cross-references: EMBL:X67386; NID:G50927; PIDN:CAA47798.1; PID:G1333920
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; Immunoglobulin

Query Match 33.8%; Score 23; DB 2; Length 12;
Best Local Similarity 44.4%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 YEKYIGREY 9
||:|
Db 3 YPYTYGSSY 11

RESULT 6
PT0215
T-cell receptor beta chain V-J region (4-1-K.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C:Accession: PT0215
R:Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restric
A:Reference number: PT0209; MUID:91217621; PMID:1902501
A:Accession: PT0215
A:Molecule type: mRNA
A:Residues: 1-10 <NAK>
C:Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEKY 4
||:|
Db 6 YEQY 9

RESULT 7
PT0214
T-cell receptor beta chain V-J region (4-1-L.6) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C:Accession: PT0214
R:Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restric
A:Reference number: PT0209; MUID:91217621; PMID:1902501
A:Accession: PT0214
A:Molecule type: mRNA
A:Residues: 1-11 <NAK>
C:Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEKY 4
||:|
Db 7 YEQY 10

RESULT 8
S47359
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47359
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
A:Reference number: S47355
A:Accession: S47359
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35683; NID:G527455; PIDN:CAA84752.1; PID:G527456
C:Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKY 4
||:|
Db 9 YEQY 12

RESULT 9
S47361
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47361
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47361
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:235685; NID:g527459; PIDN:CAA84754.1; PID:g527460
C:Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKY 4
||:|
Db 9 YEQY 12

RESULT 10
S47365
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47365; S47375; S47379; S47396; S47397; S47398; S47355
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47365
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:235690; NID:g527471; PIDN:CAA84759.1; PID:g527472; EMBL:235679;
A:Accession: S47375
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE2>
A:Cross-references: EMBL:235700; NID:g527493; PIDN:CAA84769.1; PID:g527494
A:Accession: S47379
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE3>
A:Cross-references: EMBL:235708; NID:g527509; PIDN:CAA84777.1; PID:g527510
A:Accession: S47396
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE4>
A:Cross-references: EMBL:235674; NID:g527527; PIDN:CAA84743.1; PID:g527528
A:Accession: S47397
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE5>
A:Cross-references: EMBL:235675; NID:g527529; PIDN:CAA84744.1; PID:g527530
A:Accession: S47398
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE6>
A:Cross-references: EMBL:235676; NID:g527531; PIDN:CAA84745.1; PID:g527532
C:Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKY 4
||:|
Db 9 YEQY 12

RESULT 11
S47368
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47368
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47368
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:235693; NID:g527477; PIDN:CAA84762.1; PID:g527478
C:Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKY 4
||:|
Db 9 YEQY 12

RESULT 12
S47372
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47372
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47372
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:235697; NID:g527485; PIDN:CAA84766.1; PID:g527486
C:Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKY 4
||:|
Db 9 YEQY 12

RESULT 13
S47383
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47383
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47383

Job time : 38 secs

A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35709, NID:G527513, PIDN:CAA84778.1, PID:G527514
C:Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEXY 4
||:|
Db 9 YEOY 12

RESULT 14

S47384
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47384
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994

A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
A:Reference number: S47355
A:Accession: S47384
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35704, NID:G527501, PIDN:CAA84773.1, PID:G527502
C:Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEXY 4
||:|
Db 9 YEOY 12

RESULT 15

S47374
T-cell antigen receptor VJ junction beta chain - human (fragment)

C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 25-Oct-1996 #text_change 05-Nov-1999
C:Accession: S47374, S47399, S47364
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994

A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
A:Reference number: S47355
A:Accession: S47374
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35699, NID:G527491, PIDN:CAA84768.1, PID:G527492, EMBL:Z35689;
A:Accession: S47399
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35677, NID:G527533, PIDN:CAA84746.1, PID:G527534
C:Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEXY 4
||:|
Db 9 YEOY 12

Search completed: November 1, 2005, 14:32:40

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 14:20:48 ; Search time 172 Seconds
(without alignment)

38.704 Million cell updates/sec

Title: US-10-612-162a-4

Sequence: 1 YEKYLGESEYKAV 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 4955

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*

1: uniprot_prot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	41.2	10	2 Q7WUG1	Q7WUG1 pseudomonas
2	26	38.2	12	1 S015_BACSU	P80863 bacillus su
3	23	33.8	13	2 Q50038	Q50038 mycobacteri
4	22	32.4	8	2 Q6BCE29	Q6BCE29 homo sapien
5	22	32.4	8	2 Q902V5	Q902V5 fulica leuc
6	21	30.9	10	2 Q6RTV4	Q6RTV4 carlia leuc
7	21	30.9	11	2 Q6RT302	Q6RT302 chlamydomon
8	21	30.9	11	2 Q6BLE0	Q6BLE0 pyriglena 1
9	21	30.9	11	2 Q6BLE9	Q6BLE9 myrmotherul
10	21	30.9	13	1 TEML_RANTE	P57104 rana tempor
11	20	29.4	12	2 Q9N2B8	Q9N2B8 pongo pygma
12	20	29.4	12	2 Q9N2B9	Q9N2B9 gorilla gor
13	20	29.4	12	2 Q9N2C0	Q9N2C0 pan troglod
14	20	29.4	12	2 Q7T862	Q7T862 largemouth
15	20	29.4	13	2 Q6S4R5	Q6S4R5 leishmania
16	19	27.9	9	1 NC34_STRAT	P83222 streptomyc
17	19	27.9	9	2 Q7RBS8	Q7RBS8 plasmodium
18	19	27.9	11	2 Q6QVDB	Q6QVDB phaseolus v
19	19	27.9	11	2 Q84073	Q84073 influenza a
20	19	27.9	12	1 UKA2_HUMAN	P31144 homo sapien
21	19	27.9	12	2 Q9XNR6	Q9XNR6 pyralisella 1
22	19	27.9	12	2 Q50959	Q50959 neisseria g
23	19	27.9	13	2 Q93824	Q93824 candida tro
24	19	27.9	13	2 Q86129	Q86129 vesicular s
25	18	26.5	7	2 Q8K3H6	Q8K3H6 rattus norv
26	18	26.5	10	1 SPI_HAIRO	Q10997 halocynthia
27	18	26.5	10	1 TKNI_SCYCA	P08608 scyllorhinu
28	18	26.5	10	2 Q7M500	Q7M500 aspergillus
29	18	26.5	10	2 Q51812	Q51812 plasmid f.
30	18	26.5	11	1 ASL1_BACSE	P83146 bacteroides
31	18	26.5	11	2 Q703F4	Q703F4 mus acumin

32	18	26.5	12	2 Q6DKZ0	Q6DKZ0 homo sapien
33	18	26.5	12	2 Q9T2U3	Q9T2U3 bos taurus
34	18	26.5	12	2 Q945C3	Q945C3 cryptosporidi
35	18	26.5	12	2 Q83U71	Q83U71 salmoneilla
36	18	26.5	12	2 Q9R3B3	Q9R3B3 helicobacte
37	18	26.5	12	2 Q61331	Q61331 mus muscule
38	18	26.5	12	2 Q61D52	Q61D52 mus sp. cyc
39	18	26.5	13	2 Q7M2Z6	Q7M2Z6 ovis aries
40	18	26.5	13	2 Q9TU76	Q9TU76 ovis aries
41	18	26.5	13	2 Q86260	Q86260 klebsiella
42	18	26.5	13	2 Q9RSN5	Q9RSN5 clostridium
43	17	25.0	9	2 Q61DB5	Q61DB5 homo sapien
44	17	25.0	9	2 Q8MPT4	Q8MPT4 diadema ant
45	17	25.0	9	2 Q70T12	Q70T12 staphylococ

ALIGNMENTS

RESULT 1	Q7WUG1	PRELIMINARY;	PRT;	10 AA.
AC	Q7WUG1			
DT	01-OCT-2003 (TREMBLrel. 25, Created)			
DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)			
DE	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Probable ATP-binding component of ABC transporter (fragment).			
OS	Pseudomonas fluorescens.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;			
OC	Pseudomonadaceae; Pseudomonas.			
OX	NCBI_Taxid=294;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CHAO;			
RA	Pechy-Tarr M., Bottiglieri M., Bang Lejbolle K., Gigot-Bonnefoy C.,			
RA	Keel C.;			
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY341911; AA017034.1; -			
DR	GO; GO:0005524; F:ATP binding; IEA.			
KW	ATP-binding.			
FT	NON TER			
SO	SEQUENCE	10 AA;	1262 MW;	Q8EP18CB1E8773B CRC64;
Query Match		41.2%;	Score 28;	DB 2;
Best Local Similarity		62.5%;	Pred. No. 1.3e+03;	Length 10;
Matches	5;	Conservative	1;	Mismatches 2;
				Indels 0;
				Gaps 0;
QY	2 EKYLGEEY 9			
DB	1 EYVLGHEP 8			
RESULT 2	S015_BACSU	STANDARD;	PRT;	12 AA.
ID	S015_BACSU			
AC	P80863;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Superoxide-inducible protein 5 (S015) (Fragment).			
OS	Bacillus subtilis.			
OC	Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.			
OX	NCBI_Taxid=1423;			
RN	[1]			
RP	SEQUENCE.			
RC	STRAIN=168 / ISS8;			
RX	MEDLINE=97443988; PubMed=9298659;			
RA	Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U., Hecker M.;			
RT	"First steps from a two-dimensional protein index towards a response-			
RT	regulation map for Bacillus subtilis.";			
RL	Electrophoresis 18:1451-1463 (1997).			
CC	-I- INDUCTION: By superoxide.			
CC	-I- CAUTION: Could not be found in the genome of B. subtilis 168.			

KW Direct protein sequencing.
 FT NON TER 12 12
 SQ SEQUENCE 12 AA; 1170 MW; 25718A96B37B1338 CRC64;

Query Match 38.2%; Score 26; DB 1; Length 12;
 Best Local Similarity 55.6%; Pred. No. 3.2e+03;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 5 LGEEYVKAV 13
 |||:|:|:
 DB 4 LGKEGLKAI 12

RESULT 3

OS0038 PRELIMINARY; PRT; 13 AA.

AC OS0038; 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)
 DE U22661.
 OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Smith D.R.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Robison K.;
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U15182; AAA62970.1; -
 SQ SEQUENCE 13 AA; 1589 MW; C7CCD7E47D025B06 CRC64;

Query Match 33.8%; Score 23; DB 2; Length 13;
 Best Local Similarity 57.1%; Pred. No. 1e+04;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 EKYLGEE 8
 :|||:
 DB 6 QEYLGEV 12

RESULT 4

OS06CZ9 PRELIMINARY; PRT; 8 AA.

AC OS06CZ9; 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Protein S (Fragment).
 GN Name=PROS1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Primates; Carnivora; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hamabaki N.;
 RL "Protein S variant in Exon3."
 DR EMBL; AB162156; BAD36740.1; -
 FT NON TER 1 1
 SQ SEQUENCE 8 AA; 1108 MW; D33B53277B59DB5A CRC64;

Query Match 32.4%; Score 22; DB 2; Length 8;
 Best Local Similarity 80.0%; Pred. No. 1.6e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YEKYL 5

DB 4 YPKYL 8
 |||:
 |||:

RESULT 5

OS02V5 PRELIMINARY; PRT; 8 AA.

AC OS02V5; 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Adenylate kinase (Fragment).
 OS Fulica leucopetra.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Griformes; Rallidae; Fulica.
 OX NCBI_TaxID=16758;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shapiro L.H.; Dumbacher J.P.;
 RL "Adenylate kinase intron 5: a new nuclear locus for avian systematics."
 DR Auk 118:248-255(2001).
 DR EMBL; AF307898; AAK43537.1; -
 DR GO; GO:0016301; F:kinase activity; IEA.
 KW Kinase.
 FT NON TER 1 1
 SQ SEQUENCE 8 AA; 994 MW; 96333B19CB1B1866 CRC64;

Query Match 32.4%; Score 22; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 GEEYVK 11
 |||:|:
 DB 2 GEEFEK 7

Query Match 32.4%; Score 22; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 EKYLGEE 8
 :|||:
 DB 6 QEYLGEV 12

RESULT 6

OS06R7V4 PRELIMINARY; PRT; 10 AA.

AC OS06R7V4; 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
 GN Name=GAPDH;
 OS Carlia zuma.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Scincomorpha; Scincoidae;
 OC Scincidae; Carlia.
 OX NCBI_TaxID=260893;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Doiwan G.; Phillips B.;
 RL "Single copy nuclear DNA markers characterized for comparative phylogeography in Australian wet tropics rainforest skinks."
 DR Mol. Ecol. Notes 4:185-187(2004).
 DR EMBL; AY508912; AAS09890.1; -
 FT NON TER 1 1
 SQ SEQUENCE 10 AA; 1171 MW; 9D0AB2322C9C1EA CRC64;

Query Match 30.9%; Score 21; DB 2; Length 10;
 Best Local Similarity 44.4%; Pred. No. 1.7e+04;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 5 LGEEYVKAV 13
 |||:|:|:
 DB 1 LNDHFVKLV 9

RESULT 7

06T302
ID 06T302; PRELIMINARY; PRT; 11 AA.
AC 06T302;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DE 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
GN Name=COX2B;
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
ON NCBI_TaxID=3055;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CC-2290.
RX MEDLINE=22570934; PubMed=12684385; DOI=10.1128/EC.2.2.362-379.2003;
RA Kathir P., Lavie M., Brzelton W.D., Haas N.A., Lefebvre P.A.,
RA Silflow C.D.;
RT "Molecular map of the Chlamydomonas reinhardtii nuclear genome."
RL Eukaryotic Cell 2:362-379(2003).
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1414 MW; 74EA69AD3322DB5B CRC64;

Query Match 30.9%; Score 21; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EYVK 11
| | | |
| | | |
Db 4 EYVK 7

RESULT 8
ID 068LE0 PRELIMINARY; PRT; 11 AA.
AC 068LE0;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DE 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
GN Name=NADPH;
OS Pyriglena leuconota.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Formicariidae;
OC Pyriglena.
ON NCBI_TaxID=183187;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15283860;
RA Irestedt M., Fjeldsa J., Nylander J.A., Ericson P.G.;
RT "Phylogenetic relationships of typical antbirds (Thamophilidae) and
test of incongruence based on Bayes factors."
RL BMC Evol. Biol. 4:23-23(2004).
DR EMBL; AY677056; AAT96981.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1242 MW; 9D0AEB2622C9C1EA CRC64;

Query Match 30.9%; Score 21; DB 2; Length 11;
Best Local Similarity 44.4%; Pred. No. 1.9e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 LGEYVKAV 13
| : | | |
| : | | |
Db 2 LNDHFVKLV 10

RESULT 9
ID 068LE9 PRELIMINARY; PRT; 11 AA.
AC 068LE9;

DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
GN Name=NADPH;
OS Myrmotherula fulviventris.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Thamophilidae;
OC Myrmotherula.
ON NCBI_TaxID=288045;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15283860;
RA Irestedt M., Fjeldsa J., Nylander J.A., Ericson P.G.;
RT "Phylogenetic relationships of typical antbirds (Thamophilidae) and
test of incongruence based on Bayes factors."
RL BMC Evol. Biol. 4:23-23(2004).
DR EMBL; AY677047; AAT96972.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1242 MW; 9D0AEB2622C9C1EA CRC64;

Query Match 30.9%; Score 21; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.2e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 LGEYVKAV 13
| : | | |
| : | | |
Db 2 LNDHFVKLV 10

RESULT 10
ID TEML_RANTE STANDARD; PRT; 13 AA.
AC P57104;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tempurin L.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
ON NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RX TISSUE=Skin secretion;
RC MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Tempurin, antimicrobial peptides from the European red frog Rana
temporaria."
RL Eur. J. Biochem. 242:788-792(1996).
CC -1- FUNCTION: Has antibacterial activity against Gram-negative and
CC Gram-positive bacteria.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the frog skin active peptide (PSAP) family.
KW Brevinin subfamily.
KW Amidation; Amphibian defense peptide; Antibiotic;
KW Direct protein sequencing.
FT MOD_RES 13
FT MOD_RES 13
SQ SEQUENCE 13 AA; 1641 MW; 9EBDCB1FAFF7C325 CRC64;

Query Match 30.9%; Score 21; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.2e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VEKVLG 6
| : | | |
| : | | |
Db 5 FSKFLG 10

RESULT 11

Q9N2B8
ID Q9N2B8 PRELIMINARY; PRT; 12 AA.
AC Q9N2B8;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Indolethylamine N-methyltransferase (Fragment).
GN Name=INMT;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Kitano T., Kobayakawa H., Saitou N.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB041365; BAA94454.1; -;
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Methyltransferase; Transferase.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1290 MW; CF079554917861A9 CRC64;

Query Match 29.4%; Score 20; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.9e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 GEEY 9
|:|:
Db 8 GDEY 11

RESULT 12
Q9N2B9
ID Q9N2B9 PRELIMINARY; PRT; 12 AA.
AC Q9N2B9;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Indolethylamine N-methyltransferase (Fragment).
GN Name=INMT;
OS Gorilla gorilla (Gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RA Kitano T., Kobayakawa H., Saitou N.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB041364; BAA94453.1; -;
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Methyltransferase; Transferase.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1289 MW; CF0798E2917861A9 CRC64;

Query Match 29.4%; Score 20; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.9e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 GEEY 9
|:|:
Db 8 GDEY 11

RESULT 13
Q9N2C0
ID Q9N2C0 PRELIMINARY; PRT; 12 AA.
AC Q9N2C0;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Indolethylamine N-methyltransferase (Fragment).

GN Name=INMT;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kitano T., Kobayakawa H., Saitou N.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB041363; BAA94452.1; -;
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Methyltransferase; Transferase.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1289 MW; CF0798E2917861A9 CRC64;

Query Match 29.4%; Score 20; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.9e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 GEEY 9
|:|:
Db 8 GDEY 11

RESULT 14
Q7T862
ID Q7T862 PRELIMINARY; PRT; 12 AA.
AC Q7T862;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE NTPase I (Fragment).
OS Largemouth bass ranavirus.
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Ranavirus.
OX NCBI_TaxID=79956;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IMBvscg;
RX MEDLINE=22768205; PubMed=12885900;
RA DOI=10.1128/JVI.77.16.8812-8818.2003;
RA Goldberg T.L., Coleman D.A., Grant E.C., Irendino K.R., Philipp D.P.;
RT "Strain variation in an emerging iridovirus of warm-water fishes.";
RL J. Virol. 77:8812-8818(2003).
DR EMBL; AY208993; AAP57096.1; -;
FT NON TER 1 1
SQ SEQUENCE 12 AA; 1357 MW; 108D85D5F25B73B CRC64;

Query Match 29.4%; Score 20; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.9e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 EKYLGEEY 9
|:|:
Db 3 EAYLSKLY 10

RESULT 15
Q6S4R5
ID Q6S4R5 PRELIMINARY; PRT; 13 AA.
AC Q6S4R5;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Alpha tubulin (Fragment).
OS Leishmania chagasi.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=44271;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MHOM/BR/00/1669;
RA Purdy J.E., Wilson M.E.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY466450; AAR88132.1; -.
 FT NON TER 1 1
 SQ SEQUENCE 13 AA; 148 MW; 3F361B0689741B18 CRC64;
 Query Match 29.4%; Score 20; DB 2; Length 13;
 Best Local Similarity 57.1%; Pred. No. 3.1e+04;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 5 LGGEYVK 11
 : ||| | :
 Db 5 MGSEDDVE 11

Search completed: November 1, 2005, 14:32:02
 Job time : 183 secs

THIS PAGE BLANK (USPTO)